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OM protein - protein search, using sw model

Run on: December 6, 2002, 13:19:54 ; Search time 26 Seconds

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 908470 seqs, 135250520 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A. Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: *
 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: *
 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT: *
 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT: *
 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: *
 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: *
 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: *
 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT: *
 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT: *
 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: *
 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT: *
 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: *
 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT: *
 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT: *
 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: *
 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: *
 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: *
 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: *
 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: *
 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	20	100.0	4	5	AAW40460 N-terminal polyhyd
2	20	100.0	4	13	AAW2056 Chromogenic substr
3	20	100.0	4	13	AAW26241 Alpha-keto peptide
4	20	100.0	4	15	AAW46222 Serine protease in
5	20	100.0	4	18	AAW52600 Serine protease-in
6	20	100.0	4	18	AAW52609 Cathepsin G inhibi
7	20	100.0	4	18	Cathepsin G inhibitor
8	20	100.0	4	18	AAW26078 Substrate #1 for s
9	20	100.0	4	19	AAW51453 Indicator for de
10	20	100.0	4	19	AAW51459 Indicator for dete

RESULT	1
ID	AAW40460
ID	AAW40460 standard; Protein: 4 AA.
AC	AAW40460;
DT	27-NOV-1991 (first entry)
XX	DE N-terminal polyhydroxyalkanoyl peptide.
XX	KW Polyhydroxyalkanoyl peptide; protease; peptidase; prodrug.
XX	PN ER126685-A.
XX	PD 28-NOV-1985.
XX	PF 15-MAY-1984; 84EP-0400984.
PR	16-MAY-1983; 83FR-0308051.
PA	(CNRS) CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE.
XX	PT Monsigny M., Mayer R;
XX	DR 1984-29665/48.
XX	PT N-terminal polyhydroxyalkanoyl peptide and aminoacid derivs. - opt.
PT	having C-terminal active groups, e.g. chloroquine, are water-soluble
PT	anticancer or antiparasitic cplds. and protease targets.
PS	Claim 11; page 15; 20pp; french.
XX	The peptide is polyhydroxyalkanoyl-L-Ala-L-Ala-L-Pro-L-Met-X. X is

CC R2-NH- derived from an aromatic amine, eg P-nitro-aniline, alpha-
 CC or beta-naphthylamine, or it is R3NH derived from an amino drug, eg
 CC daunorubicin or chloroquine, or it is a gp. which may confer
 CC activity, eh H, OH, CH2Cl. When X is the residue of a drug, the
 CC cpd. is a product in which the peptide is the substrate for a
 CC specific protease secreted by the target cell for the active drug,
 CC eg tumour cells or microorganism pathogens, eg plasmodium
 CC falciparum. Due to the polyhydroxy gp, the cpds. are very soluble
 CC in water or buffer soln. and are able to be used at high concn. The
 CC cpds. also allow the detection of proteases and peptidases and
 CC allow easy determination of the best substrate for a particular
 CC protease.
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 Db 1 AAPM 4

	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	4	100.0%	20	4	0	0
Best Local Similarity	100.0%	Pred. No.	7.8e+05	Mismatches	0	0
Matches	4	Conservative	0	Mismatches	0	0
Indels	0	Indels	0	Gaps	0	0

RESULT 2
 ARR22056
 ID AAR22056 standard; Peptide; 4 AA.
 XX

AC AAR22056;
 XX
 DT 06-JUL-1992 (first entry)

DE Alpha-keto peptide protease inhibitors.

KW serine protease inhibitor; cysteine protease inhibitor; chymase;
 KW chymotrypsin; elastase; trypsin; blood coagulation enzyme;
 KW antiinflammatory; anticoagulant; neuroprotectant; emphysema; ARDS;
 KW metastases; bone resorption.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acylation by MeoSuc"

FT Modified-site 4 /note= "C-terminal modification by PNA

FT /note= "(para nitro amide)"

FT WO9203542-A.

FT PD 23-JUL-1992.

XX PF 27-DEC-1991; 91WO-US99801.

XX PR 28-DEC-1990; 90US-0635287.

XX PA (GEOR-) GEORGIA TECH RES CORP.

XX Powers JC;

XX DR WPI: 1992-268589/32.

XX PT New alpha-keto:amide, alpha-keto:acid and alpha-keto:ester

PT derivs. - inhibit serine and cysteine protease(s) and are used
 PT for treating and preventing inflammation, emphysema, adult
 PT respiratory distress syndrome, etc.

XX PS Disclosure; Page 31; 88pp; English.

XX PT Abraham CR;

XX DR WPI: 1992-096886/72.

PT Treatment and diagnosis of Alzheimer's disease - by reducing
 PT beta-protein precursor proteolysis near beta-protein N-terminus
 PT by administering proteolysis inhibitor

XX Disclosure; Page 10; 29pp; English.

CC The chromogenic peptide was used to assay the activity of purified
 CC cysteine protease from Alzheimer's disease patients. The protease
 CC was incubated with the chromogenic substrate and changes in
 CC absorbance followed at 410 nm in a tittertek Multiskan ELISA reader.
 See also AAR22054, 5.

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 13; Length 4;

Qy 1 AAPM 4
 Db 1 AAPM 4

RESULT 3
 ARR26241
 ID AAR26241 standard; peptide; 4 AA.
 XX AC AAR26241;

XX DT 27-JAN-1993 (first entry)

DE Alpha-keto peptide protease inhibitors.

KW serine protease inhibitor; cysteine protease inhibitor; chymase;
 KW chymotrypsin; elastase; trypsin; blood coagulation enzyme;
 KW antiinflammatory; anticoagulant; neuroprotectant; emphysema; ARDS;
 KW metastases; bone resorption.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "MeO-Suc Ala"

FT Modified-site 4 /note= "Met-COO_R, where R denotes residue of a
 keto-acid (OH), keto-amide (NH₂) or keto-ester"

FT FT WO9212140-A.

XX PD 23-JUL-1992.

XX PF 27-DEC-1991; 91WO-US99801.

XX PR 28-DEC-1990; 90US-0635287.

XX PA (GEOR-) GEORGIA TECH RES CORP.

XX Powers JC;

XX DR WPI: 1992-268589/32.

XX PT New alpha-keto:amide, alpha-keto:acid and alpha-keto:ester

PT derivs. - inhibit serine and cysteine protease(s) and are used
 PT for treating and preventing inflammation, emphysema, adult
 PT respiratory distress syndrome, etc.

XX PS Disclosure; Page 31; 88pp; English.

XX PT Abraham CR;

XX DR WPI: 1992-096886/72.

PT Treatment and diagnosis of Alzheimer's disease - by reducing
 PT beta-protein precursor proteolysis near beta-protein N-terminus
 PT by administering proteolysis inhibitor

XX Disclosure; Page 10; 29pp; English.

CC The chromogenic peptide was used to assay the activity of purified
 CC cysteine protease from Alzheimer's disease patients. The protease
 CC was incubated with the chromogenic substrate and changes in
 CC absorbance followed at 410 nm in a tittertek Multiskan ELISA reader.
 See also AAR22054, 5.

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 13; Length 4;

Qy 1 AAPM 4
 Db 1 AAPM 4

QY 1 AAPM 4 KW Selective; serine protease inhibitor; trypsin; elastase; chymotrypsin;
 |||| antinflammatory; anticoagulant; antitumour; cathepsin G.
 Db 1 AAPM 4 XX
 XX
RESULT 4
 AAR46222 ID AAR46222 standard; peptide; 4 AA.
 XX
 AC AAR46222;
 XX
 DT 04-AUG-1994 (first entry)
 XX DE Serine protease inhibitor tetrapeptide.
 XX KW Prevention; schistosomiasis; parasite; infection; prevention;
 KW parasitic penetration; skin; cercariae; anti-penetrant.
 OS OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT Modified-site 1 /note= "BG(peptide blocking gp.) attached"
 FT /note= "PI(protease inhibitor)", other than
 FT Modified-site 4 /note= "PI(protease inhibitor)", other than
 FT chloromethyl ketone, attached"
 FT
 XX PN US5686419-A.
 XX PD 11-NOV-1997.
 XX PR 21-JAN-1994; 94US-0184286.
 XX PR 21-JAN-1994; 94US-0184286.
 PA (GEOR-) GEORGIA TECH RES CORP.
 XX PI Boduszek B., Olekyszyn J., Powers JC;
 XX DR WPI; 1997-558177/51.
 XX PS Example 7; column 20; 16pp; English.
 XX
 CC The patent discloses new peptidyl derivatives of diesters of alpha-
 CC aminoalkylphosphonic acids having basic substituents, of formula
 CC X-A(A4)-AA3-AA2-NH-(CHR-P(=O)(OZ))OZ1, in which: R = B-substituted
 CC phenyl; B = substituted benzyl or amino; Z and Z1 = 1-6C perfluoralkyl or
 CC quanidino, isothioureido or amino; Z and Z1 = 1-6C alkyl; B = amidino,
 CC optionally substituted phenyl; AA2 = an L- or D-amino acid residue;
 CC AA3 = a single bond or an L- or D-amino acid residue; AA4 = a single
 CC bond or an L- or D-amino acid residue; X = H, NH2CO, NH2CS, NH2SO2,
 CC YNHCO, YNHCS, YNHSO2, YCS, YSO2, COO, YCO; Y = optionally
 CC substituted 1-6C alkyl, 1-6C fluoralkyl, 9-fluoromethylphenyl,
 CC naphthyl, or 1-6C alkyl with 1-2, optionally substituted, attached,
 CC phenyl groups. The new compounds are inhibitors of trypsin, elastase,
 CC chymotrypsin and other serine proteases; and their inhibitory activity
 CC is selective, depending on the identity of the alpha-aminoalkylphosphonic
 CC acid ester residue. They can be used as antinflammatory agents
 CC and anticoagulants and antitumour agents. The present sequence is an
 CC example of a compound which can specifically inhibit the activity of
 CC cathepsin G.
 XX SQ Sequence 4 AA:
 Query Match 100.0%; Score 20; DB 15; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 ||||
 Db 1 AAPM 4
 XX
RESULT 5
 AAW52600 ID AAW52600 standard; peptide; 4 AA.
 XX
 AC AAW52600;
 XX
 DT 22-JUN-1998 (first entry)
 XX DE Serine protease-inhibiting peptide with C-terminal phosphonate residue.
 XX
 Query Match 100.0%; Score 20; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 ||||
 Db 1 AAPM 4
 XX
RESULT 6
 AAW52609 ID AAW52609 standard; peptide; 4 AA.
 XX
 AC AAW52609;
 XX
 DT 22-JUN-1998 (first entry)

XX	DE	23-FEB-1998	(first entry)		
XX	DE	Cathepsin G inhibitor peptide ketoamide derivative.			
KW	XX	Peptide ketoamide derivative; protease inhibitor; elastase inhibitor;			
ant-inflammatory; anticoagulant; antitumour.	KW	serine protease; cathepsin G; neurodegenerative disease;			
OS	XX	Alzheimer's disease; coagulation disorder; serine protease;			
Synthetic.	XX	cysteine protease; calpain; cathepsin G; thymase inhibitor;			
XX	KW	ischaemia; stroke; trypsin inhibitor; thrombosis; blistering; anticoagulant.			
XX	KW	tissue damage; thrombosis; blistering; anticoagulant.			
FT	OS	Synthetic.			
Key	XX	Serine protease-inhibiting peptide with C-terminal phosphonate residue.			
Modified-site	FT	Location/Qualifiers			
1	/note= "MeO-Suc-Ala"				
FT	FT	4	/note= "Met(O)(P)(Oph)2; where Met(O)(P) represents a methionine sulphoxide analogue in which the carboxyl group -COOH has been replaced by a phosphonate group -P(=O)(OH)(OH); and (Oph)2 indicates that the phosphonate has been diphenyl esterified"		
FT	FT	PN	US5686419-A.		
FT	FT	XX	XX	PD 11-NOV-1997.	
FT	FT	XX	XX	PD 21-JAN-1994; 94US-0184286.	
FT	FT	XX	XX	PR 21-JAN-1994; 94US-0184286.	
FT	FT	XX	XX	PA (GBCR-) GEORGIA TECH RES CORP.	
FT	FT	XX	XX	PI Boduszek B, Oleksyszyn J, Powers JC;	
FT	FT	XX	XX	DR WP1, 1997-558177/51.	
PS	PS	XX	New Peptidyl derivatives of alpha-aminoalkyl phosphonic acid di:ester - are serine protease inhibitors, useful e.g. for reducing blood coagulation, controlling tumour invasion or treating inflammation		
CC	PT	XX	The patent discloses new peptidyl derivatives of diesters of alpha-aminoalkylphosphonic acids having basic substituents, of formula X-AA3-(AA3-NH-CHR-P(=O)(OZ)-OZ), in which: R = B-substituted phenyl, B-substituted benzyl or B-substituted 1-6C alkyl; B = amidino, guanidino, isothiourea or amino; Z and Z1 = 1-6C perfluoroalkyl or optionally substituted phenyl; AA2 = an L- or D-amino acid residue; AA3 = a single bond or an L- or D-amino acid residue; AA4 = a single bond or an L- or D-amino acid residue; X = H, NH2CO, NH2CS, NH2SO2, YNHC, YNHCS, YNH2SO2, YSO2, YCO, YOCS or YCO; Y = optionally substituted 1-6C alkyl, 1-6C fluoroalkyl, 9-fluorenylmethyl, phenyl, naphthyl, or 1-6C alkyl with 1-2, optionally substituted, attached phenyl groups. The new compounds are inhibitors of trypsin, elastase, chymotrypsin and other serine proteases; and their inhibitory activity is selective depending on the identity of the alpha-aminoalkylphosphonic acid ester residue. They can be used as antiinflammatory agents, specific example of the new compounds.		
CC	PT	XX	Disclosure; Column 11; 16pp; English.		
CC	PT	XX	11-MAR-1997.		
CC	PT	XX	06-OCT-1995; 95US-0815073.		
CC	PT	XX	PR 27-DEC-1991; 91US-0815073.		
CC	PT	XX	PR 09-SEP-1993; 93US-0118997.		
CC	PT	XX	PR 20-MAY-1994; 94US-0247081.		
CC	PT	XX	(GEOR-) GEORGIA TECH RES CORP.		
CC	PT	XX	PI Powers JC;		
CC	PT	XX	DR WP1; 1997-178454/16.		
CC	PT	XX	New peptide keto:amide derivs - are protease inhibitors used to treat e.g. Alzheimer's disease, coagulation disorders and other neurodegenerative disorders.		
CC	PT	XX	Disclosure; Columns 17-18; 17pp; English.		
CC	CC	CC	The present sequence represents a peptide ketoamide derivative which is useful for selectively inhibiting cathepsin G. It is a specific example of a new class of peptides which selectively inhibit serine proteases or cysteine proteases, including calpains and cathepsin B. The calpain inhibitors are useful for treatment of various neurodegenerative diseases and conditions including ischemia, stroke and Alzheimer's disease. The protease inhibitors, especially the elastase, trypsin and cathepsin G, are used to control tissue damage and various inflammatory conditions mediated by proteases, such as blistering. They are also useful as anticoagulants and can be used to treat thrombosis. The peptides may also be used to identify new proteolytic enzymes encountered in research. Further, they may also be useful in research and industrially to prevent undesired proteolysis that occurs during the production, isolation, purification, transport and storage of valuable peptides and proteins; e.g. they may be added to antibodies, enzymes, plasma proteins, tissue extracts or other proteins and peptides which are widely sold for use in clinical analyses, biomedical research and for many other reasons.		
SQ	Sequence	4 AA;			
Query Match	100.0%	Score 20; DB 18; Length 4;			
Best Local Similarity	100.0%	Pred. No. 7.8e+05;			
Matches	4;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 AAPM 4				
DB	1 AAPM 4				
RESULT	7				
ID	AAW29407	standard; peptide; 4 AA.			
AC	AAW29407;				

Query Match 100.0%; Score 20; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AAPM 4	Db	1 AAPM 4
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RESULT 8
 ID AAW26078 standard; peptide: 4 AA.
 AC AAW26078;
 XX
 DT 05-NOV-1997 (first entry)
 XX
 DE Substrate #1 for serine protease.
 KW Serine protease; substrate; Streptomyces griseus; guanidine; pre-soak; cleaning composition; laundry detergent; additive composition; enzyme; dishwasher detergent; drain opener; urea; contact lens cleanser; proteinaceous stain.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 /note= "succinylated"
 FT Modified-site 4
 /note= "para-nitroanilidated"
 XX
 PN US5646028-A.
 XX
 PD 08-JUL-1997.
 XX
 PR 18-JUN-1991; 91US-0718303.
 XX
 PR 18-JUN-1991; 91US-0718303.
 PR 06-NOV-1992; 92US-0973343.
 PR 18-AUG-1994; 94US-0292924.
 PR 17-OCT-1995; 95US-0544143.
 XX
 PA (CLORX) CLOROX CO.
 XX
 PT Leigh SD;
 XX
 DR WPI; 1997 362936/33.

XX Serine protease from Streptomyces griseus ARCC 55178 - with good stability in presence of urea or guanidine, useful in cleaning compositions, including laundry and dishwashing detergents

XX Example 1; Column 12; 16pp; English.

XX AAW26078-W26096 represent substrates for the serine protease of the invention. The serine protease recognises these sequences, but is specific for the sequence shown in AAW25567. The protease has the N-terminal and C-terminal sequences represented by AAW24565 and AAW24566 respectively. The serine protease was isolated from Streptomyces griseus variety alkaliphilus No. 33 (ARCC 55178). The protease has an apparent molecular weight of 19 kD (by reducing sodium dodecyl sulphate polyacrylamide gel electrophoresis), and improved stability against urea and guanidine. The protease is inhibited by phenylmethylsulphonyl fluoride. The serine protease is useful in liquid or granular cleaning compositions, specifically laundry detergents or additive compositions. It is also useful in automatic dish washer detergents, drain openers, contact lens cleaners etc. The protease has better activity against proteinaceous stains than known enzymes and unusually high stability in the presence of chaotropic agents.

XX Sequence 4 AA:

Query Match 100.0%; Score 20; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AAPM 4	Db	1 AAPM 4
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RESULT 9
 ID AAW51453 standard; peptide: 4 AA.
 AC AAW51453;
 XX
 DT 02-SEP-1998 (first entry)
 XX
 DE Indicator for detection of leukocyte esterase activity in urine.
 KW Urine; indicator; detection; leukocyte esterase; activity; white blood cell.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 /note= "Methoxysuccinyl-suc-Ala"
 FT Modified-site 4
 /note= "Met-nitroanilide"
 XX
 PN US5776780-A.
 XX
 PD 07-JUL-1998.
 XX
 PR 12-APR-1996; 96US-0631581.
 XX
 PR 12-APR-1996; 96US-0631581.
 PR 28-MAY-1993; 93US-0568956.
 PR 24-ARR-1995; 95US-0422929.
 PA (CHIM) CHIMERA RES & CHEM INC.
 XX
 PI Carter JM, Smith JV;
 XX
 DR WPI; 1998-39 8049734.
 XX
 PT Automated measurement of white blood cell esterase activity in urine
 PT - comprises adding reagent composition to the sample containing an indicator, placing sample in a analyser and comparing absorbance with a standard measurement
 XX
 PS Claim 11; Column 14; 8pp; English.

XX The invention relates to a method for the measurement of white blood cell esterase activity in urine. It comprises: (i) placing an aliquot of the urine in an automated analyser sampling cup; (ii) placing the cup in a sampling tray with the automated analyser, transferring the urine to a cuvette and injecting at least one reagent composition in an aqueous medium into the cuvette, where the reagent composition comprises a buffer to adjust the pH of the urine to 7-9, an activator and surfactant selected from benzalkonium chloride, 2,5-dimethylbenzenesulphonic acid and benzethonium chloride, and an indicator to determine leukocyte esterase activity in the urine; (iii) reading the aliquot of urine at specified intervals, in accordance with a preprogrammed code introduced into the automated analyser, at a preprogrammed monochromatically specified wavelength, to compare absorbance of the urine sample and reagent composition complex with that of a standard containing a known concentration of leukocyte esterase and determining the quantitative amount of leukocyte esterase in the patient's urine. The method provides a fully automated method for determining white blood cells in urine. The method is preferable to the old dipstick method as it reduces consumable material and labour costs. It also offers increased accuracy, sensitivity

CC and reduction of interference by substances which affected prior art tests. The present sequence represents a specifically claimed indicator.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 19; Length 4;
Matches 4; Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
AAW51449 standard; peptide; 4 AA.
Db 1 AAPM 4

RESULT 10
XX AC AAW51449;
DT 02-SEP-1998 (first entry)
DE Indicator for detection of leukocyte esterase activity in urine.
XX KW Urine; indicator; detection; leukocyte esterase; activity;
KW white blood cell.
OS Synthetic.

Key Location/Qualifiers
FT Modified-site I /note= "Methoxysuccinyl-suc-Ala"
FT Modified-site 4 /note= "Met-nitroanilide"

XX US5776780-A.
PD 07-JUL-1998.
XX PF 12-APR-1996; 96US-0631581.
XX PR 12-APR-1996; 96US-0331581.
PR 28-MAY-1993; 93US-0088956.
PR 24-APR-1995; 95US-0429292.
PA (CHIM-) CHIMERA RES & CHEM INC.
PI Carter JM, Smith JV;
XX DR WPI; 1998-398049/34.

Automated measurement of white blood cell esterase activity in urine - comprises adding reagent composition to the sample containing an indicator, placing sample in a analyser and comparing absorbance with a standard measurement

XX PS Claim 11; Column 14; 8pp; English.

The invention relates to a method for the measurement of white blood cell esterase activity in urine. It comprises: (i) placing an aliquot of the urine in an automated analyser sampling cup; (ii) placing the cup in a sampling tray with the automated analyser, transferring the urine to a cuvette and injecting at least one reagent composition in an aqueous medium into the cuvette, where the reagent composition comprises a buffer to adjust the pH of the urine to 7.9, an activator and surfactant selected from benzalkonium chloride, 2,5-dimethylbenzenesulphonic acid and benzethonium chloride, and an indicator to determine leukocyte esterase activity in the urine; (iii) reading the aliquot of urine at specified intervals, in accordance with a preprogrammed code introduced into the automated analyser, at a preprogrammed monochromatically specified wavelength, to compare absorbance of the urine sample and reagent composition complex with that of a standard containing a known concentration of leukocyte esterase and determining the quantitative

CC amount of leukocyte esterase in the patient's urine. The method provides a fully automated method for determining white blood cells in urine. The method is preferable to the old dipstick method as it reduces consumable material and labour costs. It also offers increased accuracy, sensitivity and reduction of interference by substances which affected prior art tests. The present sequence represents a specifically claimed indicator.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 19; Length 4;
Matches 4; Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
AAW51611 standard; peptide; 4 AA.
Db 1 AAPM 4

RESULT 11
XX AC AAW51611;
DE Peptide conjugated to lipid for use in liposomal drug delivery.
XX KW Liposome; conjugate; drug delivery; peptidase-secreting cell;
KW tumour; diagnosis; therapy.
XX OS Synthetic.

XX PN WO9816240-A1.
XX PD 23-APR-1998.
XX PF 15-OCT-1997; 97WO-US18538.
XX PR 15-OCT-1996; 96US-0027544.
XX PA (LIPO) LIPOSOME CO INC.
XX PI Ali S, Cabral Lilly D, Erukulla RK, Franklin JC;
PI Janoff AS, Meers PR, Pak C;
XX DR WPI; 1998-261025/23.

New peptide-lipid conjugates are incorporated into liposome(s) - to selectively destabilise the liposome(s) in the vicinity of target peptidase-secreting cells, e.g., tumour cells; useful in diagnosis and therapy

XX PS Claim 6; Page 33; 55pp; English.

The invention relates to peptide-lipid conjugates and their use in the preparation of liposomes which are predisposed to degradation in the presence of peptidase-secreting cells and hence are targeted to these cells. The liposomes can be used to treat mammalian diseases, disorders and conditions, e.g. tumours, microbial infections and inflammation. The liposomes allow selective delivery of an active agent to desired cells. The liposomes are stable when the peptide remains conjugated to the lipid. However, once the peptide portion of the conjugate is cleaved from the lipid, by the action of cell-secreted peptidases, the liposomes destabilise and release their contents in the vicinity of, or into, the secreting cells. The liposomes can thus be used to treat conditions characterised by the occurrence of peptidase-secreting cells. For example, the breast cancer cell line MCF-7 is known to secrete elastase, the levels of which are inversely correlated to overall survival in breast cancer patients. The present sequence represents a specifically claimed peptide which forms part of the peptide-lipid conjugate.

XX SQ Sequence 4 AA;

	Query Match	100.0%	Score	20;	DB	19;	Length	4;	Raw8244
	Best Local Similarity	100.0%	Pred.	No.	7.8e-05;	Mismatches	0;	Indels	0;
	Matches	4;	Conservative	0;	Mismatches	0;	Gaps	0;	ID Raw8244 standard; peptide: 4 AA.
y	1 AAPM 4								AC AAW8244;
b	1 AAPM 4								XX XX
									DT 24-FEB-1999 (first entry)
									DE Seq ID 13 from US5849560.
									KW Anyloid beta-protein precursor; endoprotease; human; brain; screening; pheophytin sulphonyl fluoride; protease inhibitor.
									XX XX
									XX KW Alzheimer's disease; O-pheanthroline; metal chelator; treatment; pheophytin sulphonyl fluoride; protease inhibitor.
									XX XX
									XX OS Unknown.
									XX US5849560-A.
									PN PA PD 15-DEC-1998.
									XX PF 26-FEB-1993; 93US-0025321.
									XX PR 26-FEB-1993; 93US-0025321.
									PR 17-AUG-1990; 90US-0568806.
									PR 05-APR-1991; 91US-0681093.
									XX PA (UYBO-) UNIV BOSTON.
									XX PI Abraham CR;
									DR WI; 1999-069739/06.
									XX PT Purified endoprotease associated with Alzheimer's disease - is prepared from fractions of brain tissue homogenate and is useful for drug screening.
									PT XX PS Disclosure: Column 23-24; 27PP; English.
									XX CC This invention related to the discovery of a human amyloid beta-protein precursor N-terminal domain which is cleaved by a purified endoprotease from human brain tissue homogenate. This endoprotease is identical to an endoprotease found in the brains of humans with Alzheimer's disease. The endoprotease is inhibited by O-pheanthroline and by metal chelators and is not inhibited by pheophytin sulphonyl fluoride. The endoprotease is useful to screen for protease inhibitors that might be useful for treating Alzheimer's disease by inhibiting cleavage of the N-terminal domain of amyloid beta-protein precursor.
									CC NOTE: This sequence does not appear in the specification but is represented in the Sed ID listing.
									CC XX SQ Sequence 4 AA:
									Query Match 100.0%; Score 20; DB 20; Length 4;
									Best Local Similarity 100.0%; Pred. No. 7.8e-05; Mismatches 0; Indels 0; Gaps 0;
									Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
									RESULT 14
									AAB97634 ID AAB97634 standard; peptide: 4 AA.
									XX XX AC AAB97634;
									XX DT 21-SEP-2001 (first entry)
									XX DE Alpha-ketoamide cathepsin G inhibitor peptide.
									XX KW Peptide ketamide; cysteine protease inhibitor; serine protease inhibitor; transition state analogue; KW

XX	OS	KW	neurodegenerative disease; ischaemia; stroke; Alzheimer's disease;
XX	FH	KW	anticoagulant; thrombosis; adult respiratory distress syndrome;
FT	Key	KW	emphysema; rheumatoid arthritis; pancreatitis; viral infection;
FT	Modified-site	KW	muscular dystrophy; myocardial tissue damage; tumour metastasis;
FT	Modified-site	KW	bone resorption; cathepsin inhibitor.
XX	Synthetic.		
XX	Location/Qualifiers		
XX	1		
PN	/note= "MeO-Suc-Ala"		
XX	4		
XX	/note= "Met-CO-NR3R4"		
PD	22-MAY-2001.		
XX	PF	27-DEC-1996;	96US-0777354.
XX	PR	27-DEC-1991;	91US-0815073.
PR	09-SEP-1993;	93US-0118997.	
PR	20-MAY-1994;	94US-0246511.	
PR	06-OCT-1995;	95US-0539944.	
XX	PA	(GEOR-) GEORGIA TECH RES CORP.	
XX	PI	Powers JC;	
XX	DR		
XX	WPI:	2001-440210/47.	
PT	New tripeptide ketoamide derivatives are serine and cysteine protease inhibitors, useful as anticoagulants and for treating neurodegenerative diseases, thrombosis, emphysema and rheumatoid arthritis -		
PT			
XX	PS		
XX			
CC	The invention relates to peptide ketoamide derivatives useful for selectively inhibiting serine proteases and cysteine proteases, and for generally inhibiting all members of these classes of enzymes. The peptide ketoamides are derivatives of substrate peptides of serine and cysteine proteases and act as transition state analogues. The peptides of the invention have the formula MI-AA1-AA2-AA3-COO-NR4 where:		
CC	MI is NH2CO-, NH2C(S)-, NH2SO2-, XNHC(O)-, X2NCOO-, XNHCS(-, X2NCS-, XNH2CO-, X2NSO2-, XCO-, XCS-, XSO2-, XCOO- or XCS(-,		
CC	X is 1-10C (fluoro)alkyl (optionally substituted by J), 1-adamantyl, 9-fluorenyl, phenyl or naphthyl (optionally substituted by J), 1-10C alkylphenyl, 1-10C alkylidiphenyl or 1-10C alkylphenoxy (all optionally substituted by K);		
CC	J is halo, COOH, OH, CN, NO2, NH2, 1-10C alkoxy, 1-10C alkylamine, 2-12C dialkylamine, 1-10C alkyl-OOC-, 1-10C alkyl-OCONH- or 1-10C alkyl-thio;		
CC	K is halo, 1-10C (perfluoro)alkyl, 1-10C alkoxy, NO2-, CN, OH, COOH, NH2, 1-10C alkylamino, 2-12C dialkylamino, 1-10C acyl, 1-10C alkoxy-CO or 1-10C alkylthio;		
AA1, AA2 are independently Ala, Val, Leu, Ile, Gly, Ser, Asp or Glu;			
AA3 is Asp or Glu, in either the L or D form;			
R3 is 2-3C alkyl-phenyl, 3-20C cycloalkylphenyl, 1-20C alkylphenyl (substituted by up to 3 of K), 3-20C cycloalkyl-phenyl (substituted by R4 = H, 3-20C alkyl, cycloalkyl, 1-20C alkylphenyl (optionally substituted by up to 3 of K), 3-20C cycloalkylphenyl (optionally substituted by K), NH2CH2CH2-(4-hydroxyphenyl) or NH-CH2CH2-(3-indolyl); and			
NH2CH2CH2-(3-indolyl).			
The peptide ketoamides are useful for treating neurodegenerative diseases and for treating thrombosis. They are also useful for treating emphysema, adult respiratory distress syndrome, rheumatoid arthritis, pancreatitis, viral infections, muscular dystrophy, myocardial tissue damage, tumour metastasis and bone resorption. The present sequence represents a cathepsin G (cysteine protease) peptide inhibitor.			

RESULT 16
 AAB6278 standard; peptide; 4 AA.
 AC AAB6278;
 XX DT 03-APR-2001 (first entry)
 DE peptide-lipid conjugate peptide #3.
 XX KW peptide-lipid conjugate; liposome; liposomal drug delivery; cancer;
 KW peptidase-secreting cell; phosphatidylethanolamine;
 KW inflammatory disorder; neuropathy.
 XX OS Synthetic.
 XX FH key Location/Qualifiers
 FT Modified-site 1
 /label= "OTHER
 /note= "optionally modified by succinyl, methoxysuccinyl
 or carboxy sugar group"
 PR 4
 FT Modified-site /label= "OTHER
 /note= "C-terminal phosphatidylethanolamine"
 PR XX PN WO200100247-A1.
 PR XX PA (ELIAN-) ELAN PHARM TECHNOLOGIES INC.
 PR XX PT Meers PR, Pak C, Ali S, Janoff A, Franklin JC, Erukulla RK;
 PR XX PI Cabral-Lilly D, Ahl PL;
 PR XX DR WPI; 2002-266419/31.
 XX CC This invention relates to a method of administering a bioactive agent
 CC to a mammal by administering a composition which comprises a carrier
 CC and a Liposome. The Liposome is delivered to the vicinity of cells in
 CC the mammal which secrete a peptide which recognizes the amino acid
 CC residue. The composition in considered cytostatic, antibacterial
 CC anti-inflammatory and antifungal. The composition is used to treat
 CC animals for diseases such as tumors, cancer, microbial infection or
 CC inflammatory disorders. The peptide-lipid conjugate selectively
 CC destabilising the Liposomes in the vicinity of target peptidase-secreting
 CC cells and hence delivers the Liposomes to the vicinity of the target
 CC cells or directly into the cells. The present sequence represents
 CC an enzyme cleavable peptide which is of sufficient length to project
 CC above the lipid-based carriers of which they have been incorporated.
 XX SQ Sequence 4 AA;
 XX Query Match 100.0%; score 20; DB 22; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OY 1 AAPM 4
 XX Db 1 AAPM 4
 XX SQ Sequence 4 AA;
 XX Query Match 100.0%; score 20; DB 23; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OY 1 AAPM 4
 XX Db 1 AAPM 4
 RESULT 17
 ABB83504 standard; peptide; 4 AA.
 ID ABB83504
 XX AC ABB83504;
 XX OS Synthetic.
 XX DT 18-SEP-2002 (first entry)
 DE Enzyme cleavable peptide to project from lipid-based carrier #19.
 XX DE Enzyme cleavable peptide to project from lipid-based carrier #4.
 XX KW Cytostatic; antibacterial; anti-inflammatory; antifungal;
 KW tumour; cancer; microbial infection; inflammatory disorder;
 KW liposome.
 XX OS Synthetic.
 XX PN US6339069-B1.
 XX DD 15-JAN-2002.
 XX PF 29-JUN-1999; 99US-0343650.
 XX PR 15-OCT-1996; 99US-027544P.
 PR 27-FEB-1997; 97US-039183P.
 PR 15-OCT-1997; 97US-0950610.
 PR 07-OCT-1998; 98US-0168010.
 XX PA (ELIAN-) ELAN PHARM TECHNOLOGIES INC.
 XX PT Meers PR, Pak C, Ali S, Janoff A, Franklin JC, Erukulla RK;
 PR XX PI Cabral-Lilly D, Ahl PL;
 PR XX DR WPI; 2002-266419/31.
 XX CC This invention relates to a method of administering a bioactive agent
 CC to a mammal by administering a composition which comprises a carrier
 CC and a Liposome. The Liposome is delivered to the vicinity of cells in
 CC the mammal which secrete a peptide which recognizes the amino acid
 CC residue. The composition in considered cytostatic, antibacterial
 CC anti-inflammatory and antifungal. The composition is used to treat
 CC animals for diseases such as tumors, cancer, microbial infection or
 CC inflammatory disorders. The peptide-lipid conjugate selectively
 CC destabilising the Liposomes in the vicinity of target peptidase-secreting
 CC cells and hence delivers the Liposomes to the vicinity of the target
 CC cells or directly into the cells. The present sequence represents
 CC an enzyme cleavable peptide which is of sufficient length to project
 CC above the lipid-based carriers of which they have been incorporated.
 XX SQ Sequence 4 AA;
 XX Query Match 100.0%; score 20; DB 23; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OY 1 AAPM 4
 XX Db 1 AAPM 4
 RESULT 18
 ABB83518 standard; peptide; 4 AA.
 ID ABB83518
 XX AC ABB83518;
 XX DT 18-SEP-2002 (first entry)
 DE Enzyme cleavable peptide to project from lipid-based carrier #19.
 XX DE Enzyme cleavable peptide to project from lipid-based carrier #4.
 KW Cytostatic; antibacterial; anti-inflammatory; antifungal;
 KW tumour; cancer; microbial infection; inflammatory disorder;
 KW liposome.
 XX OS Synthetic.

XX	Key	Location/Qualifiers
FT	Modified-site	I
FT	/label= MeOSuc	1
FT	/note= "Methoxy succinyl"	1
PN	US6339069-B1.	1
XX	PD	16-MAY-2002.
XX	PF	02-NOV-2001; 2001WO-US51172.
FT	PR	03-NOV-2000; 2000US-245737P.
XX	PA	(GLAD-) GLADSTONE INST J DAVID.
XX	PI	Huang Y, Mahley RW;
XX	DR	WPI; 2002-490051/52.
XX	PT	Inhibiting neurofibrillary tangles formation, useful for treating e.g. Alzheimer's, coronary artery disease or stroke, by reducing the formation of carboxyl-terminal truncated form of apolipoprotein E in a neuron of the individual -
XX	PT	Inhibiting neurofibrillary tangles formation, useful for treating e.g. Alzheimer's, coronary artery disease or stroke, by reducing the formation of carboxyl-terminal truncated form of apolipoprotein E in a neuron of the individual -
XX	PT	Inhibiting neurofibrillary tangles formation, useful for treating e.g. Alzheimer's, coronary artery disease or stroke, by reducing the formation of carboxyl-terminal truncated form of apolipoprotein E in a neuron of the individual -
XX	PS	Claim 30; Page 63; 7/5pp; English.
CC	The present invention relates to a method of inhibiting the formation of neurofibrillary tangles in an individual, which involves reducing the formation of a carboxyl-terminal truncated form of apolipoprotein E (apoE) in a neurone in the individual. The method is useful for inhibiting the formation of neurofibrillary tangles in an individual. The reduction in the formation of carboxyl-terminal truncated apoE treats a disorder related to apoE in an individual, specifically Alzheimer's disease, coronary artery disease, head trauma or stroke. The present sequence is a peptide capable of inhibiting the formation of the C-terminal truncated form of apoE.	
CC	Sequence 4 AA;	
CC	Query Match 100.0%; Score 20; DB 23; Length 4;	
CC	Best Local Similarity 100.0%; Pred. No. 7.8e+05;	
CC	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AAPM 4	
Db	1 AAPM 4	
XX	RESULT 20	
ID	ABB83531	
XX	ABB83531 standard; peptide; 5 AA.	
AC	ABB83531;	
XX	DT 18-SEP-2002 (first entry)	
XX	DE Enzyme cleavable peptide to project from lipid-based carrier #32.	
XX	KW Cytostatic; antibacterial; anti-inflammatory; antifungal;	
KW	KW tumour; cancer; microbial infection; inflammatory disorder;	
KW	KW liposome.	
XX	OS Synthetic.	
XX	Location/Qualifiers	
FH	Key	
FT	Modified-site	
FT	/label= Suc	
FT	/note= "Succinyl"	
XX	PN US6339069-B1.	
XX	PD 15-JAN-2002.	
XX	PR 29-JUN-1999; 99US-0345650.	
PR	15-OCT-1996; 96US-027544P.	
PR	27-FEB-1997; 97US-039183P.	
PR	15-OCT-1997; 97US-0950118.	
PR	07-OCT-1998; 98US-0168010.	
XX	SYNTHETIC.	
XX	WO200238108-A2.	

XX (ELAN-) ELAN PHARM TECHNOLOGIES INC.
 XX PA Cabral-Lilly D, Ahl PL;
 XX PI WPI; 2002-266419/31.
 PI Cabral-Lilly D, Ahl PL;
 XX DR Liposome composition useful in the treatment of e.g. tumours comprises
 PT liposome containing a bioactive agent and a lipid component which is
 PT delivered to the vicinity of cells in the mammal.
 XX DR WPI; 2002-266419/31.
 PS Disclosure: Column 15; 50pp; English.
 CC This invention relates to a method of administering a bioactive agent
 CC to a mammal by administering a composition which comprises a carrier
 CC and a liposome. The liposome is delivered to the vicinity of cells in
 CC the mammal which secrete a peptidase which recognizes the amino acid
 CC residue. The composition in considered cytostatic, antibacterial
 CC anti-inflammatory and antifungal. The composition is used to treat
 CC animals for diseases such as tumours, cancer, microbial infection or
 CC inflammatory disorders. The peptide-lipid conjugate selectively
 CC destabilizing the liposomes in the vicinity of target peptidase-secreting
 CC cells and hence delivers the liposomes to the vicinity of the target
 CC cells or directly into the cells. The present sequence represents
 CC an enzyme cleavable peptide which is of sufficient length to project
 CC above the lipid-based carriers of which they have been incorporated.
 XX SQ Sequence 5 AA;

Query	Match	Score	DB	Length
Best Local	Similarity	100.0%	23;	5;
Matches		4;	Pred. No.	7.8e+05;
Qy	1 AAPM 4			
Db	2 AAPM 5			

RESULT 21
 ABB83532
 ID ABB83532 standard; peptide; 5 AA.
 XX AC AAB06270
 XX DT 03-OCT-2000 (first entry).
 XX DE Human proBDNF signal peptide cleavage site.
 XX KW Human; pro-brain-derived neurotrophic factor; proBDNF; SKI-1;
 KW subtilisin-kexin isoenzyme; antilipaemic; cytostatic; vasotropin;
 KW SKI-1 inhibitor; hypercholesterolaemia; liver steatosis;
 KW Ras-dependent cancer; restenosis; amyloid protein formation.
 OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 XX PN WO200026348-A2.
 XX PD 11-MAY-2000.
 XX PF 04-NOV-1999; 99W0-CA01058.
 XX PR 04-NOV-1998; 98CA-2249648.
 XX PA (RECL-) INST RECH CLINIQUES MONTREAL.
 XX PI Seidah N, Chretien M, Marcinkiewicz M, Laksonen R, Davignon J;
 XX DR WPI; 2000-365601/31.
 XX PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
 PT producing a polypeptide useful for treating hypercholesterolemia, liver
 PT steatosis and amyloidosis, comprises a specific amino acid sequence

XX (ELAN-) ELAN PHARM TECHNOLOGIES INC.
 PI Meers PR, Pak C, Ali S, Janoff A, Franklin JC, Brukulla RK;
 XX PI Cabral-Lilly D, Ahl PL;
 XX DR Liposome composition useful in the treatment of e.g. tumours comprises
 PT liposome containing a bioactive agent and a lipid component which is
 PT delivered to the vicinity of cells in the mammal.
 XX DR WPI; 2002-266419/31.
 PS Disclosure: Column 15; 50pp; English.
 CC This invention relates to a method of administering a bioactive agent
 CC to a mammal by administering a composition which comprises a carrier
 CC and a liposome. The liposome is delivered to the vicinity of cells in
 CC the mammal which secrete a peptidase which recognizes the amino acid
 CC residue. The composition in considered cytostatic, antibacterial
 CC anti-inflammatory and antifungal. The composition is used to treat
 CC animals for diseases such as tumours, cancer, microbial infection or
 CC inflammatory disorders. The peptide-lipid conjugate selectively
 CC destabilizing the liposomes in the vicinity of target peptidase-secreting
 CC cells and hence delivers the liposomes to the vicinity of the target
 CC cells or directly into the cells. The present sequence represents
 CC an enzyme cleavable peptide which is of sufficient length to project
 CC above the lipid-based carriers of which they have been incorporated.
 XX SQ Sequence 5 AA;

Query	Match	Score	DB	Length
Best Local	Similarity	100.0%	23;	5;
Matches		4;	Pred. No.	7.8e+05;
Qy	1 AAPM 4			
Db	2 AAPM 5			

RESULT 22
 ABB83532
 ID ABB83532 standard; peptide; 9 AA.
 XX AC AAB06270;
 XX DT 03-OCT-2000 (first entry).
 XX DE Human proBDNF signal peptide cleavage site.
 XX KW Human; pro-brain-derived neurotrophic factor; proBDNF; SKI-1;
 KW subtilisin-kexin isoenzyme; antilipaemic; cytostatic; vasotropin;
 KW SKI-1 inhibitor; hypercholesterolaemia; liver steatosis;
 KW Ras-dependent cancer; restenosis; amyloid protein formation.
 OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 XX PN US6339069-B1.
 XX PD 15-JAN-2002.
 XX PF 29-JUN-1999; 99US-0343650.
 XX PR 15-OCT-1998; 96US-027544P.
 XX PR 27-FEB-1997; 97US-039183P.
 XX PR 15-OCT-1997; 97US-0390618.
 XX PR 07-OCT-1998; 98US-0168010.
 XX PA (ELAN-) ELAN PHARM TECHNOLOGIES INC.
 PI Meers PR, Pak C, Ali S, Janoff A, Franklin JC, Brukulla RK;

PS Example 1; Page 22; 119pp; English.

XX The present sequence is the site at which human pro-brain-derived CC neurotrophic factor (proBDNF) is cleaved to remove the 18 amino acid CC signal peptide. proBDNF is a substrate of subtilisin-kexin isoenzyme 1 CC (SK1-1), a type-1 membrane-bound proteinase. SK1-1 cleaves at a specific CC threonine residue within the N-terminal segment of human proBDNF. CC Peptides which bind to and are cleaved by SK1-1 may be used for monitoring SK1-1 activity, for screening inhibitors of SK1-1 activity, or CC for screening enhancers of SK1-1 activity. Proteic fragments of SK1-1 CC which bind to the SK1-1 catalytic site may be used as inhibitors of SK1-1 activity. They may be used to treat diseases involving overexpression of CC SK1-1 or SK1-1 substrate. Such diseases include hypercholesterolaemia, CC high levels of fatty acids, lipids or farnesyl pyrophosphate, liver steatosis, Ras-dependent cancer, restenosis and amyloid protein formation. CC

XX

SQ Sequence 9 AA:

Query Match	100.0%	Score	20;	DB	21;	Length	9;
Best Local Similarity	100.0%	Pred. No.	7.8e+05;				
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Qy 1 AAPM 4
Db 5 AAPM 8

RESULT 23

AAB10855 standard; Protein; 14 AA.

ID AAB10855;
XX
AC AAB10855;
XX
DT 02-FEB-2001 (first entry)
XX
DB pSectag-VEGF protein fragment VEGF back1.
XX
KW MVP; multivalent protein; treatment; dressing; skin; mucus; musculature; nervous system; inner organ; hematopoietic system; immune system; joint; support tissue; immunization.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO20053790-A1.
XX
PD 14-SEP-2000.
XX
PF 26-FEB-2000; 2000WO-EP01612.
XX
PR 10-MAR-1999; 99DE-1010419.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Kontermann R, Nettelbeck D, Sedlacek H, Mueller R;
XX
DR WPI; 2000-57227/53.
XX
N-PSDB; AAA98162.

PT Cell specific multivalent proteins useful for targeting specific cells PT for the treatment of disease -

XX

PS Example 1; Page 54; 81pp; German.

CC This invention describes a method for the production of a novel cell CC specific multivalent protein (MVP). The invention also describes (1) a CC nucleic acid construct, which encodes an MVP; (2) a bacterium, yeast or CC mammalian cell, in which the nucleic acid construct of (1) is introduced; CC (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP CC comprising a scFv with a binding site for the adenoviral fibre protein or CC CD3 molecule and two VEFB units bound by a peptide linker; and (6) a CC complex comprising at least two MVPs as above (in which each single

CC ligand can be 0-1). The MVP, optionally bound to a vector, is useful for CC production of a remedy to treat cells outside tissue by dressings for CC skin, mucus, nervous systems, inner organs, hematopoietic systems, CC immune systems, musculature, support tissues or joints and to immunize to CC prevent or treat diseases.

XX

SQ Sequence 14 AA:

Query Match	100.0%	Score	20;	DB	21;	Length	14;
Best Local Similarity	100.0%	Pred. No.	1.9e+02;				
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Qy 1 AAPM 4
Db 4 AAPM 7

RESULT 24

AAB98208
ID AAB98208 standard; Peptide; 15 AA.

XX
AC AAB98208;
XX
DT 17-AUG-2001 (first entry)
XX
DB Human P24 protein-22 N-terminal peptide SEQ ID NO:7.
XX
KW Human; P24 protein-22; diagnosis; treatment; cancer; haemopathy; HIV; KW human immunodeficiency virus; infection; immunological disease; KW inflammation.
XX
OS Homo sapiens.
XX
PN WO20129076-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-CN00332.
XX
PR 18-OCT-1999; 99CN-0116990.
XX
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
XX
PT Mao Y, xie Y;
XX
DR WPI; 2001-290896/30.
XX
PT Human P24 protein-22 and encoded polynucleotide, applicable in PT diagnosis and treatment of cancer, hemopathy, immunological diseases PT and various inflammations -
XX
PS Example 6; Page. 15; 29pp; Chinese.

XX
CC The present invention describes the human P24 protein-22. The P24 CC protein-22 polypeptide and polynucleotide can be used in the diagnosis CC and treatment of cancer, haemopathy, HIV (human immunodeficiency virus) CC infection, immunological diseases and various inflammation. The present CC sequence represents a the human P24 protein-22 N-terminal peptide, which CC is used in an example from the present invention.

XX

SQ Sequence 15 AA:

Query Match	100.0%	Score	20;	DB	22;	Length	15;
Best Local Similarity	100.0%	Pred. No.	2.1e+02;				
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Qy 1 AAPM 4
Db 2 AAPM 5

RESULT 25

AAR42608

ID AAR42608 standard; Protein; 17 AA.
 XX
 AC AAR42608;
 XX DT 28-OCT-1993 (first entry)
 XX DE Encoded by human VEGF-165 exon II.
 XX KW angiogenesis; wound healing; mitogen; vascular endothelial cells;
 KW vascular Endothelial Cell Growth Factor; hVEGF-165; hVEGF-121;
 KW alternative RNA splicing.
 XX OS Homo sapiens.
 XX FH
 KEY Location/Qualifiers
 FT Cleavage-site 4..5 /note= "signal peptide-mature protein junction"
 FT PN US5219739-A.
 XX PD 15-JUN-1993.
 XX PR 27-JUL-1989; 89US-0387545.
 XX PR 27-JUL-1989; 89US-0387545.
 PR 14-DEC-1990; 90US-0450883.
 PR 27-JUL-1990; 90US-0539041.
 XX PA (SC10-) SCS NOVA INC.
 XX PI Abraham JA, Fiddes JC, Mitchell RL, Tischer EG;
 DR WPI; 1993 205302/25.
 DR N-PSDB; AAQ49604.
 PT Isolated DNA sequences, expression vectors and transformant cells - used for large scale prodn. of vascular endothelial cell growth factor, for treating wounds in which neo-vascularisation is required
 XX PS claim 8; Fig 8; 40pp; English.
 CC The sequences of the 8 possible exons encoding human vascular endothelial cell growth factor, together with contiguous splice junctions, were obtained from overlapping genomic inserts. A method for producing VEGF is claimed comprising culturing mammalian cells transformed with an expression vector containing exons I-V and VIII. See AAQ4261 for exon I and AAQ49604-049610 for exons II-VIII.
 CC Sequence 17 AA:
 SQ Query Match 100.0%; Score 20; DB 14; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 Db 4 AAPM 7.
 RESULT 26
 AAR94034
 ID AAR94034 standard; Protein; 17 AA.
 AC AAR94034;
 XX DE 10-OCT-1996 (first entry)
 VNGF exon II.
 XX KW vascular endothelial growth factor; VEGF; human; conjugate; tumour; iris; proliferation inhibition; VEGF-mediated pathophysiological condition; dermatological disorder; VEGF receptor; vascular proliferation; retina;
 KW OS Homo sapiens.
 XX FH Location/Qualifiers

KW ophthalmic disorder; hyperproliferating blood vessel; therapy; psoriasis; conjunctival; vitreous humour; rheumatoid arthritis; skin cancer;
 KW varicose veins; gene therapy.
 XX OS Homo sapiens.
 XX PN WC9606641-A1.
 XX PD 07-MAR-1996.
 XX PR 29-AUG-1995; 95WO-US10973.
 XX PR 16-MAY-1995; 95US-0341979.
 XX PR 29-AUG-1994; 94US-0297961.
 XX PA (PRIZ-) PRIM PHARM INC.
 PI Fleurbaaij GA, Freund E, Houston LL, Nova MP, Sosnowski BA;
 DR WPI; 1996 160151/16.
 DR N-PSDB; AAT11742.
 XX PT Vascular endothelial cell growth factor (VEGF) conjugates - having of VEGF linked to targeted agent, used for inhibiting proliferation of cells, e.g. for gene therapy
 XX PS Disclosure; Page 118; 193PP; English.
 XX CC AAR94033-894038, AAR94041, AAR94042 and AAW00582 represent vascular endothelial growth factors (VEGF) exons. This sequence represents exon II. These sequences were used in VEGF conjugates of the invention. In the conjugates, VEGF (or fragments of it) are linked to a targeted agent (this can be via a linker sequence), so that the conjugate binds to a VEGF receptor. Cys-modified forms of VEGF are particularly suitable for chemical conjugation to linkers and targeted agents. The conjugates are used for inhibiting proliferation of cells bearing VEGF receptors. They can be used for treating a VEGF-mediated pathological condition, including dermatological disorders with underlying vascular proliferation, solid tumours or an ophthalmic disorder of hyperproliferating blood vessels of the retina, iris, conjunctiva or vitreous humour. The conjugates can also be used for treating psoriasis, rheumatoid arthritis, skin cancers and other tumours, or varicose veins. They are also suitable for use in gene therapy.
 XX SQ Sequence 17 AA:
 Query Match 100.0%; Score 20; DB 17; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 Db 4 AAPM 7.
 RESULT 27
 AAR94035
 ID AAR94035 standard; Peptide; 19 AA.
 AC AAU00655;
 XX DT 07-SEP-2001 (first entry)
 XX DE Human targeting peptide sequence #1.
 XX DE Human targeting peptide sequence #1.
 XX KW Membrane translocating peptide; MTRP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system;
 KW targeting peptide.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers

FT Modified-site 1
 FT /note= "N-terminus has a dansyl group"
 FT Modified-site 19
 FT /note= "C-terminal amide"
 XX WO200127154-A2.
 XX 19-APR-2001.
 XX PD 27-SEP-2000; 2000WO-1B01491.
 XX PR 27-SEP-1999; 99US-015246.
 XX PA (OMAH/) O'MAHONY D J.
 PA (LAMB/) LAMBKIN I J.
 PI O'mahony DJ, Lambkin IJ;
 XX DR WPI; 2001-300212/31.
 XX PT Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic of the peptides -
 XX PS Example 1; Page 22; 42pp; English.
 XX The sequence represents a human targeting peptide which is used to identify the presence of a human membrane translocated peptide (MTLP) and quantify the amount, to bind the MTLP to the surface of a particle, or to localise the MTLP in a cell or tissue sample. MTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of MTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP, for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder.

XX Sequence 19 AA;

Query Match 100.0%; Score 20; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPM 4
 Db 13 AAPM 16

RESULT 28
 ABG62530 ID ABG62530 standard; Peptide; 25 AA.
 AC ABG62530;
 XX DT 21-AUG-2002 (first entry)
 XX DE Eubacterial MutS1 DNA polymerase III beta subunit binding peptide #35.
 XX KW DNA polymerase III; beta subunit; eubacteria; antibacterial;
 KW eubacterial infection.
 XX OS Burkholderia cepacia.
 XX PN wo200230596-A1.

XX Sequence 25 AA;

Query Match 100.0%; Score 20; DB 23; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPM 4
 Db 16 AAPM 19

RESULT 29
 AAM19115 ID AAM19115 standard; Protein; 31 AA.
 XX AC AAM19115;
 XX DT 12-OCT-2001 (first entry)

XX DE Peptide #5549 encoded by probe for measuring cervical gene expression.
 XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX OS Homo sapiens.
 XX PN WO200157278-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US00670.
 XX PR 04-FEB-2000; 2000US-0180312.
 XX PR 26-MAY-2000; 2000US-0207456.
 XX PR 30-JUN-2000; 2000US-0568408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-0224687.
 XX PR 27-SEP-2000; 2000US-0226359.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488901/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for
 analyzing gene expression in human cervical epithelial cells -
 XX PS Claim 27; SEQ ID NO 23941; 487PP; English.
 XX CC The present invention relates to human single exon nucleic acid probes
 (SENP; see AA110068-AA18459). The present sequence is a peptide encoded
 by one such probe. The SNPs are derived from human HeLa cells. The SNPs
 can be used to produce a single exon microarray, which can be used for
 measuring human gene expression in a sample derived from human cervical
 epithelial cells. By measuring gene expression the probes are therefore
 useful in grading and/or staging of diseases of the cervix, notably
 cervical cancer.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 31 AA:
 Query Match 100.0%; Score 20; DB 22; Length 31;
 Best Local Similarity 100.0%; pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC OY 1 AAPM 4
 CC Db 14 AAPM 17

RESULT 31
 ABG41275
 ID4 ABG41275 standard; Peptide; 31 AA.
 XX AC ABG41275;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 30940.
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesis; pulmonary hypertension;
 KW hyaline membrane disease.
 XX OS Homo sapiens.
 XX PN WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PR 30-JAN-2001; 2001WO-US00665.
 XX PR 04-FEB-2000; 2000US-180312P.
 XX PR 26-MAY-2000; 2000US-20456P.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0652366.
 XX PR 21-SEP-2000; 2000US-0334687.
 XX PR 27-SEP-2000; 2000US-0336369.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-48897/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for
 analyzing gene expression in human placenta.
 XX PS Claim 27; SEQ ID NO 32033; 654PP; English.
 XX CC The present invention relates to single exon nucleic acid probes (SENP;
 see AA131315-AA157546). The present sequence is a peptide encoded by one
 predicting, measuring and displaying gene expression in samples derived
 from human placenta. The probes are useful for producing a microarray for
 human genetic disorders.

XX SQ Sequence 31 AA:
 Query Match 100.0%; Score 20; DB 22; Length 31;
 Best Local Similarity 100.0%; pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2002-114183/15.

PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 XX PS Claim 27; SEQ ID NO 30940; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring single exon nucleic acid expression in a sample derived from human lung comprising one or more nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising: (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarray having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangiomatosis, pulmonary alveolar proteinosis, Kartagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences.

XX Sequence 31 AA;

SQ	Query Match	Best Local Similarity	Score	DB	Length
	100.0%	20	DB 23	31	
Matches	100.0%	Pred. No. 4.1e+02			
4	Conservative 0	Mismatches 0			
Oy	1 AAPM 4	Indels 0	Gaps 0		
Db	14 AAPM 17				

XX RESULT 32

ID	Query Match	Best Local Similarity	Score	DB	Length
AAB39021	100.0%	20	DB 21	42	
ID AAB39021 standard	100.0%	Pred. No. 5.5e+02			
XX Matches 4	Conservative 0	Mismatches 0			
Oy 1 AAPM 4	Indels 0	Gaps 0			
Db 18 AAPM 21					

XX RESULT 33

ID	Query Match	Best Local Similarity	Score	DB	Length
ABG27642	100.0%	20	DB 21	42	
ID ABG27642 standard	100.0%	Pred. No. 4.3 AA..			
XX AC ABG27642					
XX DT 18-FEB-2002 (first entry)					
XX DE Novel human diagnostic protein #27633.					

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PP 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-054217.
 XX PR 23-AUG-2000; 2000US-0649157.
 XX PA (HYSE-) HYSQ INC.
 XX PI Dumanac RT, Liu C, Tang YR;
 DR WPI; 2001-639362/73.
 XX DR N-PSDB; AAS91829.
 PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 XX
 PS Claim 20; SEQ ID NO 58001; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABC0010-ABG03077 represent novel human CC diagnostic amino acid sequences of the invention.
 Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp://wipo.int/pub/published_pct_sequences.
 XX Sequence 43 AA:
 Query Match 100.0%; Score 20; DB 22; Length 43;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 Db 25 AAPM 28
 SQ Sequence 50 AA:
 Query Match 100.0%; Score 20; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 Db 31 AAPM 34
 RESULT 34
 AAU64697 ID AAU64697 standard; Protein; 50 AA.
 XX AC AAU64697;
 XX DT 27-FEB-2002 (first entry)
 XX DE Propionibacterium acnes immunogenic protein #25593.
 XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthalmitis; bone; joint; central nervous system; ELISA;
 KW

KW Inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; KW dermatological; osteopathic; neuroprotectant.
 XX OS Propionibacterium acnes.
 XX PN WO200181581-A2.
 XX PD 01-NOV-2001.
 XX PP 20-APR-2001; 2001WO-US12865.
 XX PR 21-APR-2000; 2000US-199047P.
 XX PR 02-JUN-2000; 2000US-209841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59648.
 PT Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for PT treating acne vulgaris -
 XX PS Example 1; SEQ ID NO 25892; 1069pp; English.
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include Sapho syndrome (synovitis; acne; CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies CC specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA).
 Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp://wipo.int/pub/published_pct_sequences.
 XX

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PR 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US 208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORT-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59659.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 26300; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU69017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC *P. acnes*. The disorders include sapho syndrome (*synovitis*), acne,
 CC *pustulosis*, *hyperkeratosis* and *osteomyelitis*, uveitis and endophthalmitis.
 CC *P. acnes* is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of *P. acnes* in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for *P. acnes* proteins. These antibodies can be used to
 CC downregulate expression and activity of *P. acnes* polypeptides and
 CC therefore treat *P. acnes* infections. The antibodies may also be used as
 CC diagnostic agents for determining *P. acnes* presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 Note: The sequence data for this patient did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://ipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 50 AA;
 Query Match 100.0%; Score 20; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 |||||
 Db 46 AAPM 49
 RESULT 36
 AA65229
 ID AA65229 standard; Protein; 51 AA.
 AC
 AC AAY65229;
 AC
 DT 01-FEB-2000 (first entry)
 DE Human 5' EST related polypeptide SEQ ID NO:1390.
 KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
 KW gene therapy; chromosome mapping; upstream regulatory sequence;
 KW
 KW forensic; location; development; protein synthesis; stability;
 KW regulation; identification.
 XX
 OS Homo sapiens.
 XX
 PN WO9953051-A2.
 XX
 PD 21-OCT-1999.
 XX
 PR 09-APR-1999; 99WO-1B00712.
 XX
 PR 09-APR-1998; 98US-0057719.
 PR 28-APR-1998; 98US-0069047.
 XX
 PA (GEST-) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 DR WPI; 2000-038446/03.
 DR N-PSDB; AAZ242843.
 XX
 PT Novel secreted protein 5' expressed sequence tag sequences used in
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures
 PS
 XX
 CC AZ42265 to AA243075 represent novel 5' expressed sequence tag (EST)
 CC sequences, corresponding to human secreted proteins. AAY64651 to
 CC AAY65438 represent the EST-related proteins corresponding to AA42265 to
 CC AZ42052. The 5' ESTs can be used for producing secreted human gene
 CC products. They can be used to identify and isolate 5' untranslated
 CC regions (UTRs) and upstream regulatory regions which control the
 CC location, development stage, rate, and quantity of protein synthesis, as
 CC well as stability of mRNA. The ESTs are also useful as probes for
 CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
 CC also be used in forensic procedures to identify individuals, or in
 CC diagnostic procedures to identify individuals having genetic diseases
 CC resulting from abnormal gene expression. The products may also be used in
 CC gene therapy protocols. The nucleic acids encoding signal peptides can be
 CC used for directing extracellular secretion of a polypeptide or the
 CC insertion of a polypeptide into a membrane, or importing a polypeptide
 CC into a cell. The proteins encoded by the EST sequences may be useful in
 CC treating a variety of human conditions. Secreted proteins have
 CC therapeutic value and the identification of new secreted proteins is
 CC valuable. AAZ2249 to AA42264 and AAY64644 to AAY64650 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 51 AA;
 Query Match 100.0%; Score 20; DB 21; Length 51;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 |||||
 Db 42 AAPM 45
 RESULT 37
 ABG0125
 ID ABG0125 standard; Protein; 53 AA.
 XX
 AC ABG0125;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #116.
 XX
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PR 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-ABR-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PT Dermanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 XX
 DR N-PSDB; AAS64312.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 XX
 PS claim 20; SEQ ID NO 30484; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG3037 represent novel human diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 53 AA;

Query Match 100.0%; Score 20; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; OS

Oy 1 AAPM 4
 Db 21 AAPM 24

RESULT 38
 AAU64950
 ID AAU64950 standard; Protein; 56 AA.
 XX
 AC AAU64950;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #25846.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX

RESULT 39
 AAU67577
 ID AAU67577 standard; Protein; 59 AA.
 XX
 AC AAU67577;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #28473.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.

PN WO200181581-A2.
 XX
 PC 01-NOV-2001.
 XX
 PR 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORTI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Parsing DH, Mitcham JL, Wang SS, Bhatia A;
 PT L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; ABN59575.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 Example 1; SEQ ID NO 28772; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC *P. acnes* is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of *P. acnes* in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The invention
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for *P. acnes* proteins. Those antibodies can be used to
 CC downregulate expression and activity of *P. acnes* polypeptides and
 CC therefore treat *P. acnes* infections. The antibodies may also be used as
 CC diagnostic agents for determining *P. acnes* presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 59 AA;

Query Match	100 %;	Score 20;	DB 22;	Length 59;
Best Local Similarity	100.0 %;	Pred. No. 7.5e+02;		
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

Qy 1 AAPM 4
 Db 48 AAPM 51

RESULT 40
 XX
 ABP10723
 ID ABP10723 standard; Protein: 60 AA.
 XX
 AC ABP10723;
 XX
 DT 25-JUN-2002 {first entry}
 XX
 DE Human ORFX protein sequence SEQ ID NO:21428.

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;

PN WO200192523-A2.
 XX
 OS Homo sapiens.
 XX
 PR 06-DEC-2001.
 XX
 PN WO200192523-A2.
 XX
 PD 29-MAY-2001; 2001WO-US10836.
 XX
 PR 30-MAY-2000; 2000US-206132P.
 PR 29-AUG-2000; 2000US-228716P.
 XX
 DR WPI; 2002-106308/14.
 XX
 DR N-PSDB; ABN26475.
 XX
 PS Disclosure; SEQ ID 21428; 1037pp; English.
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN2725 encode the human ORFX
 CC proteins given in ABP0010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 60 AA;

Query Match	100.0 %;	Score 20;	DB 23;	Length 60;
Best Local Similarity	100.0 %;	Pred. No. 7.7e+02;		
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

Qy 1 AAPM 4
 Db 48 AAPM 51

Search completed: December 6, 2002, 13:28:01
 Job time : 26 secs

Copyright (c) 1993 - 2002 CompuGen Ltd.	GenCore version 5.1.3			
OM protein - protein search, using SW model				
Run on: December 6, 2002, 13:26:14 ; Search time 9.33333 Seconds	(Without alignments)			
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Searched: US-10-033-526-2				
Perfect-score: 20				
Sequence: 1. AARM 4				
Total number of hits satisfying chosen parameters: 262574				
Minimum DB seq length: 0				
Maximum DB seq length: 2000000000				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 45 summaries				
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3: /cgn2_6/podata/1/iaa/5A_COMBO.pep:*				
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5: /cgn2_6/podata/1/iaa/PCTUS_COMBO.pep:*				
6: /cgn2_6/podata/1/iaa/backfilest1.pep:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
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1	20	100.0	4 1 US-08-004-643C-3	Sequence 3, Appli
2	20	100.0	4 1 US-08-460-338-60	Sequence 4, Appli
3	20	100.0	4 1 US-08-777-208-3	Sequence 50, Appli
4	20	100.0	4 1 US-08-398-028B-60	Sequence 3, Appli
5	20	100.0	4 1 US-08-693-653-2	Sequence 60, Appli
6	20	100.0	4 2 US-08-501-265B-60	Sequence 2, Appli
7	20	100.0	4 2 US-08-025-322C-13	Sequence 60, Appli
8	20	100.0	4 2 US-08-907-840A-1	Sequence 13, Appli
9	20	100.0	4 3 US-08-168-618-4	Sequence 1, Appli
10	20	100.0	4 3 US-08-950-618-19	Sequence 4, Appli
11	20	100.0	4 3 US-08-950-618-32	Sequence 19, Appli
12	20	100.0	4 3 US-08-950-618-33	Sequence 32, Appli
13	20	100.0	4 4 US-09-343-650-19	Sequence 33, Appli
14	20	100.0	4 4 US-09-168-010-4	Sequence 4, Appli
15	20	100.0	4 4 US-09-578-303-11	Sequence 19, Appli
16	20	100.0	4 4 US-09-168-010-33	Sequence 32, Appli
17	20	100.0	4 4 US-09-519-739-28	Sequence 33, Appli
18	20	100.0	4 4 US-09-343-650-4	Sequence 4, Appli
19	20	100.0	4 4 US-09-343-650-9	Sequence 19, Appli
20	20	100.0	4 4 US-09-343-650-32	Sequence 32, Appli
21	20	100.0	4 4 US-09-343-650-33	Sequence 33, Appli
22	20	100.0	4 4 US-09-578-303-11	Sequence 11, Appli
23	20	100.0	4 6 5 194596-23	Sequence 5, Appli
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25	20	100.0	106 4 US-09-188-930-136	Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
26	20	100.0	106 4 US-08-905-223-336	Sequence 136, Appli
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ALIGNMENTS				
RESULT 1	US-08-004-643C-3			
SEQUENCE 3, Application US-08004643C	; Sequence 3, Appli			
PATENT NO. 5480779	Sequence 9, Appli			
GENERAL INFORMATION:	Sequence 3, Appli			
APPLICANT: Gunter & Gerhard Kllerz	Sequence 9, Appli			
TITLE OF INVENTION: Cyclosporine Assay	Sequence 13, Appli			
NUMBER OF SEQUENCES: 7	Sequence 58, Appli			
CORRESPONDENCE ADDRESS:	Sequence 59, Appli			
ADRESSEEE: Gunter Fischer et al. c/o G. P. Katona	Sequence 60, Appli			
STREET: 230 Park Avenue, Room 2200	Sequence 61, Appli			
CITY: New York	Sequence 62, Appli			
STATE: New York	Sequence 63, Appli			
COUNTRY: USA	Sequence 64, Appli			
ZIP: 10161 USA	Sequence 3, Appli			
COMPUTER READABLE FORM:	Sequence 3, Appli			
MEDIUM TYPE: FLOPPY disk	Sequence 3, Appli			
COMPUTER: IBM PC compatible	Sequence 3, Appli			
OPERATING SYSTEM: MS-DOS	Sequence 3, Appli			
SOFTWARE: conf. to Patentin Release #1.0, ver. #1.25	Sequence 3, Appli			
APPLICATION NUMBER: US/08/004, 643C	Sequence 3, Appli			
FILING DATE: 12 January 1993	Sequence 3, Appli			
CLASSIFICATION: 435	Sequence 3, Appli			
PRIORITY APPLICATION DATA:	Sequence 3, Appli			
APPLICATION NUMBER: 703 590	Sequence 3, Appli			
FILED DATE: 20 May 1991	Sequence 3, Appli			
APPLICATION NUMBER: 398, 992	Sequence 3, Appli			
FILED DATE: 24 August 1989	Sequence 3, Appli			
APPLICATION NUMBER: DD WP 601 F/319 577W	Sequence 3, Appli			
FILED DATE: 07 September 1988	Sequence 3, Appli			
ATTORNEY/AGENT INFORMATION:	Sequence 3, Appli			
NAME: Katona, Gabriele.	Sequence 3, Appli			
REGISTRATION NUMBER: 20,829	Sequence 3, Appli			
REFERENCE/DOCKET NUMBER: 691-003	Sequence 3, Appli			
TELECOMMUNICATION INFORMATION:	Sequence 3, Appli			
TELEPHONE: (212)986-3377	Sequence 3, Appli			
TELEFAX: (212)986-6126	Sequence 3, Appli			
TELEX:	Sequence 3, Appli			
INFORMATION FOR SEQ ID NO: 3:	Sequence 3, Appli			
SEQUENCE CHARACTERISTICS:	Sequence 3, Appli			
LENGTH: 4 amino acid residues	Sequence 3, Appli			
TYPE: amino acid	Sequence 3, Appli			
SEQUENCE:	Sequence 3, Appli			
STRANDEDNESS: single	Sequence 3, Appli			
TOPOLOGY: linear	Sequence 3, Appli			
US-08-004-643C-3	Sequence 3, Appli			
Query Match Score: 20; DB: 1; Length: 4;	Sequence 3, Appli			
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;	Sequence 3, Appli			

RESULT 2
 Qy 1 AAPM 4
 Sequence 4, Application US/08544143A
 ;
 Patent No. 5646028
 General Information:
 ;
 APPLICANT: Leigh, Scott D.
 TITLE OF INVENTION: NOVEL ALKALINE PROTEASE AND USES
 NUMBER OF SEQUENCES: 22
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/544,143A
 FILING DATE: 17-OCT-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: de Runtz, K. Alison
 REGISTRATION NUMBER: 37,119
 REFERENCE/DOCKET NUMBER: 0409.054US3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-362-5556
 TELEFAX: 415-362-5418
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 ;
 US-08-544-143A-4

Query Match 100.0%; Score 20; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 4;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 Db 1 AAPM 4

RESULT 3
 US-08-460-343B-60
 ; Sequence 60, Application US/08460343B
 ;
 Patent No. 5741664
 General Information:
 ;
 APPLICANT: Marcus D. Ballinger and James A. Wells
 TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING
 TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:

RESULT 4
 US-08-777-208-3
 ; Sequence 3, Application US/08777208
 ;
 Patent No. 5763576
 General Information:
 ;
 APPLICANT: Powers, James C.
 TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Deveau, Colton & Marquis
 STREET: Two Midtown Plaza, Suite 1400
 CITY: Atlanta
 STATE: GA
 COUNTRY: USA
 ZIP: 30309
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Microsoft Windows 95
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/777,208
 FILING DATE: 27-DEC-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/539944
 FILING DATE: 06-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colton, Laurence P.
 REGISTRATION NUMBER: 33371
 REFERENCE/DOCKET NUMBER: 10733-191B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 875-3555
 TELEFAX: (404) 875-8505
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: no
US-08-777-208-3

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 5
US-08-348-02BB-60
Sequence 60, Application US/08398028B
; Sequence 60, Application US/08398028B
; Patent No. 5780285
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBTILISIN VARIANT CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/950,143
; FILING DATE: 13-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Battle, Carl
; REGISTRATION NUMBER: 30,731
; REFERENCE/DOCKET NUMBER: 510-5747
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 503-8532
; TELEFAX: (201) 503-8807
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; STRANDEDNESS: single
; TOPOLogy: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= "2a
; OTHER INFORMATION: /note= "succinyl derivative"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= "2b
; OTHER INFORMATION: /note= "-p-nitro-anilide derivative"
; US-08-348-02BB-60

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 6
US-08-653-2
Sequence 2, Application US/086693653
; Sequence 2, Application US/086693653
; Patent No. 5780439
; GENERAL INFORMATION:
; APPLICANT: Meny, Francois
; APPLICANT: Kahn, Jean-Maurice
; APPLICANT: Roger, Loic
; TITLE OF INVENTION: Improvements in or relating to organic
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

RESULT 7
US-08-504-265B-60
Sequence 60, Application US/08504265B
; Sequence 60, Application US/08504265B
; Patent No. 5837516
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBTILISIN VARIANT CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: New Jersey
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: NJ07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/086693653
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/353,652
; FILING DATE:
; APPLICATION NUMBER: US 07/950,143
; FILING DATE: 13-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Battle, Carl
; REGISTRATION NUMBER: 30,731
; REFERENCE/DOCKET NUMBER: 510-5747
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 503-8532
; TELEFAX: (201) 503-8807
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; STRANDEDNESS: single
; TOPOLogy: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= "2a
; OTHER INFORMATION: /note= "succinyl derivative"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= "2b
; OTHER INFORMATION: /note= "-p-nitro-anilide derivative"
; US-08-653-2

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 7
US-08-504-265B-60
Sequence 60, Application US/08504265B
; Sequence 60, Application US/08504265B
; Patent No. 5837516
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBTILISIN VARIANT CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: New Jersey
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: NJ07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/086693653
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/353,652
; FILING DATE:
; APPLICATION NUMBER: US 07/950,143
; FILING DATE: 13-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Battle, Carl
; REGISTRATION NUMBER: 30,731
; REFERENCE/DOCKET NUMBER: 510-5747
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 503-8532
; TELEFAX: (201) 503-8807
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; STRANDEDNESS: single
; TOPOLogy: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= "2a
; OTHER INFORMATION: /note= "succinyl derivative"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= "2b
; OTHER INFORMATION: /note= "-p-nitro-anilide derivative"
; US-08-653-2

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504, 265B
FILING DATE: 19-JUL-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/925-8228
TELEFAX: 650/922-9881

INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-504-265B-60

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 8
US-08-025-321C-13
Sequence 13, Application US/08025321C
; Patent No. 5843560

GENERAL INFORMATION:
APPLICANT: Abraham Ph.D., Carmela R.
TITLE OF INVENTION: PROTEASES CRUSING ABNORMAL DEGRADATION
TITLE OF INVENTION: OF AMYLOID BETA-PROTEIN PRECURSOR
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Deveau, Colton & Marquis
STREET: Two Midtown Plaza, Suite 1400
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907, 840A
FILING DATE: 14-AUG-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184286
FILING DATE: 21-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Colton, Laurence C.
REGISTRATION NUMBER: 33371

REFERENCE/DOCKET NUMBER: 10733-175CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 875-3555
TELEFAX: (404) 875-8505

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
US-08-907-840A-1

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 9
US-08-907-840A-1
Sequence 1, Application US/08907840A
; Patent No. 5952307

GENERAL INFORMATION:
APPLICANT: Powers, James C.
TITLE OF INVENTION: Basic Alpha-Aminoalkylphosphonate
TITLE OF INVENTION: Derivatives
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEE: Deveau, Colton & Marquis
STREET: Two Midtown Plaza, Suite 1400
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907, 840A
FILING DATE: 14-AUG-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184286
FILING DATE: 21-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Colton, Laurence C.
REGISTRATION NUMBER: 33371

REFERENCE/DOCKET NUMBER: 10733-175CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 875-3555
TELEFAX: (404) 875-8505

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
US-08-907-840A-1

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 10
US-08-930-618-4
Sequence 4, Application US/08930618
; Patent No. 6087325
; GENERAL INFORMATION:

```

; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950.618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; US-08-950-618-4

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indexes 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 11
US 08-950-618-19
; Sequence 19, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; CURRENT APPLICATION NUMBER: US/08/950.618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE: 
; NAME/KY: BINDING
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal succinyl group
; US-08-950-618-32

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indexes 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 13
US-08-950-618-33
; Sequence 33, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950.618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE: 
; NAME/KY: BINDING
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal methoxy succinyl group
; US-08-950-618-19

Query Match 100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indexes 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 12
US-08-950-618-32

```

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 14
US-09-168-010-4
; Sequence 4, Application US/09168010A
; Patent No. 6143716
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; US-09-168-010-4

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 15
US 09-168-010-19
; Sequence 19, Application US/09168010A
; Patent No. 6143716
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 32
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal succinyl group
; US-09-168-010-32

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

RESULT 17
US-09-168-010-33
; Sequence 33, Application US/09168010A
; Patent No. 6143716
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal methoxy succinyl group
; US-09-168-010-19

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 1 AAPM 4

Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 1 AAPM 4

RESULT 18
 US-09-343-650-4
 Sequence 4, Application US/09343650
 Patent No. 6339069
 GENERAL INFORMATION:
 APPLICANT: The Liposome Company Inc.
 APPLICANT: Meers, Paul
 APPLICANT: Pak, Charles
 APPLICANT: Ali, Shaukat
 APPLICANT: Janoff, Andrew S.
 APPLICANT: Franklin, J. Craig
 APPLICANT: Erukulla, Ravi K.
 TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
 Title of Invention: Liposomal Drug Delivery
 FILE REFERENCE: TLC 215C
 CURRENT APPLICATION NUMBER: US/09/343, 650
 CURRENT FILING DATE: 1999-06-29
 EARLIER APPLICATION NUMBER: US 08/950, 618
 EARLIER FILING DATE: 1997-10-15
 SEQ ID NO: 44
 SOFTWARE: FASTSEQ for Windows Version 3.0
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Peptides
 US-09-343-650-4

Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 1 AAPM 4

RESULT 19
 US-09-343-650-19
 Sequence 19, Application US/09343650
 Patent No. 6339069
 GENERAL INFORMATION:
 APPLICANT: The Liposome Company Inc.
 APPLICANT: Meers, Paul
 APPLICANT: Pak, Charles
 APPLICANT: Ali, Shaukat
 APPLICANT: Janoff, Andrew S.
 APPLICANT: Franklin, J. Craig
 APPLICANT: Erukulla, Ravi K.
 APPLICANT: Meers, Paul
 APPLICANT: Pak, Charles
 APPLICANT: Ali, Shaukat
 APPLICANT: Janoff, Andrew S.
 APPLICANT: Franklin, J. Craig
 APPLICANT: Erukulla, Ravi K.
 TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
 Title of Invention: Liposomal Drug Delivery
 FILE REFERENCE: TLC 215C
 CURRENT APPLICATION NUMBER: US/09/343, 650
 CURRENT FILING DATE: 1999-06-29
 EARLIER APPLICATION NUMBER: US 08/950, 618
 EARLIER FILING DATE: 1997-10-15
 SEQ ID NO: 32
 SOFTWARE: FASTSEQ for Windows Version 3.0
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Peptides
 FEATURE:
 NAME/KEY: BINDING
 LOCATION: (1)..(1)
 OTHER INFORMATION: N-terminal succinyl group
 US-09-343-650-32

Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 1 AAPM 4

RESULT 21
 US-09-343-650-33
 Sequence 33, Application US/09343650
 Patent No. 6339069
 GENERAL INFORMATION:
 APPLICANT: The Liposome Company Inc.
 APPLICANT: Meers, Paul
 APPLICANT: Pak, Charles
 APPLICANT: Pak, Charles

APPLICANT: Ali, Shaukat
 APPLICANT: Janoff, Andrew S.
 APPLICANT: Franklin, J. Craig
 APPLICANT: Erukulla, Ravi K.
 APPLICANT: Cabral-Lilly, Donna
 TITLE OF INVENTION: Peptide-Lipid conjugates, Liposomes and
 NUMBER OF SEQ ID NOS: 44
 FILE REFERENCE: TLC 215C
 CURRENT APPLICATION NUMBER: US/09/343, 650
 CURRENT FILING DATE: 1999-06-29
 EARLIER APPLICATION NUMBER: US 08/250, 618
 EARLIER FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 33
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Peptides
 FEATURE:
 NAME/KEY: BINDING
 LOCATION: (1)..(1)
 OTHER INFORMATION: N-terminal carboxy sugar group
 US-09-343-650-33

RESULT 22
 US-09-578-303-11
 ; Sequence 11, Application US/09578303
 ; GENERAL INFORMATION:
 ; Patent No. 6395959
 ; APPLICANT: Trevis, James
 ; APPLICANT: Whitworth, S. Troy
 ; APPLICANT: Blum, Murray S.
 ; TITLE OF INVENTION: Ant Proteases and Methods of Inhibition
 ; FILE REFERENCE: 235.0010101
 ; CURRENT APPLICATION NUMBER: US/09/578, 303
 ; CURRENT FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/136, 331
 ; PRIOR FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 11
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: para-nitronanilide substrate
 ; NAME/KEY: SITE
 ; LOCATION: (1)
 ; OTHER INFORMATION: succinyl end cap
 ; NAME/KEY: SITE
 ; LOCATION: (4)
 ; OTHER INFORMATION: para-nitronanilide end cap
 ; OTHER INFORMATION: para-nitronanilide end cap
 ; US-09-578-303-11

Query Match 100.0%; Score 20; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 1 AAPM 4

RESULT 23
 US-08-988-842-5
 ; Sequence 5, Application US/08988842
 ; Patent No. 5462173
 ; GENERAL INFORMATION:
 ; APPLICANT: Lu, Jun Ping
 ; APPLICANT: Cantley, Lewis C.
 ; APPLICANT: Yaffe, Michael
 ; APPLICANT: Fischer, Gunter
 ; TITLE OF INVENTION: INHIBITORS OF PHOSPHOTREONINE AND
 ; FILE REFERENCE: BIDMC97-02PA
 ; CURRENT APPLICATION NUMBER: US/08/988, 842
 ; CURRENT FILING DATE: 1997-12-11
 ; EARLIER APPLICATION NUMBER: 60/058, 164
 ; EARLIER FILING DATE:
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 5
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: synthetic nucleotide
 ; FEATURE:
 ; NAME/KEY: PHOSPHORYLATION
 ; LOCATION: (5)..(5)
 ; US-08-988-842-5

Query Match 100.0%; Score 20; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 1 AAPM 4

RESULT 24
 5194596-23
 ; Patent No. 5194596
 ; APPLICANT: TISCHER, EDMUND G.; ABRHAM, JUDITH A.; FIDDES, JOHN
 ; C.; MITCHELL, RICHARD L.
 ; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
 ; GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 32
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/450, 883
 ; FILING DATE: 14-DEC-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 387, 745
 ; FILING DATE: 27-JUL-1989
 ; SEQ ID NO:23:
 ; LENGTH: 8
 ; 5194596-23

Query Match 100.0%; Score 20; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 4 AAPM 7

RESULT 25
 5219739-28
 ; Patent No. 5219739
 ; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
 ; JOHN C.; MITCHELL, RICHARD L.
 ; TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
 ; HVEGF121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
 ; VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
 ; NUMBER OF SEQUENCES: 40
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/559,041
 FILING DATE: 27-JUL-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 430,883
 FILING DATE: 14-DEC-1989
 APPLICATION NUMBER: 397,545
 FILING DATE: 27-JUL-1989
 SEQ ID NO: 28
 LENGTH: 8
 ; 5219739-28

Query Match 100.0%; Score 20; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 4 AAPM 7

RESULT 26
 US-09-188-930-136
 ; Sequence 136, Application US/09188930A
 ; Patent No. 6130502
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Siachan, Lorna
 ; APPLICANT: Siebecker, Mattew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Marison, James Greg
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; FILE REFERENCE: 11000_101C1
 ; CURRENT APPLICATION NUMBER: US/09/188,930A
 ; CURRENT FILING DATE: 1998-11-09
 ; NUMBER OF SEQ ID NOS: 348
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 136
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Rat

Query Match 100.0%; Score 20; DB 4; Length 106;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 4 AAPM 7

RESULT 27
 US-08-905-223-356
 ; Sequence 356, Application US/08905223
 ; Patent No. 6222029
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, Jean-Baptiste D.
 ; APPLICANT: Duetert, Aymeric
 ; APPLICANT: Lacroix, Bruno
 ; TITLE OF INVENTION: ESTS FOR SECRETED PROTEINS
 ; NUMBER OF SEQUENCES: 503
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Krobbe, Martens, Olson & Bear
 ; STREET: 501 West Broadway
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-3505
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: WInd95

Query Match 100.0%; Score 20; DB 4; Length 116;
 Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 29 AAPM 32

RESULT 29
 US-08-940-316-3
 ; Sequence 316, Application US/08840316
 ; Patent No. 6054567

SOFTWARE: Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/905,223
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned A.
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-0176
 TELEFAX: (619) 235-8550
 INFORMATION FOR SEQ ID NO: 336:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 110 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 ORIGINAL SOURCE:
 ORGANISM: Homo Sapiens
 TISSUE TYPE: Brain
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: -104..-1
 IDENTIFICATION METHOD: Von Heijne matrix
 OTHER INFORMATION: score 5.1
 OTHER INFORMATION: seq SSVASLITATPSLA/SP
 ; US-08-905-223-336

Query Match 100.0%; Score 20; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 71 AAPM 74

RESULT 28
 US-09-134-001C-3725
 ; Sequence 3725, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIORITY NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3725
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-3725

Query Match 100.0%; Score 20; DB 4; Length 116;
 Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 29 AAPM 32

GENERAL INFORMATION:

APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,

APPLICANT: Tsarev, Sergei A., and Robinson, Robin A.

TITLE OF INVENTION: Recombinant Proteins Of

TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08478, 507

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/279, 823

FILING DATE: 25-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/681, 078

FILING DATE: 05-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/505, 888

FILING DATE: 05-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/420, 921

FILING DATE: 13-OCT-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/367, 486

FILING DATE: 16-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/336, 672

FILING DATE: 11-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/208, 997

FILING DATE: 17-JUN-1988

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38, 615

REFERENCE/DOCKET NUMBER: 4600-0183.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 324-0880

TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-478-507-9

RESULT 30

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 30

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

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Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 123;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 7 AAPM 10

RESULT 31

Query Match

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,523
 FILING DATE: 28-MAY-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13102
 FILING DATE: 03-OCT-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US08/316,765
 FILING DATE: 03-OCT-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/947,263
 FILING DATE: 18-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Richard W. Bork
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4032US4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6549
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acid residues
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
; US-08-809-523-3

Query Match 100.0%; Score 20; DB 4; length 123;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Gaps 0;

QY	1 AAPM 4	1 1 1	Db	7 AAPM 10
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RESULT 32
 US-09-128-275A-9
 Sequence 9, Application US/09128275A
 Patent No. 6229005
 GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R
 APPLICANT: Yarbrough, Patrice O
 APPLICANT: Bradley, Daniel W
 APPLICANT: Krawczyński, Krzysztof Z
 APPLICANT: Tam, Albert
 APPLICANT: Fly, Kirk E
 TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dahlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/128-275A
 FILING DATE: 03-AUG-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/279,823
 FILING DATE: 25-JUL-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/681,078
 FILING DATE: 05-APR-1991

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/505,888
 FILING DATE: 05-APR-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/420,921
 FILING DATE: 13-OCT-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/367,486
 FILING DATE: 16-JUN-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/336,672
 FILING DATE: 11-APR-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/208,997
 FILING DATE: 17-JUN-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Peclitory, Joanne R.
 REGISTRATION NUMBER: 42,995
 REFERENCE/DOCKET NUMBER: 4600-0183-24
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0980
 TELEFAX: (650) 324-0960
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
; US-09-128-275A-9

MOLECULE TYPE: protein
; US-09-128-275A-9

Query Match 100.0%; Score 20; DB 4; length 123;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Gaps 0;

QY	1 AAPM 4	1 1 1	Db	7 AAPM 10
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RESULT 33
 US-08-471-971-3
 Sequence 3, Application US/08471971
 Patent No. 6207759
 GENERAL INFORMATION:
 APPLICANT: Tsarev, Sergei A.; Emerson, Suzanne U.; Purcell, Robert H.
 APPLICANT: Suzanne U.; Purcell, Robert H.
 TITLE OF INVENTION: Recombinant Proteins Of A Pakistani Strain Of Hepatitis E And Their
 TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEMAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,971
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US08/316,765
 FILING DATE: 03-OCT-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US07/947,263
 FILING DATE: 18-SEP-1992

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid residues
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLogy: unknown
; US-08-471-971-3

Query Match, Best Local Similarity 100.0%; Score 20; DB 4; Length 123;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPM 4
Db 7 AAPM 10

RESULT 34
US-09-553-427-9
; Sequence 9, Application US/09553427
; Patent No. 6379891
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Patricia O
APPLICANT: Bradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
NUMBER OF INVENTION: NO. 6379891-A/NO. 6379891-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/553,427
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672

Query Match, Best Local Similarity 100.0%; Score 20; DB 4; Length 123;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPM 4
Db 7 AAPM 10

RESULT 34
US-09-553-427-9
; Sequence 9, Application US/09553427
; Patent No. 6379891
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Patricia O
APPLICANT: Bradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
NUMBER OF INVENTION: NO. 6379891-A/NO. 6379891-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/553,427
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672

RESULT 35
US-09-462-606-13
; Sequence 13, Application US/09462606
; Patent No. 64,324,08
GENERAL INFORMATION:
APPLICANT: Meng, Xiang-Jin
APPLICANT: Emeison, Suzanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
FILE REFERENCE: 2026426701
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 60/053069
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: PCT/US98/14665
PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 123
TYPE: PRT
ORGANISM: Hepatitis E virus
; US-09-462-606-13

Query Match, Best Local Similarity 100.0%; Score 20; DB 4; Length 123;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPM 4
Db 7 AAPM 10

RESULT 36
US-09-462-606-58
; Sequence 58, Application US/09462606
; Patent No. 64,324,08
GENERAL INFORMATION:
APPLICANT: Meng, Xiang-Jin
APPLICANT: Emeison, Suzanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
FILE REFERENCE: 2026426701
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-06-12

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; LENGTH: 123
; TYPE: PRT
; ORGANISM: Hepatitis E virus
; US-09-462-606-60

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 123;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 7 AAPM 10

RESULT 37
US-09-462-606-59
; Sequence 59, Application US/09462606
; Patent No. 6432408
; GENERAL INFORMATION:
; APPLICANT: Meng, Xiang-Jin
; APPLICANT: Emerson, Suzanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
; FILE REFERENCE: 20264267US1
; CURRENT APPLICATION NUMBER: US/09/462,606
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 60/053069
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/14665
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Hepatitis E virus
; US-09-462-606-59

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 123;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 7 AAPM 10

RESULT 39
US-09-462-606-61
; Sequence 61, Application US/09462606
; Patent No. 6432408
; GENERAL INFORMATION:
; APPLICANT: Meng, Xiang-Jin
; APPLICANT: Emerson, Suzanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
; FILE REFERENCE: 20264267US1
; CURRENT APPLICATION NUMBER: US/09/462,606
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 60/053069
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/14665
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Hepatitis E virus
; US-09-462-606-61

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 123;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 7 AAPM 10

RESULT 40
US-09-462-606-62
; Sequence 62, Application US/09462606
; Patent No. 6432408
; GENERAL INFORMATION:
; APPLICANT: Meng, Xiang-Jin
; APPLICANT: Emerson, Suzanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
; FILE REFERENCE: 20264267US1
; CURRENT APPLICATION NUMBER: US/09/462,606
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 60/053069
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/14665
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Hepatitis E virus
; US-09-462-606-62

Query Match
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 7 AAPM 10

RESULT 38
US-09-462-606-60
; Sequence 60, Application US/09462606
; Patent No. 6432408
; GENERAL INFORMATION:
; APPLICANT: Meng, Xiang-Jin
; APPLICANT: Emerson, Suzanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
; FILE REFERENCE: 20264267US1
; CURRENT APPLICATION NUMBER: US/09/462,606
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 60/053069
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/14665
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Hepatitis E virus
; US-09-462-606-60

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 123;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 7 AAPM 10

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Fri Dec 6 14:08:53 2002

us-10-033-526-2.mod.rai

Page 14

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Db	7	AAPM 10							

Search completed: December 6, 2002, 13:31:50
Job time : 9.3333 secs

Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 13:30:14 ; Search time 4.88889 Seconds
 (without alignments)
 13.289 Million cell updates/sec

Title: US-10-033-526-2
 perfect score: 20
 Sequence: 1 AAMP 4

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues
 Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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 2: /cgn2_6/ptodata/1/pupbaa/PCT_NEW_PUB_pep: *
 3: /cgn2_6/ptodata/1/pupbaa/US06_NEW_PUB_pep: *
 4: /cgn2_6/ptodata/1/pupbaa/US06_PUBCOMB_pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

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2	20	100.0	31	10	US-09-864-761-48187 Sequence 48187, A
3	20	100.0	85	10	US-09-867-550-500 Sequence 500, App
4	20	100.0	112	10	US-09-867-869-939 Sequence 939, App
5	20	100.0	117	10	US-09-764-1182 Sequence 1182, Ap
6	20	100.0	120	10	US-09-764-265-21 Sequence 21, Appli
7	20	100.0	124	10	US-09-864-761-44327 Sequence 44327, A
8	20	100.0	124	10	US-09-769-066-221 Sequence 21, Appli
9	20	100.0	126	10	US-09-815-242-922 Sequence 4902, Ap
10	20	100.0	127	10	US-09-815-242-0542 Sequence 10542, Ap
11	20	100.0	128	10	US-09-864-761-3702 Sequence 43702, A
12	20	100.0	128	10	US-09-815-242-13224 Sequence 13224, A
13	20	100.0	132	10	US-09-815-242-13224 Sequence 36620, A
14	20	100.0	136	10	US-09-864-761-36620 Sequence 36620, A
15	20	100.0	156	10	US-09-815-242-10329 Sequence 10329, A
16	20	100.0	156	10	US-09-815-242-13886 Sequence 13886, A
17	20	100.0	171	10	US-09-812-133-2 Sequence 2, Appli
18	20	100.0	191	9	US-09-870-759-122 Sequence 152, Appli
19	20	100.0	191	10	US-09-349-954-2 Sequence 2, Appli

RESULT	1	US-10-033-526-2
;	;	Sequence 1, Application US/10033526
;	;	; Sequence 2, Application US/10033526
;	;	; Patent No. US20020147999A1
;	;	; GENERAL INFORMATION:
;	;	; APPLICANT: Robert W. Mahley
;	;	; TIME OF INVENTION: Methods of Treating Disorders Related to
;	;	; TIME OF INVENTION: APOE
;	;	; FILE REFERENCE: UCAL217
;	;	; CURRENT APPLICATION NUMBER: US/10/033,526
;	;	; CURRENT FILING DATE: 2001-11-02
;	;	; PRIORITY APPLICATION NUMBER: 60/245,737
;	;	; PRIORITY FILING DATE: 2000-11-03
;	;	; NUMBER OF SEQ ID NOS: 4
;	;	; SOFTWARE: FASTSEQ for Windows Version 4.0
;	;	; SEQ ID NO: 2
;	;	; LENGTH: 4
;	;	; TYPE: PRT
;	;	; ORGANISM: Artificial Sequence
;	;	; FEATURE: OTHER INFORMATION: synthetic peptide
;	;	US-10-033-526-2
;	;	Query Match 100.0%; Score 20; DB 12; Length 4;
;	;	Best Local Similarity 100.0%; Score: 20; DB: 12; Length: 4;
;	;	Matches 4; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	AAMP 4
Db	1	AAMP 4
;	;	RESULT 2
;	;	US-09-864-761-48187
;	;	; Sequence 48187, Application US/09864761
;	;	; Patent No. US2002048763A1
;	;	; GENERAL INFORMATION:
;	;	; APPLICANT: Penn, Sharron G.
;	;	; APPLICANT: Rank, David R.
;	;	; APPLICANT: Hanzel, David K.
;	;	; APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Aeonica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,751
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/235,359
 PRIOR FILING DATE: 2000-03-27
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
 SEQ ID NO 48187
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL021707.2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
 OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.5
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
 US-09-864-761-48187

RESULT 3
 US-09-867-550-500
 ; Sequence 500, Application US/09867550
 ;
 GENERAL INFORMATION:
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Mehraban, Firdaus
 ; APPLICANT: Conley, Pamela
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Topper, James

Qy 1 AAPM 4
 |||||
 Db 14 AAPM 17

Query Match 100.0%; Score 20; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 |||||
 Db 3 AAPM 6

Query Match 100.0%; Score 20; DB 10; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 |||||
 Db 3 AAPM 6

RESULT 5
 US-09-764-864-1182
 ; Sequence 1182, Application US/09764864
 ;
 GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PTZ23
 ; CURRENT APPLICATION NUMBER: US/09/774,864
 ; CURRENT FILING DATE: 2001-01-17

Query Match 100.0%; Score 20; DB 10; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 |||||
 Db 44 AAPM 47

RESULT 4
 US-09-764-869-939
 ; Sequence 939, Application US/09764869
 ; Patent No. US2002061521A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC007
 ; CURRENT APPLICATION NUMBER: US/09/774,869
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 2442
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 939
 ; LENGTH: 112
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (44)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (63)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-764-869-939

Query Match 100.0%; Score 20; DB 10; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Prior application data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 1792
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1182
 LENGTH: 117
 TYPE: prn
 ORGANISM: Homo sapiens
 FEATURE: SITE
 NAME/KEY: SITE
 LOCATION: (22)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (23)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (93)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (116)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 ; US-09-764-864-1182

Query Match 100.0%; Score 20; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 34 AAPM 37

RESULT 6
 US-09-917-265-21
 ; Sequence 21, Application US/09917265
 ; Patent No. US2002020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wondering, Ramani S.
 ; BOROUGH, Karen L.
 ; TITLE OF INVENTION: CANINE AND FELLINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREIN
 ; FILE REFERENCE: IM-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/223,016
 ; PRIOR FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 21
 ; LENGTH: 120
 ; TYPE: prn
 ; ORGANISM: Felis catus
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (473); (473)
 ; OTHER INFORMATION: n = unknown at position 473
 ; US-09-917-265-21

Query Match 100.0%; Score 20; DB 10; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 9 AAPM 12

RESULT 7
 US-09-864-761-44327
 ; Sequence 44327, Application US/09864761
 ; Patent No. US2002020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rank, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.

Query Match 100.0%; Score 20; DB 10; Length 124;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 Db 119 AAPM 122

RESULT 8
 US-09-169-066-21
 ; Sequence 21, Application US/09769066
 ; Patent No. US20020107360A1

GENERAL INFORMATION:

APPLICANT: Fuerst, Thomas R.

McAtee, C. Patrick

Yarbough, Patrice O.

Zhang, Yifan

TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/769,066

FILING DATE: 24-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/542,634

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid

STRANDEDNESS: Hepatitis E Virus (Mexico Strain)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid

STRANDEDNESS: Hepatitis E Virus (Mexico Strain)

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

RESULT 9
US-09-769-066-21Query Match 100.0%; Score 20; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 AAPM 4
Dy 7 AAPM 10RESULT 10
US-09-815-242-4902
Sequence 4902, Application US/09815242
patent No. US20030061569A1

GENERAL INFORMATION:

APPLICANT: Haselebeck, Robert

APPLICANT: Ohlssen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Travick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes In

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIORITY FILING DATE: 2001-03-21

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

RESULT 9
US-09-769-066-22
Query Match 100.0%; Score 20; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 AAPM 4
Db 7 AAPM 10RESULT 10
US-09-815-242-4902
Sequence 4902, Application US/09815242
patent No. US20030061569A1

GENERAL INFORMATION:

APPLICANT: Haselebeck, Robert

APPLICANT: Ohlssen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Travick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes In

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIORITY FILING DATE: 2001-03-21

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

RESULT 9
US-09-769-066-21
Query Match 100.0%; Score 20; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 AAPM 4
Dy 7 AAPM 10RESULT 10
US-09-815-242-4902
Sequence 4902, Application US/09815242
patent No. US20030061569A1

GENERAL INFORMATION:

APPLICANT: Haselebeck, Robert

APPLICANT: Ohlssen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Travick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes In

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIORITY FILING DATE: 2001-03-21

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

RESULT 9
US-09-769-066-22
Query Match 100.0%; Score 20; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 AAPM 4
Dy 7 AAPM 10RESULT 10
US-09-815-242-4902
Sequence 4902, Application US/09815242
patent No. US20030061569A1

GENERAL INFORMATION:

APPLICANT: Haselebeck, Robert

APPLICANT: Ohlssen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Travick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes In

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIORITY FILING DATE: 2001-03-21

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

RESULT 9
US-09-769-066-21
Query Match 100.0%; Score 20; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 AAPM 4
Dy 7 AAPM 10RESULT 10
US-09-815-242-4902
Sequence 4902, Application US/09815242
patent No. US20030061569A1

GENERAL INFORMATION:

APPLICANT: Haselebeck, Robert

APPLICANT: Ohlssen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Travick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes In

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIORITY FILING DATE: 2001-03-21

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

RESULT 9
US-09-769-066-22
Query Match 100.0%; Score 20; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 AAPM 4
Dy 7 AAPM 10RESULT 10
US-09-815-242-4902
Sequence 4902, Application US/09815242
patent No. US20030061569A1

GENERAL INFORMATION:

APPLICANT: Haselebeck, Robert

APPLICANT: Ohlssen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Travick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes In

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIORITY FILING DATE: 2001-03-21

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2000-07-23

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 4902
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-815-242-4902

Query Match 100.0%; Score 20; DB 10; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPM 4
Db 117 AAPM 120

RESULT 11
US-09-815-242-10542
Sequence 10542, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: BLITRA_01A
; CURRENT APPLICATION NUMBER: US/09/815, 242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191, 078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SEQ ID NO: 10542
; SOFTWARE: FASTSEQ for Windows Version 4.0
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-815-242-10542

Query Match 100.0%; Score 20; DB 10; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPM 4
Db 117 AAPM 120

RESULT 12
US-09-864-761-43702
; Sequence 43702, Application US/09864761
; Patent No. US20020048703A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.

APPLICANT: Hanszel, David K.
; APPLICANT: Chen, Weishang
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CURRENT APPLICATION NUMBER: US/09/864,761
; FILE REFERENCE: Aeonica-X-1
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263, 6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608, 408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Animax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 43702
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003693.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW HIT: AA41611.1, EVALUE 1.90e+00
; US-09-864-761-43702

Query Match 100.0%; Score 20; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPM 4
Db 123 AAPM 126

RESULT 13
US-09-815-242-13224
; Sequence 13224, Application US/09815242
; Patent No. US20020061569A1

GENERAL INFORMATION:
 APPLICANT: Hasebeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITRA.01A

CURRENT APPLICATION NUMBER: US/09/815, 242

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206, 848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242, 578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257, 931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269, 308

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSSO for Windows Version 4.0

SEQ ID NO: 13224

LENGTH: 128

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-815-242-13224

Query Match 100.0%; Score 20; DB 10; Length 128;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 ||||
 Db 119 AAPM 122

RESULT 14

US 09-864-761-36620

Sequence 30620, Application US/09864761

PATENT NO. US20020041763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wansheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeonica-X-1

CURRENT APPLICATION NUMBER: US/09/864, 761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180, 312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632, 366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263, 6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236, 359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

RESULT 15

US-09-815-242-10329

Sequence 10329, Application US/09815242

PATENT NO. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Hasebeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITRA.01A

CURRENT APPLICATION NUMBER: US/09/815, 242

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR FILING DATE: 2000-03-21

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; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 10329
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-815-242-10329

Query Match 100.0%; Score 20; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 49 AAPM 52

RESULT 16
; Sequence 13886, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Title of Invention: Prokaryotes
; FILE REFERENCE: ELITRA.01IA
; CURRENT APPLICATION NUMBER: US/09/815, 242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191, 078
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/259, 308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 13886
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Salmonella typhi
; US-09-815-242-13886

Query Match 100.0%; Score 20; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 49 AAPM 52

RESULT 17
; Sequence 2, Application US/09812133
; Patent No. US20020061240A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Kenneth A., Jr.
; APPLICANT: Kendall, Richard L.
; APPLICANT: Bett, Andrew J.
; APPLICANT: Huckle, William R.
; TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF
; Title of Invention: ANGIOGENESIS
; FILE REFERENCE: 20013P
; CURRENT APPLICATION NUMBER: US/09/812,133
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: PCT/US88/22668
; PRIOR FILING DATE: 1988-10-23
; PRIOR APPLICATION NUMBER: 60/063, 629
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Human
; US-09-812-133-2

Query Match 100.0%; Score 20; DB 10; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 26 AAPM 29

RESULT 18
; Sequence 122, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 122
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-870-759-122

Query Match 100.0%; Score 20; DB 9; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 26 AAPM 29

RESULT 19
; Sequence 2, Application US/09349954A
; Patent No. US20020019027A1

```

GENERAL INFORMATION:
 ; APPLICANT: Hayward, Nicholas K.
 ; APPLICANT: Weber, Gunther
 ; APPLICANT: Grimmond, Sean
 ; APPLICANT: Larson, Catharina
 TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
 FILE REFERENCE: Dav. Col. Cave
 CURRENT APPLICATION NUMBER: US/09/349, 954A
 CURRENT FILING DATE: 1995-07-08
 PRIOR APPLICATION NUMBER: 08/765, 588
 PRIOR FILING DATE: 1996-02-22
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 191
 TYPE: PRT
 ORGANISM: Nucleotide Sequence of VEGF165
 ; US-09-349-954A-2

Query Match Similarity 100.0%; Score 20; DB 10; Length 191;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 26 AAPM 29

RESULT 20
 US-09-932-451A-2
 ; Sequence 2, Application US/09932451A
 ; PATENT NO. US2002011324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OZAWA, Keiya
 ; APPLICANT: SHIMPO, Masahisa
 ; APPLICANT: IKEDA, Uichi
 ; APPLICANT: SHIMADA, Kazuyuki
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-MEDIATED DELIVERY OF ANGIOGENIC
 ; TITLE OF INVENTION: FACTORS
 ; FILE REFERENCE: 0800-0026
 ; CURRENT APPLICATION NUMBER: US/09/932, 451A
 ; CURRENT FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/226, 056
 ; PRIOR FILING DATE: 2000-08-17
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 2
 ; LENGTH: 191
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-165
 ; US-09-932-451A-2

Query Match Similarity 100.0%; Score 20; DB 10; Length 191;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 26 AAPM 29

RESULT 21
 US-09-907-007-2
 ; Sequence 2, Application US/09907007
 ; PATENT NO. US20020143395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harvard, Nicholas K.
 ; APPLICANT: Weber, Gunther

RESULT 22
 US-09-795-006A-2
 ; Sequence 2, Application US/09795006A
 ; PATENT NO. US20020151680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALITALO, et al
 ; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
 ; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
 ; FILE REFERENCE: 28967/3597B
 ; CURRENT APPLICATION NUMBER: US/09/795, 006A
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: US 60/205, 331
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 60/185, 205
 ; PRIOR FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 191
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-795-006A-2

Query Match Similarity 100.0%; Score 20; DB 10; Length 191;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 26 AAPM 29

RESULT 23
 US-09-832-209A-8
 ; Sequence 8, Application US/09852209A
 ; PATENT NO. US20020164687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ERIKSSON, Ulf
 ; APPLICANT: AASE, Karin
 ; APPLICANT: LEE, Xuri
 ; APPLICANT: PONTEN, Annica
 ; APPLICANT: UUTELA, Marko
 ; APPLICANT: ALITALO, Kari
 ; APPLICANT: OESTMAN, Arne
 ; APPLICANT: HEIJLIN, Carl-Henrik
 ; APPLICANT: BETSHOLTZ, Christo

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
 TITLE OF INVENTION: THEREFOR, AND USES THEREOF
 FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
 CURRENT APPLICATION NUMBER: US/09/852,209A
 CURRENT FILING DATE: 2001-05-10
 PRIORITY APPLICATION NUMBER: 09/410,349
 PRIORITY FILING DATE: 1999-09-30
 PRIORITY APPLICATION NUMBER: 60/110,749
 PRIORITY FILING DATE: 1998-12-03
 PRIORITY APPLICATION NUMBER: 60/113,002
 PRIORITY FILING DATE: 1998-12-18
 PRIORITY APPLICATION NUMBER: 60/135,426
 PRIORITY FILING DATE: 1999-05-21
 PRIORITY APPLICATION NUMBER: 60/144,022
 PRIORITY FILING DATE: 1999-07-15
 NUMBER OF SEQ ID NOS.: 39
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 8
 LENGTH: 192
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-852-209A-8

Query Match 100.0%; Score 20; DB 9; Length 192;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 APM 4
 Db 26 APM 29

RESULT: 24

US-09-992-598-401

; Sequence 401, Application US/09992598
 ; Patent No. US20020160384A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Bozstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerbertsen, Marc E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Guiney, Austin L.
 ; APPLICANT: Kijavil, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watatabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ;
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C20
 ; CURRENT APPLICATION NUMBER: US/09/992,598
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIORITY APPLICATION NUMBER: 60/049787
 ; PRIORITY FILING DATE: 1997-06-16
 ; PRIORITY APPLICATION NUMBER: 60/062250
 ; PRIORITY FILING DATE: 1997-10-17
 ; PRIORITY APPLICATION NUMBER: 60/065186
 ; PRIORITY FILING DATE: 1997-11-12
 ; PRIORITY APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/0666770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088126
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088229
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088255
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088905
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/088940
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089112
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089314
 PRIOR FILING DATE: 1998-06-16


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PRIORITY APPLICATION NUMBER: 60/091633
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091978
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/091982
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/092182
PRIORITY FILING DATE: 1998-07-09

Query Match Similarity Score 20; DB 9; Length 198;
Best Local 100%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAPM 4
Db      21 AAPM 24

RESULT 26
US-09-989-722-401
Sequence 401, Application US/09989722
Patent No. US2002007067A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Destroyes, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-03
PRIORITY APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-05
PRIORITY APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIORITY APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIORITY APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIORITY APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIORITY APPLICATION NUMBER: 60/088226
PRIOR FILING DATE: 1998-06-09
PRIORITY APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIORITY APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIORITY APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIORITY APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIORITY APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIORITY APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIORITY APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIORITY APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIORITY APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIORITY APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIORITY APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIORITY APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIORITY APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIORITY APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIORITY APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIORITY APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIORITY APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIORITY APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIORITY APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIORITY APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18

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PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-05-04
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PRIOR FILING DATE: 1998-05-04
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PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-05-04
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Query Match 100.0%; Score 20; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence	401, Application US/09989279
PATENT NO.	US20020077496A1
GENERAL INFORMATION:	
APPLICANT:	Ashkenazi, Avi J.
APPLICANT:	Baker, Kevin P.
APPLICANT:	Botsstein, David
APPLICANT:	Desnoyers, Luc
APPLICANT:	Barton, Dan L.
APPLICANT:	Rerar, Napoleone
APPLICANT:	Fong, Sherman
APPLICANT:	Gerbier, Hans Peter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Kljavin, Ivar J.
APPLICANT:	Napier, Mary A.
APPLICANT:	Pan, James
APPLICANT:	Paon, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunes, Daniel
APPLICANT:	Watanae, Colin K.
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William T.
APPLICANT:	Zemlin, Zenin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
FILE REFERENCE: P2730F1C6	
CURRENT APPLICATION NUMBER:	US/09/989,279
CURRENT FILING DATE:	2001-11-19
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PRIOR FILING DATE:	1997-06-16
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PATENT NO. US2003007249A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeier
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: K-Javvin, Tavar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C65
 CURRENT APPLICATION NUMBER: US09/989,727
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
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Query Match 100.0%; Score 20; DB 10; Length 198;
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RESULT 30
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Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      21 APM 24
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APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Naylor, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paon, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William T.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2710P1C70

CURRENT APPLICATION NUMBER: US/09/989,731

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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 20; DB 10; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 AAPM 4
 QY 21 AAPM 24
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RESULT 31
 US-09-889-732-401.
 ; Sequence 401 Application US/09989732
 ; Patent No. US002012353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyes, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Andrej
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
 APPLICANT: Klaavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Marguerite Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumeis, Daniel
 APPLICANT: Watnabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2710P1C57
 CURRENT APPLICATION NUMBER: US/09/989,732
 CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 20; DB 10; Length 198;
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Indels 0; Gaps 0;

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; Patent No. US2002127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boiststein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
 APPLICANT: Watansabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730FIC15
 CURRENT APPLICATION NUMBER: US/09/991,073
 CURRENT FILING DATE: 2001-11-14
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; APPLICANT: Ashkenazi Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bottstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watnabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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TITLE OF INVENTION: Acids Encoding the Same

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; PRIOR FILING DATE: 1998-07-09

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Db          111
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; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurley, Austin L.
; APPLICANT: Kijaviv, Var J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watansabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Zhai, Zemin
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 20; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0;
Matches   4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy      1  AAMP 4
Db      21  AAMP 24

RESULT 35

US-09-93-604-401
; Sequence 401 Application US/09993604
; Patent No. US0020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KjJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watansabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.

APPLICANT: Zhang, Zenin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C25
; CURRENT APPLICATION NUMBER: US/09/993, 604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-06-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-06-17

; PRIOR FILING DATE: 1998-02-25
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091549
PRIOR FILING DATE: 1998-05-07

Qy 1 AAPM 4

Db	21 AAPM 24
RESULT 36	
US-09-990-456-401	
; Sequence 401, Application US/09990456	
; Patent No. US20020137890A1	
; GENERAL INFORMATION:	
; APPLICANT: Ashkenazi, Avi J.	
; APPLICANT: Baker, Kevin P.	
; APPLICANT: Botstein, David	
; APPLICANT: Destroyers, Luc	
; APPLICANT: Eaton, Dan L.	
; APPLICANT: Ferrara, Napoleone	
; APPLICANT: Fong, Sherman	
; APPLICANT: Gerber, Hans Peter	
; APPLICANT: Gerritsen, Mary E.	
; APPLICANT: Goddard, Audrey	
; APPLICANT: Godowski, Paul J.	
; APPLICANT: Grimaldi, J. Christopher	
; APPLICANT: Gurley, Austin L.	
; APPLICANT: Kjellvin, Ivar J.	
; APPLICANT: Napier, Mary A.	
; APPLICANT: Pan, James	
; APPLICANT: Paon, Nicholas F.	
; APPLICANT: Roy, Margaret Ann	
; APPLICANT: Steeart, Timothy A.	
; APPLICANT: Tumas, Daniel	
; APPLICANT: Waranabe, Colin K.	
; APPLICANT: Williams, P. Mickey	
; APPLICANT: Wood, William T.	
; APPLICANT: Zhang, Zemin	
TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic	
FILE REFERENCE: P2730P1C22	
CURRENT APPLICATION NUMBER: US/09/990456	
CURRENT FILING DATE: 2001-11-14	
PRIOR APPLICATION NUMBER: 60/049787	
PRIOR FILING DATE: 1997-06-16	
PRIOR APPLICATION NUMBER: 60/062250	
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PRIOR APPLICATION NUMBER: 60/066770	
PRIOR FILING DATE: 1997-11-24	
PRIOR APPLICATION NUMBER: 60/075945	
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PRIOR APPLICATION NUMBER: 60/078910	
PRIOR FILING DATE: 1998-03-20	
PRIOR APPLICATION NUMBER: 60/083322	
PRIOR FILING DATE: 1998-04-28	
PRIOR APPLICATION NUMBER: 60/084600	
PRIOR FILING DATE: 1998-05-07	


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; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091549
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 20; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Gaps 0;

RESULT 38
US-09-244-694-3
; Sequence 3, Application US/09244694
; Patent No. US20020026037A1
; GENERAL INFORMATION:
; APPLICANT: HU, Jing Shan S.
; APPLICANT: Olsen, Henrik A.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 3
; FILE REFERENCE: 1998-10-0003
; CURRENT APPLICATION NUMBER: US/09/244,694
; CURRENT FILING DATE: 1998-02-10
; EARLIER APPLICATION NUMBER: US 09/132,088
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: US 09/033,662
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: US 08/469,641
; EARLIER FILING DATE: 1998-06-06
; NUMBER OF SEQ ID NOS.: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-694-3

Query Match 100.0%; Score 20; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Gaps 0;
Indels 0; Gaps 0;

QY      1  AAPM 4
Db      21  AAPM 24

RESULT 39
US-09-291-299A-8
; Sequence 8, Application US/09291299A
; Patent No. US20030074405A1
; GENERAL INFORMATION:
; APPLICANT: YONG, Xie
; TITLE OF INVENTION: Antigenized Antibody Vaccine for Foot-and-Mouth Disease
; FILE REFERENCE: 09/291,299
; CURRENT APPLICATION NUMBER: US/09/291,299A
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS.: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-291-299A-8

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Matches 4; Conservative 0; Gaps 0;
Indels 0; Gaps 0;

QY      1  AAPM 4
Db      115  AAPM 118

RESULT 40
US-09-299-967
; Sequence 967, Application US/09925299
; Patent No. US2002005627A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1536
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 967
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-967

Query Match 100.0%; Score 20; DB 10; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPM	4
Db	48	AAPM	51

Search completed: December 6, 2002, 13:42:06
Job time : 5.88889 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 13:25:59 ; Search time 10.2222 Seconds

Perfect score: 1 AAFM 4
Sequence: 37.618 Million cell updates/sec

Title: US-10-033-526-2

Scoring table: BL0SPM62
Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73;*: 1; pir1;*
2; pir2;*
3; pir3;*
4; pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	41	1 B40236	structural protein
2	20	100.0	60	1 H3NJUJ	cytotoxin 1 - cobr
3	20	100.0	60	1 H3NJUJ	hypothetical prote
4	20	100.0	79	1 T30118	probable transcri
5	20	100.0	83	2 H95974	hypothetical prote
6	20	100.0	83	2 F97400	proteinase inhibit
7	20	100.0	102	1 TISYD2	hypothetical prote
8	20	100.0	105	2 T36139	hypothetical prote
9	20	100.0	105	2 D75580	acetyl-CoA acetyl
10	20	100.0	106	2 G97841	hypothetical prote
11	20	100.0	106	2 C97505	conserved hypothet
12	20	100.0	108	2 AD2794	hypothetical prote
13	20	100.0	109	2 F82556	hypothetical prote
14	20	100.0	121	2 T22303	hypothetical prote
15	20	100.0	121	2 D75584	structural protein
16	20	100.0	123	1 VHWHHE	Residues: 1-160 <L00>
17	20	100.0	123	1 C44212	Röttig, G.; Steinmetz, W.E.; Bougis, P.E.; Rochat, H.; Wuethrich, K.
18	20	100.0	126	2 C86883	Eur. J. Biochem. 168, 609-620, 1987
19	20	100.0	128	2 H95027	A;Title: Sequence-specific ¹ H-NMR assignments and determination of the secondary st
20	20	100.0	128	2 H97838	A;Reference number: S02517; PMID: 88029481; PMID: 822421
21	20	100.0	130	2 T06394	A;Contents: annotation; solution structure by NMR
22	20	100.0	131	2 AC0717	C;Superfamily: snake toxin
23	20	100.0	133	2 F75544	C;Keywords: cytotoxin
24	20	100.0	133	2 D87701	F;3-21,14-38,42-53,54-59/Disulfide bonds: #status predicted
25	20	100.0	140	2 T01170	Query Match
26	20	100.0	142	2 G64952	best Local Similarity 100.0%; Pred. No. 1.3e-02; Matches 4; Conservative 0;
27	20	100.0	142	2 C90954	Indels 0; Gaps 0;
28	20	100.0	142	2 H85802	polyketide cyclase
29	20	100.0	146	2 H57956	ribozyme

30	20	100.0	147	2 AG3578	hypothetical prote
31	20	100.0	152	2 G98370	tolR protein (tolR)
32	20	100.0	152	2 AH3013	tolR protein (imp)
33	20	100.0	152	2 C75544	hypothetical prote
34	20	100.0	154	2 T06396	isoprenylated prot
35	20	100.0	156	1 BK8C9	acetyl-CoA carboxy
36	20	100.0	156	2 T49921	ribosomal protein-1
37	20	100.0	156	2 C85890	acetyl-CoA carboxy
38	20	100.0	156	2 G91144	acetyl-CoA carboxy
39	20	100.0	156	2 AH0312	biotin carboxyl ca
40	20	100.0	159	2 D87658	hypothetical prote
41	20	100.0	159	2 A82219	transcription regu
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44	20	100.0	170	2 G86300	L10 ribosomal prot
45	20	100.0	171	2 S35248	nifQ protein - Ent

ALIGNMENTS

RESULT 1

B40236 structural protein 1 - hepatitis E virus (strain Indian)

C;Species: hepatitis E virus

C;Accession: B40236 R;Ray, R.; Jameel, S.; Manivel, V.; Ray, R.

Virology 189, 359-362, 1992

A;Title: Indian hepatitis E virus shows a major deletion in the small open reading fr

A;Reference number: A40236; MUID:92295577; PMID:1534953

A;Accession: A40236

A;Molecule type: genomic RNA

A;Residues: 1-41 <RA>

C;Superfamily: hepatitis E virus structural protein 1

C;Keywords: structural protein

QY	1 AAFM 4	1111
Db	7 AAFM 10	1111

RESULT 2

H3NJUJ cytotoxin 1 - Mozambique cobra (tentative sequence)

N;Alternate names: cardiotoxin gamma; cardiotoxin XIIb; cytotoxin XIIb

C;Species: Naja mossambica mossambica (Mozambique cobra)

C;Accession: A30050; A01728; S02517

R;Low, A.I.

Biochim. Biophys. Acta 336, 481-495, 1974

A;Title: Snake venom toxins. The amino acid sequences of three cytotoxin homologues f

A;Reference number: A01728

A;Accession: A30050

A;Molecule type: protein

A;Residues: 1-160 <L00>

R;Orting, G.; Steinmetz, W.E.; Bougis, P.E.; Rochat, H.; Wuethrich, K.

Eur. J. Biochem. 168, 609-620, 1987

A;Title: Sequence-specific ¹H-NMR assignments and determination of the secondary st

A;Reference number: S02517; PMID: 88029481; PMID: 822421

A;Contents: annotation; solution structure by NMR

C;Superfamily: snake toxin

C;Keywords: cytotoxin

F;3-21,14-38,42-53,54-59/Disulfide bonds: #status predicted

QY 1 AAPM 4
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 Db 28 AAPM 31

RESULT 3
 H3N1B
 cytotoxin 1 - cobra (Naja mossambica pallida) (tentative sequence)
 N;Alternate names: cardiotoxin gamma
 C;Species: Naja mossambica pallida
 C;Dbat: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Mar-2000
 C;Accession: A37578; A01728
 R;Pfroklund, L.; Baker, D.
 Biochemistry 14, 2065-2071, 1975
 A;Title: The complete covalent structure of a cardiotoxin from the venom of Naja nigricollis
 A;Reference number: A37578; MUID:75205552; PMID:1148181
 A;Molecule type: protein
 A;Residues: 1-60 <FR>
 C;Superfamily: snake toxin
 C;Keywords: cytotoxin; hemolysis
 F;3-21,14-38,42-53,54-59/Disulfide bonds: #status experimental

Query Match 100.0%; Score 20; DB 1; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 |||||
 Db 28 AAPM 31

RESULT 4
 T30118
 hypothetical protein F22H10.3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Dbat: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 R;Langston, Y.; Hawkins, J.
 submitted to the EMBL Data Library, September 1996
 A;Reference number: Z20740
 A;Accession: T30118
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-79 <LAN>
 A;Experimental source: EMBL:U70845; PIDN:AKB0098.1; GSDB:GN00028; CESP:F22H10.3
 C;Genetics:
 A;Gene: CESP:F22H10.3
 A;Map position: X

Query Match 100.0%; Score 20; DB 2; Length 79;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 |||||
 Db 47 AAPM 50

RESULT 5
 B95974
 probable transcription regulator protein [imported] - *Sinorhizobium meliloti* (strain 102)
 C;Species: *Sinorhizobium meliloti*
 C;Accession: B95974
 C;Dbat: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C;Accession: S32243; JG2244; A01303; B01303; S29559
 C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 R;Inian, T.M.; Weldner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9839-9844, 2001
 A;Title: The complete sequence of the 1,683-kb PSYMB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: B95974
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-83 <KUR>
 A;Cross-references:
 A;Experimental source: strain 1021, megaplasmid PSYMB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubel
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Fedderspiel, N.A.; Fischer, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaudi, P.; Vandebriel, M.; Vorhoelter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:2136824; PMID:11474104
 A;Contents: annotation
 A;Genetics:
 A;Genes: exsl; Smb20935
 A;Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 |||||
 Db 13 AAPM 16

RESULT 6
 F97400
 hypothetical protein AGR_C_597 [imported] - *Agrobacterium tumefaciens* (strain C58, Ce
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C;Accession: F97400
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldm
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*
 A;Reference number: A97359; PMID:11743194
 A;Accession: F97400
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-88 <KUR>
 A;Cross-references: GB:AE00769; PIDN:AKB86159.1; PID:915155250; GSDB:GN00169
 A;Genetics:
 A;Gene: AGR_C_597
 A;Map position: circular chromosome

Query Match 100.0%; Score 20; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 |||||
 Db 64 AAPM 67

RESULT 7
 T1SP2
 protease inhibitor (Bowman-Birk) D-II precursor - soybean
 N;Contains: protease inhibitor (Bowman-Birk) E-I (Pi-II)
 C;Species: Glycine max (soybean)
 C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 C;Accession: S32243; JG2244; A01303; B01303; S29559
 R;Song, J.C.; Baek, J.M.; Kim, S.I.
 submitted to the EMBL Data Library, October 1992
 A;Title: Molecular cloning of a genomic DNA encoding the soybean bowman-birk pr
 A;Reference number: S32243
 A;Accession: S32243
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-102 <SON>
 A;Cross-references: EMBL:X68707; NID:9288618; PIDN:CAA48658.1; PID:9288619
 R;Baek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
 Biosci. Biotechnol. Biochem. 58, 843-846, 1994

A;Title: Nucleotide sequence homology of cDNAs encoding soybean Bowman-Birk type protein
A;Reference number: JC2224; MUID:94289861; PMID:7764974
A;Accession: JC2224
A;Molecule type: mRNA
A;Residues: 1-102 <BA2>
A;Cross-references: EMBL:X68706; NID:918571; PIDN:CRA48657; 1; PID:918572
A;Experimental source: clone PB26
R;Ooani, S.; Ikenaka, T.
J. Biochem. 83, 737-745, 1978
A;Title: Studies on soybean trypsin inhibitors. XII. Linear sequences of two soybean dous
A;Reference number: A01503; MUID:78150870; PMID:641033
A;Accession: A01503
A;Molecule type: protein
A;Residues: 28-102 <OPI1>
A;Accession: B01303
A;Molecule type: protein
A;Residues: 37-57 <OPI2>
R;Chen, P.; Rose, J.; Love, R.; Wei, C.H.; Wang, B.C.
J. Biol. Chem. 267, 1990-1994, 1992
A;Title: Reactive sites of an anticarcinogenic Bowman-Birk proteinase inhibitor are simi
A;Reference number: A42052; MUID:92112932; PMID:1730730
A;Contents: annotation; X-ray crystallography of inhibitor PI-II at 2.5 anstroms
C;Comment: This protein regulates endogenous proteinase during germination, stores sulf
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C;Keywords: duplication; seed; serine proteinase inhibitor; storage protein
F;-27;/domain: signal sequence; #status predicted <SIG>
F;28-102;/product: proteinase inhibitor (Bowman-Birk) D-II #status experimental <MAT>
F;41-70;/domain: Bowman-Birk inhibitor repeat homology <BB1>
F;71-96;/domain: Bowman-Birk inhibitor repeat homology <BB2>
F;43-77,44-59,47-93,49-57,67-74,71-86,76-84;/disulfide bonds: #status experimental
F;78;/Inhibitory site: Arg (trypsin) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 43 AAPM 46

RESULT 10

97841 Query Match 100.0%; Score 20; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 43 AAPM 46

Query Match 100.0%; Score 20; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 18 AAPM 21

RESULT 8

T36139 Query Match 100.0%; Score 20; DB 1; Length 105;
hypothetical protein SCE19A.16c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C;Accession: T36139
R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: 221598
A;Accession: T36139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <UR>
A;Cross-references: GB:AB006914; PIDN:AAL03673.1; PID:91562061; GSPDB:GN00173
A;Gene: RC1135
C;Genetics:

Query Match 100.0%; Score 20; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 26 AAPM 29

RESULT 11

C97545 Query Match 100.0%; Score 20; DB 2; Length 105;
hypothetical protein AGR_C-2012 [imported] - Agrobacterium tumefaciens (strain C58, C
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: C97545
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; William, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markez,
Science 294, 2333-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; PMID:11743194
A;Accession: C97545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAR87316.1; PID:915156613; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C-2012
A;Map position: circular chromosome

Query Match 100.0%; Score 20; DB 2; Length 108;

RESULT 9

C7280 Query Match 100.0%; Score 20; DB 2; Length 108;
hypothetical protein APE1923 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix

Qy	1 AAPM 4	Oy	1 AAPM 4	A;Gene: XE2441		
Db	15 AAPM 18	Db	36 AAPM 39	Query Match 100.0%; Score 20; DB 2; Length 109; Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
				Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
				RESULT 12		
AD2764	conserved hypothetical protein Atu1525 [imported] - Agrobacterium tumefaciens (strain C5)	C;Accession: AD2764	C;Accession: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, P.; Karp, P.; Romero, P.; Zhang, S.	Science 294, 2317-2323, 2001	C;Species: Agrobacterium tumefaciens	C;Species: Agrobacterium tumefaciens	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kresspan, W.; Perry, M.; Gordon-Kamm, E.W.	A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.	A;Status: preliminary	A;Status: preliminary	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Reference number: AB2577; PMID:11743193	A;Accession: AD2764	A;Molecule type: DNA	A;Molecule type: DNA	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Residues: 1-108 <KUR>	A;Cross-references: GB:AEO08688; PIDN:ALA42530.1; PID:917739951; GSPDB:GN00186	A;Genetics:	A;Genetics:	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Experimental source: strain C58 (Dupont)	A;Gene: Atu1525	A;Map position: circular chromosome	A;Map position: circular chromosome	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
				RESULT 13		
F8256	hypothetical protein XF2441 [imported] - Xylella fastidiosa (strain 9a5c)	C;Species: Xylella fastidiosa	C;Species: Xylella fastidiosa	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000	C;Accession: F8256	R;janonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen	R;janonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
Nature 406, 151-157, 2000	A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.	A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.	A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Reference number: A82515; MUID:2036517; PMID:1091347	A;Note: for a complete list of authors see reference number A59328 below	A;Accession: F8256	A;Accession: F8256	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Status: preliminary	A;Molecule type: DNA	A;Residues: 1-109 <SIM>	A;Residues: 1-109 <SIM>	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Cross-references: GB:AE004053; GB:AE003849; NID:93107631; PIDN:AAF85240.1; GSPDB:GN001	A;Experimental source: strain 9a5c	D75584	D75584	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acecio, M.; Alvarenga, R.; A	R;jonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen	C;Species: Deinococcus radiodurans	C;Species: Deinococcus radiodurans	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camarao, L.E.A.; Carraro, D.M.; Carrer, H	A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.	C;Accession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000	C;Accession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A.S.Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.	A;Reference number: A82515; MUID:2036517; PMID:1091347	R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J	R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
submitted to GenBank, June 2000	A;Note: for a complete list of authors see reference number A59328 below	S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.	S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm	A;Accession: F8256	Science 266, 1571-1577, 1999	Science 266, 1571-1577, 1999	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieber, J.E.; Kurata, E.E.; Laing	A;Status: preliminary	A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.	A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
chado, M.A.; Madeira, A.M.B.N.; Madeira, C.L.; Marques, M.V.; Martins, E	A;Molecule type: DNA	A;Accession: D75584	A;Accession: D75584	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.	A;Residues: 1-121 <WHL>	A;Gene: DRA0303	A;Gene: DRA0303	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Reference number: A82515; MUID:2036517; PMID:1091347	A;Cross-references: GB:AB001863; GB:AE001825; NID:96460670; PIDN:AAFL12515.1; PID:9646	C;Genetics:	C;Genetics:	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
A;Contents: annotation	C;Superfamily: Deinococcus radiodurans hypothetical protein DRA0303	A;Map position: 2	A;Map position: 2	Best Local Similarity 100.0%; Pred. NO. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;		
C;Genetics:	Query Match 100.0%; Score 20; DB 2; Length 121; Best Local Similarity 100.0%; Pred. NO. 2.7e+02; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1 AAPM 4	Qy	1 AAPM 4	Query Match 100.0%; Score 20; DB 2; Length 121; Best Local Similarity 100.0%; Pred. NO. 2.7e+02; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		Db	40 AAPM 43	Db	40 AAPM 43	Query Match 100.0%; Score 20; DB 2; Length 121; Best Local Similarity 100.0%; Pred. NO. 2.7e+02; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
 VRWHE
 structural protein 1 - hepatitis E virus (strain Burma)
 C:Species: hepatitis E virus
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
 C:Accession: BA0778; AA0235
 R:Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.; Virology, 185, 120-131, 1991
 A:Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
 A:Reference number: A40778; MUID:92024067; PMID:1926770
 A:Molecule type: genomic RNA
 A:Residues: 1-123 <PAM>
 A:Cross-references: GB:NM7456; NID:9330023; PIDN:AAA45735.1; PID:9330025
 R:RAY, R.; Jameel, S.; Manivel, V.; Ray, R.
 A:Title: Indian hepatitis E virus shows a major deletion in the small open reading frame
 A:Reference number: A40236; MUID:92295577; PMID:1534953
 A:Molecule type: genomic RNA
 A:Residues: 1-57; P' 59-102; P' 104-123 <RAV>
 C:Superfamily: hepatitis E virus structural protein 1
 C:Keywords: structural protein

Query Match 100.0%; Score 20; DB 1; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 DB 7 AAPM 10

RESULT 17
 C44212
 structural protein 1 - hepatitis E virus (strain Mexico)
 C:Species: hepatitis E virus
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999
 C:Accession: C44212
 R:Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.
 A:Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE
 A:Reference number: A44212; MUID:93079857; PMID:1448913
 A:Molecule type: genomic RNA
 A:Cross-references: GB:NM7456; NID:9330017; PIDN:AAA45731.1; PID:9330019
 C:Superfamily: hepatitis E virus structural protein 1
 C:Keywords: structural protein

Query Match 100.0%; Score 20; DB 1; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 DB 7 AAPM 10

RESULT 18
 C80883
 50S ribosomal protein L17 [imported] - lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: C66883
 R:Bolotin, A.; Wincher, P.; Mauger, S.; Jaillon, O.; Malarrie, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-126 <STO>

RESULT 19
 H5027
 ribosomal protein L17 [imported] - *Streptococcus pneumoniae* (strain TIGR4)
 C:Species: *Streptococcus pneumoniae*
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
 C:Accession: H95027
 R:Tettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
 on, J.D.; Umeyan, L.K.; White, D.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp
 son, T.; Hickie, E.K.; Holt, T.E.
 Science, 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
 A:Title: Complete Genome Sequence of a Virulent Isolate of *Streptococcus pneumoniae*.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: H95027
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-128 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK74417.1; PID:914971706; GSPDB:GN0164; TIGR:
 A:Experimental source: strain TIGR4
 C:Genetics:
 C:Gene: SP0237
 C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 100.0%; Score 20; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 DB 119 AAPM 122

RESULT 20
 H97898
 50S ribosomal protein L17 [imported] - *Streptococcus pneumoniae* (strain R6)
 C:Species: *Streptococcus pneumoniae*
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
 C:Accession: H97898
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehoff, B.S.
 e, R.; LeBlanc, D.J.; Lee, L.N.; Letkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
 A:Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: H97898
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-128 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAK9020.1; PID:91545761; GSPDB:GN00174
 C:Genetics:
 C:Gene: rpIQ
 C:Superfamily: Escherichia coli ribosomal protein L17
 Query Match 100.0%; Score 20; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 119 AAPM 122

RESULT 21

T06394
isoprenylated protein - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C;Accession: T06394
R;Biermann, B.J.; Morehead, T.A.; Tate, S.E.; Price, J.R.; Randall, S.K.; Crowell, D.N.
J. Biol. Chem. 269, 25251-25254, 1994
A;Title: Novel isoprenylated proteins identified by an expression library screen.
A;Reference number: 215647; MUID:9501311; PMID:7929216
A;Accession: T06394
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-130 <BIE>
A;Cross-references: EMBL:U13180; NID:9532702; PIDN:AAA65012.1; PID:9532703
A;Experimental source: Strain Mandarin

Query Match 100.0%; Score 20; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 57 AAPM 60

RESULT 22

AC0747
conserved hypothetical protein SRY2136 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Accession: AC0747
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
R;Perkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th., T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulie, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Little, C.; Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi; Reference number: AB0502; PMID:11677608
A;Accession: AC0747
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05678.1; PID:916503173; GSPDB:GN00176
A;Gene: STM2136
C;Genetics:
C;Superfamily: universal stress protein A

Query Match 100.0%; Score 20; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 50 AAPM 53

RESULT 23

F77544
probable holo-acyl carrier protein synthase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Accession: F77544
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: F77544
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Mau, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

Query Match 100.0%; Score 20; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 71 AAPM 74

RESULT 24

D87701
conserved hypothetical protein CC3646 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: D87701
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
R;Nierman, W.C.; Relphelyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laiu, M.T.; Beboy, R.T.; Douson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Emblebaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Accession: D87701
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-139 <STO>
A;Cross-references: GB:AE005673; NID:913425402; PIDN:AAK25608.1; GSPDB:GN00148
C;Genetics:
C;Gene: CC3646

Query Match 100.0%; Score 20; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 71 AAPM 74

RESULT 25

T01170
ferredoxin [2Fe-2S] 2 - maize
C;Species: Zea mays (maize)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Jun-2000
C;Accession: T01170
R;Matsumura, T.; Kimata-Ariga, Y.; Sakakibara, H.; Sugiyama, T.; Murata, H.; Takao, T submitted to the ENB Data Library, August 1998
A;Description: cDNA cloning and characterization of ferredoxin localized in bundle sheath cells
A;Accession: T01170
A;Reference number: ZI4252
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Accession: T01170
A;Molecule type: mRNA
A;Residues: 1-140 <MAT>
A;Cross-references: EMBL:AB016810; PIDN:BA32348.1
C;Genetics:
C;Gene: PDF2
C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein
F;68-122-Domain: ferredoxin [2Fe-2S] homology <PDF2>
F;83, 88, 91, 121/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 20; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 Db 33 AAPM 35

RESULT 26

G6452 hypothetical 17.1 kd protein in f1hd-otsA intergenic region - Escherichia coli (strain K-12) [imported] - Escherichia coli (strain K-12) [imported]

C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C;Accession: G6452
 R;Blattner, F.R.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimambato, E.; Potamitis, K.; Apoda, N.; Rose, D.J.; Mau, B.; Shao, Y.; Science 277, 1455-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:9742617; PMID:9278503
 A;Accession: G6452
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-142 <BLAT>
 A;Cross-references: GB:AE000263; GB:U00096; NID:91788200; PIDN:AAC74965.1; PID:91788205;
 A;Experimental source: strain K-12, substrain MG1655
 C;Genetics:
 A;Gene: yecG
 C;Superfamily: universal stress protein A

Query Match 100.0%; Score 20; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 Db 50 AAPM 53

RESULT 27

C9054 probable regulator [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C;Accession: C9054
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; DNA Res 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genetic comparison with O157:H7 strains [imported]
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: C9054
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-142 <HY>
 A;Cross-references: GB:BA00007; PIDN:BAB36026.1; PID:913362071; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain RIMD 0509952

Query Match 100.0%; Score 20; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 Db 26 AAPM 29

RESULT 29

AG378 hypothetical protein BMEL10552 [imported] - Brucella melitensis (strain 16W)

C;Species: Brucella melitensis
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C;Accession: AG378
 R;Belvecechio, V.G.; Kapatral, V.; Reckaw, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov, I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Prok. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis [imported]
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AG378
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-147 <KOR>
 A;Cross-references: GB:AB008918; PIDN:AAL53794.1; PID:917984725; GSPDB:GN00191
 A;Experimental source: strain 16W
 A;Gene: BMEL10552
 A;Map position: II

Query Match 100.0%; Score 20; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
 Db 50 AAPM 53

RESULT 28

H8502 probable regulator yecG [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

hypothetical protein - *Deinococcus radiodurans* (strain R1)

Qy 1 AAPM 4
|||
Db 26 AAPM 29

C;Species: *Deinococcus radiodurans*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C;Accession: C75544
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, R.; Liu, F.; Wollen, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A;Reference number: A97359; PMID:11743194
A;Accession: G98270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89689.1; PID:915159595; GSPPDB:GN00170
C;Genetics:
A;Map position: linear chromosome
A;Gene: AGR_L_2238
A;Superfamily: tolR protein

Query Match 100.0%; Score 20; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31

AH013
AH013 tolR protein [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C;Species: *Agrobacterium tumefaciens*
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AH3013
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Ergec, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClelland, P.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A.;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AH3013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KUR>
A;Cross-references: GB:AE00689; PIDN:AAL41526.1; PID:g17742138; GSPPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: tolR
A;Map position: linear chromosome
C;Superfamily: tolR protein

Query Match 100.0%; Score 20; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31

G98270
G98270 tolR protein (tolR) rp310 [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)
C;Species: *Agrobacterium tumefaciens*
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jun-2002
C;Accession: G98270
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, R.; Liu, F.; Wollen, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A;Reference number: A97359; PMID:11743194
A;Accession: G98270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KWH>
A;Cross-references: GB:AE001886; GB:AE000513; NID:96457921; PIDN:AAF09834.1; PID:9645
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0244
A;Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32

T06396
T06396 isoprenylated protein - soybean (fragment)
C;Species: Glycine max (soybean)
C;Accession: T06396
R;Biermann, B.J.; Morehead, T.A.; Tate, S.E.; Price, J.R.; Randall, S.K.; Crowell, D. J. Biol. Chem. 269, 25251-25254, 1994
A;Title: Novel isoprenylated proteins identified by an expression library screen.
A;Reference number: Z15647; NID:95014311; PMID:929216
A;Accession: T06396
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-154 <EBIE>
A;Cross-references: EMBL:U13181; NID:9532704; PIDN:AAA65013.1; PID:9532705
A;Experimental source: strain Mandarin

Query Match 100.0%; Score 20; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33

Qy 1 AAPM 4
|||
Db 49 AAPM 52

Qy 1 AAPM 4
|||
Db 81 AAPM 84

RESULT 34

T06396
T06396 isoprenylated protein - soybean (fragment)
C;Species: Glycine max (soybean)
C;Accession: T06396
R;Biermann, B.J.; Morehead, T.A.; Tate, S.E.; Price, J.R.; Randall, S.K.; Crowell, D. J. Biol. Chem. 269, 25251-25254, 1994
A;Title: Novel isoprenylated proteins identified by an expression library screen.
A;Reference number: Z15647; NID:95014311; PMID:929216
A;Accession: T06396
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-154 <EBIE>
A;Cross-references: EMBL:U13181; NID:9532704; PIDN:AAA65013.1; PID:9532705
A;Experimental source: strain Mandarin

Query Match 100.0%; Score 20; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 35

BKEC9
BKEC9 acetyl-CoA carboxylase (EC 6.4.1.2) biotin carboxyl carrier protein [validated] - Escherichia coli
C;Species: *Escherichia coli*
C;Accession: 30-Nov-1980 #sequence_revision 31-Dec-1989 #text_change 01-Mar-2002
R;Muramatsu, S.; Mizuno, T. Nucleic Acids Res. 17, 3982, 1989
A;Title: Nucleotide sequence of the fabE gene and flanking regions containing a bent
A;Reference number: A93687; NID:89283408; PMID:2660106
A;Accession: A93687
A;Molecule type: DNA
A;Residues: 1-156 <MR>
A;Cross-references: GB:X14825; NID:941361; PIDN:CAA32933.1; PID:g41362
A;Experimental source: strain La2-22
R;Sutton, M.R.; Fall, R.R.; Nervi, A.M.; Alberts, A.W.; Vagelos, P.R.; Bradshaw, R.A. J. Biol. Chem. 252, 3934-3940, 1977

RESULT 33

C75544
C75544

A; Title: Amino acid sequence of *Escherichia coli* biotin carboxyl carrier protein (9100).
A; Reference number: A92204; MUID:77187896; PMID:324999
A; Accession: A92204
A; Molecule type: protein
A; Residues: 75-156 <SUR>
R; Li, S.J.; Cronan Jr., J.E.
J. Biol. Chem. 267, 855-863, 1992
A; Title: The gene encoding the biotin carboxylase subunit of *Escherichia coli* acetyl-CoA:acetyl-CoA acetyltransferase (EC 2.3.1.7)
A; Reference number: JS0686; MUID:92112819; PMID:1370469
A; Accession: JS0686
A; Molecule type: protein
A; Residues: 1-156 <LIS1>
A; Cross-references: GB:W04528; NID:9145172; PIDN:AAA23408.1; PID:9145174
A; Experimental source: strain K12
A; accession: PS0357
A; Molecule type: protein
A; residues: 1-23 <LIS1>
R; Alix, J.H.
DNA 8, 779-789, 1989
A; Title: A rapid procedure for cloning genes from lambda libraries by complementation of A; reference number: A33643; MUID:90126231; PMID:2575489
A; accession: A33643
A; Molecule type: DNA
A; Residues: 1-156 <LIS1>
A; Cross-references: GB:M32214; NID:9145899; PIDN:AAA23744.1; PID:9145890
R; Li, S.J.; Cronan Jr., J.E.
J. Bacteriol. 175, 332-340, 1993
A; Title: Growth rate regulation of *Escherichia coli* acetyl coenzyme A carboxylase, which A; reference number: A40637; MUID:93123150; PMID:7678242
A; accession: C00637
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-25 <LIS1>
A; Cross-references: GB:S552912; NID:9126399; PIDN:ABA24892.1; PID:926401
A; Note: sequence extracted from NCBI backbone (NCBInr:122315 NCBIp:122319)
R; Kondo, H.; Shirasuchi, K.; Yoshino, T.; Masuda, T.; Kitazono, A.; Tsuru, D.; Anai, Proc. Natl. Acad. Sci. U.S.A. 88, 9130-9133, 1991
A; Title: Acetyl-CoA carboxylase from *Escherichia coli*: gene organization and nucleotide A; reference number: JS0632; MUID:92052166; PMID:1683920
A; accession: PS0272
A; Molecule type: DNA
A; Residues: 133-156 <KON>
A; Cross-references: GB:MT9446
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perera, N.T.; Burland, V.; Riley, M.; Co-Science 27, 1453-162, 1997
A; Title: The complete genome sequence of *Escherichia coli* K-12.
A; Reference number: A65118
A; accession: A65118
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-156 <BLAT>
A; Cross-references: GB:AE000404; GB:U000956; NID:92367207; PIDN:AACT67687.1; PID:9178953;
A; Experimental source: strain K-12, substrain MG1655
R; Chapman-Smith, A.; Turner, D.L.; Cronan Jr., J.E.; Morris, T.W.; Wallace, J.C.
Biochem. J. 302, 881-887, 1995
A; Title: Expression, biotinylation and purification of a biotin-domain peptide from the A; reference number: S7877; MUID:95031932; PMID:945216
A; accession: S7877
A; Molecule type: protein
A; Residues: 2-20 <CHA>
C; Genetics:
A; Gene: accB; fabE
A; Map position: 72 min
C; Complex: In *E. coli*, acetyl-CoA carboxylase is composed of biotin carboxylase complex Iota in carboxyl carrier protein (BCCP, homodimer) (PIR:BKEC9)
C; Function: <ACCo>
A; Description: EC 6.4.1.2 [validated; MUID:75035569]; the acetyl-CoA carboxylase complex
A; Pathway: fatty acid biosynthesis
C; Function: <BCC>
A; Description: a specific lysine residue within the biotin carboxyl carrier protein (BCCP) is modified
A; Note: the C-terminal 87 amino acids of the biotin carboxyl carrier protein (BCCP) form a superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

C;Keywords: biotin binding; fatty acid biosynthesis; homodimer; ligase
F;1-156/product: biotin carboxyl carrier protein BCCP; long form #status experimental
F;2-156/product: biotin carboxyl carrier protein #status experimental <MAT>
F;76-156/product: biotin carboxyl carrier protein BCCP87; short form #status experimental
F;76-156/domain: lipoyl/biotin binding homology <LBB>
F;122/Binding site: biotin (lys) (covalent) #status experimental

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Qy 1 AAPM 4	100.0%	Score 20;	DB 1;	Length 156;	0;	0;
Db 49 AAPM 52	100.0%	Pred. No. 3.4e+02;		Mismatches 0;	0;	0;

RESULT 36
T49921
ribosomal protein-like - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
N;C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C;Accession: T49921
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandst, A.; Duesterhoeft, A.; Bancro
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24990
A;Accession: T49921
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <BEV>
A;Cross-references: EMBL:AL353994; GSPDB:GN00063; ATSP:F17114.40
A;Experimental source: cultivar Columbia; BAC clone F17114
C;Genetics:
A;Gene: ATSP:F17114.40
A;Map position: 5
A;Introns: 1/9/2; 3/7/3; 5/4/3; 85/2; 111/2
C;Superfamily: Escherichia coli ribosomal protein L17

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Qy 1 AAPM 4	100.0%	Score 20;	DB 2;	Length 156;	0;	0;
Db 104 AAPM 107	100.0%	Pred. No. 3.4e+02;		Mismatches 0;	0;	0;

RESULT 37
C85990
acetyl-CoA carboxylase (EC 6.4.1.2) biotin carboxyl carrier protein [similarity] - Es
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: C85990
R;Perna, N-T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, F.J.; Davis, N.W.; Lim, A.; Dimmler, S.; Potamousis, K.; Apoda
Nature, 409, 539-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: AB5480; MUID:21074935; PMID:11206551
A;Accession: C85990
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <STO>
A;Cross-references: GB:AE005174; NID:912517882; PIDN:AAG58383.1; GSPDB:GN00145; UMGD:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: accB
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology
C;Keywords: ligase

Query Match Score 20; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 49 AAPM 52

RESULT 38

C;Accession: DB7658
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
C;Accession: G91144
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kuromoto, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37550.1; PID:91363600; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECG4127
C;Superfamily: biotin carboxyl carrier protein; Lipoyl/biotin-binding homology
C;Keywords: ligase

Query Match 100.0%; Score 20; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 49 AAPM 52

RESULT 39

AH0912

biotin carboxyl carrier protein [imported] - *Salmonella enterica* subsp. *enterica* serovar
C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A;Note: this species has also been called *Salmonella typhi*
C;Accession: AH0912
R;Parkhill, J.R.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Threlfall, T.J.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Reference number: AB0502; PMID:11677608
A;Accession: AH0912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <PARZ>
A;Cross-references: GB:AL513382; PIDN:CAD07894.1; PID:91650441; GSPDB:GN00176
C;Genetics:
A;Gene: STY3559
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match 100.0%; Score 20; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
Db 49 AAPM 52

RESULT 40

DB7658

hypothetical protein CC3302 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

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OM protein - protein search, using sw model

Run on: December 6, 2002, 13:20:29 ; Search time 5.5556 Seconds

(Without alignments) 29.863 Million cell updates/sec

Title: US-10-033-526-2
 Perfect score: 20

Sequence: 1 AAPM 4

Scoring table: BL0SUM62
 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	20	100.0	19	1 HHP_THICU	P80487 thiobacillus
2	20	100.0	60	1 CXI_NAJMO	P01467 naja mossm
3	20	100.0	60	1 CXI_NAJMO	P01468 naja pallid
4	20	100.0	71	1 GROL_RABIT	P30782 oryctolagus
5	20	100.0	98	1 GRO_BOVIN	P046675 bos tauris
6	20	100.0	103	1 GRO_SHEEP	P046578 ovis aries
7	20	100.0	116	1 DIXD_DROME	P52880 drosophila
8	20	100.0	121	1 YAFIC_ECOLI	P29325 hepatitis e
9	20	100.0	123	1 VSTL_HEVBU	P03449 hepatitis e
10	20	100.0	123	1 VSTL_HEVME	P0061 hepatitis e
11	20	100.0	123	1 VSTL_HEVWY	P01461 hepatitis e
12	20	100.0	133	1 ACPS_DEIRRA	P07072 deinococcus
13	20	100.0	142	1 YECG_ECOLI	P46888 escherichia
14	20	100.0	142	1 YECG_SALIVY	P09m66 salmonella
15	20	100.0	146	1 VEGA_SHEEP	P50412 ovis aries
16	20	100.0	154	1 NAPB_BROSH	P053177 rhodobacter
17	20	100.0	156	1 BCC_ECOLI	P02935 escherichia
18	20	100.0	159	1 CYPC_STREOC	P23194 streptomyce
19	20	100.0	161	1 BFR_RHOC	P059138 rhodobacter
20	20	100.0	170	1 RLI0_CHLPN	P09-9a2 chlamydia p
21	20	100.0	172	1 RLI0_CHLMI	P09-78 chlamydia m
22	20	100.0	172	1 RLI0_CHLTR	P08313 chlamydia t
23	20	100.0	190	1 VEGA_BOVIN	P15091 bovis tauris
24	20	100.0	190	1 VEGA_HORSE	P09490 equus cabal
25	20	100.0	190	1 VEGA_PIG	P49151 sus scrofa
26	20	100.0	191	1 CBP2_ARATH	P30187 arabidopsis
27	20	100.0	198	1 ACDZ_CLOPE	P08X99 clavigeratum
28	20	100.0	200	1 ACPD_ECO57	P08X99 escherichia
29	20	100.0	200	1 ACPD_ECOLI	P41407 escherichia
30	20	100.0	200	1 ACPD_SALIV	P8x1P4 salmonella
31	20	100.0	200	1 ACPD_YERPE	P08x60 yersinia pe
32	20	100.0	213	1 PSEAE	P09x17 pseudomonas
33	20	100.0	214	1 VEGA_CANPA	P09my3 canis famili

ALIGNMENTS

RESULT 1
 HHP_THICU STANDARD; PRT; 19 AA.
 ID HHP_THICU P00487;
 DT 01-OCT-1996 (Rel. 34, created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last annotation update)
 DE Heterotroph-specific protein (fragment).
 OS Thiomonas cuprinus.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.
 RN NCBI_TaxID=36660;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Martin I., Amaro A.M., Jerez C.A., Anills R., Abad J.P.;
 RL Submitted (SPP=1993) to the SWISS-PROT data bank.
 CC - MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 CC HETEROTROPHICALLY.
 FT NON_TER 19 AA; 19 19 AA; 1786 MW; C549197D0A492B07 CRC64;
 SQ SPQUENCE

Query Match 100.0%; Score 20; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 DB 12 AAPM 15
 RESULT 2
 CXL_NAJMO STANDARD; PRT; 60 AA.
 ID CXL_NAJMO P01467;
 AC P01467;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUN-2002 (Rel. 41, Last annotation update)
 DT CYTotoxin 1 (cardiotoxin XIB) (Cytox IIB).
 OS Naja mossmambica (Mozambique cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Elapidae; Elapinae; Naja.
 OC Naja_TaxID=8644;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RA Louw A. I.;
 RT Snake venom toxins. The amino acid sequences of three cytotoxin
 homologues from Naja mossmambica mossmambica venom.;
 RT Blachon. Biophys. Acta 336:481-495(1974).
 RN [2]
 RT STRUCTURE BY NMR.
 RT MEDLINE-BB802411; PubMed=2822421;
 RA Oetting G., Steinmetz W.E., Bouis P.E., Rochat H., Wuethrich K.;
 RT Sequence-specific 1H-NMR assignments and determination of the secondary structure in aqueous solution of the cardiotoxins CTXIIA
 RT

RT and CTXrib from *Naja mossambica mossambica*.";
 RL Eur. J. Biochem. 168:609-620(1987).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE-93279339; PubMed-8504828;
 RA O'Connell J.F., Bougis P.E., Wuehrich K.;
 RT "Determination of the nuclear-magnetic-resonance solution structure
 of cardiotoxin CTX Iib from *Naja mossambica mossambica*.";
 RL Eur. J. Biochem. 213:891-900(1993).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MISCELLANEOUS: LD(50) IS 0.83 MG/KG BY INTRAVENOUS INJECTION.
 CC -!- SIMILARITY: BELONGS TO THE SNAKE TOXIN FAMILY.
 DR PIR: A01728; H3NJB1.
 DR PIR: S02517.
 DR PDB: 2C CX; 3J-JAN-94.
 DR InterPro: IPR00352; Cytotoxin.
 DR InterPro: IPR03571; Snake_toxin.
 DR Pfam: PF00087; toxin; 1.
 DR PROSITE: PS00272; SNAKE_TOXIN; 1.
 KW Venom; Cytotoxin; Cardiotoxin; Multigene family; 3D-structure.
 FT DISULFID 3 21
 FT DISULFID 14 38
 FT DISULFID 42 53
 FT DISULFID 54 59
 FT STRAND 2 3
 FT TURN 9 10
 FT STRAND 12 13
 FT TURN 16 17
 FT STRAND 21 26
 FT TURN 30 31
 FT STRAND 35 37
 FT STRAND 49 54
 FT TURN 57 58
 SQ SEQUENCE 60 AA; 6826 MW; 68BB50B776B6491C CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 60;
 Best Local Similarity 100.0%; Pred. No. 72; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 28 AAPM 31

RESULT 3
 CXL_NAJPA STANDARD: PRT; 60 AA.
 ID CXL_NAJPA
 AC P01468;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cytoxin 1 (Cardiotoxin gamma).
 OS *Naja pallida* (Red spitting cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scincoglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapine; *Naja*.
 OX NCBI_TaxId=8658;
 RN {1}
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=venom;
 RX MEDLINE-7520552; PubMed-1148181;
 RA Fryklund L.; Eaker D.;
 RT "The complete covalent structure of a cardiotoxin from the venom of
 RT *Naja nigricollis* (African black-necked spitting cobra).";
 RL Biochemistry 14:2865-2871(1995).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
 RX MEDLINE-94224084; PubMed-8195041;
 RA Blwes A.; Rees B.; Moras D.; Menez R.; Menez A.;
 RT "X-ray structure at 1.55 Å of toxin gamma, a cardiotoxin from *Naja*
 RT nigricollis venom. Crystal packing reveals a model for insertion into
 RT membranes";
 RL J. Mol. Biol. 239:122-136(1994).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- CAUTION: THE VENOM OF THIS SNAKE WAS ORIGINALLY THOUGHT TO BE THAT
 OF *N. NIGRICOLLIS* WHILE IT IS REALLY FROM *N. PALLIDA*.
 DR PIR: A37578; H3NJB1.
 DR PDB: 1GX; 30-APR-94.
 DR PDB: 1CXN; 20-DEC-94.
 DR PDB: 1CXO; 20-DEC-94.
 DR InterPro: IPR003572; Cytotoxin.
 DR InterPro: IPR03571; Snake_toxin.
 DR Pfam: PF00087; toxin; 1.
 DR PROSITE: PS00272; Cytotoxin.
 DR PROSITE: PS00272; SNAKE_TOXIN; 1.
 KW Venom; Cytotoxin; Cardiotoxin; Multigene family; 3D-structure.
 FT DISULFID 3 21
 FT DISULFID 14 38
 FT DISULFID 42 53
 FT DISULFID 54 59
 FT STRAND 2 4
 FT TURN 8 9
 FT STRAND 11 13
 FT TURN 16 17
 FT STRAND 20 26
 FT TURN 27 28
 FT STRAND 29 29
 FT TURN 30 31
 FT STRAND 35 39
 FT TURN 49 54
 FT TURN 57 58
 SQ SEQUENCE 60 AA; 6827 MW; 68BB50B996B6491C CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 60;
 Best Local Similarity 100.0%; Pred. No. 72; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 28 AAPM 31

RESULT 4
 GRO1_RABBIT STANDARD: PRT; 71 AA.
 ID GRO1_RABBIT
 AC P30782;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Permeability factor 2 (KPF2) (Fragment).
 OS *Oryctolagus cuniculus* (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=New Zealand white; TISSUE=Alveolar macrophage;
 RA MEDLINE-95129889; PubMed-7828903;
 RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
 RA Martin T.R.;
 RT "Cloning of two rabbit GRO homologues and their expression in
 RT alveolar macrophages";
 RL Gene 151:337-338(1994).
 RN [2]
 RP SEQUENCE OF 1-36.
 RC STRAIN-New Zealand white; TISSUE=Peritoneal cavity;
 RX MEDLINE-91378900; PubMed-1898341;
 RA Jose P.J., Collins P.D., Perkins J.A., Beaubien B.C., Totty N.F.,
 RA Waterfield M.D., Hsuan J., Williams T.J.;
 RT "Identification of a second neutrophil-chemoattractant cytokine

RT generated during an inflammatory reaction in the rabbit peritoneal cavity in vivo; purification, partial amino acid sequence and
 RT structural relationship to melanoma-growth-stimulatory activity.";
 RL Biochem. J. 278:493-497(1991).
 CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS (BY
 CC SUBUNIT) HOMODIMER (PROBABLE).
 CC -!- INDUCTION: GENERATED DURING AN INFLAMMATORY REACTION.
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE_CXC).
 CC
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 CC
 DR EMBL; IJ9107; AAA64357.1; -.
 DR PIR; S17507; S17507.
 DR HSSP; P19875; IQNK.
 DR InterPro; IPR001089; CXC_chmkine_sm1.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 98 GROWTH REGULATED PROTEIN HOMOLOG GAMMA.
 DT DISULFID 39 65 BY SIMILARITY.
 FT N -> S (IN REF. 2).
 FT CONFLICT 23 23 N -> S (IN REF. 2).
 FT NON_TER 71 71 DE Growth regulated protein precursor (CXCL1).
 SQ SEQUENCE 71 AA: E91387CB382C8008 CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 85; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; OvY 1 AAPM 4
 RN 1111
 Db 53 AAPM 56
 RESULT 5
 GROG_BOVIN STANDARD; PRM; 98 AA.
 ID GROG_BOVIN
 AC 044675;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth regulated protein homolog gamma precursor (GRO-gamma).
 OS Bos taurus (Bovine)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Caprinae; Ovis.
 OC OX NCBI_TaxId=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9152612; PubMed=10028286;
 RA Mori W.S.; Yoshimura T.;
 RT "Isolation of novel GRO genes and a phylogenetic analysis of the CXC
 RT chemokine subfamily in mammals";
 RL Mol. Biol. Evol. 16:180-193(1999).
 CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE_CXC).
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 CC
 DR EMBL; 095814; RAB93930.1; -.
 DR HSSP; P19875; IQNK.
 DR InterPro; IPR001089; CXC_chmkine_sm1.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PRO037; SMALLCYTKC.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 103 GROWTH REGULATED PROTEIN.
 DT DISULFID 39 65 BY SIMILARITY.
 FT N -> S (IN REF. 2).
 FT CONFLICT 41 81 BY SIMILARITY.
 SQ SEQUENCE 103 AA: C59827F346716695 CRC64;

Query Match	100.0%	Score 20;	DB 1;	Length 103;	RL
Best Local Similarity	100.0%	Pred. No.	1.2e+02;	-	CC
Matches	4;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
1 AAPM 4					
b	85 AAPM 88				
RESULT 7					
IUX-DROME	STANDARD;	PRT;	116 AA.		
D-DIUX-DROME					
C 09V4K;					
T 16-OCT-2001 (Rel. 40, Created)					
T 16-OCT-2001 (Rel. 40, Last sequence update)					
E Diuretic hormone class-II precursor (Diuretic peptide) (DP) (DH(31)).					
CG13094.					
S Drosophila melanogaster (Fruit fly)					
Bukaryota; Metazoa; Arthropoda; Pancrustacea; Hexapoda;					
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;					
Muscomorpha; Ephydriodea; Drosophilidae; Drosophila;					
NCBI_TaxID:7227;					
[1]					
P SEQUENCE FROM N_A.					
X STRAIN=Berkeley;					
X MEDLINE=20196006; PubMed=10731132;					
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,					
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,					
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,					
A Suttor G.G., Wormit J.R., Yandell M.D., Zhang Q., Chen L.X.,					
A Brandon R.C., Rogers Y.H.C., Blazek R.G., Champé M., Miklos G.L.G.,					
A Wan K.H., Doyle C.J., Baxter E.G., Helt G., Nelson C.R., Preiffer B.D.,					
A Balliew R.M., Basu A., Boxendale J., Bayraktaroglu L., Beasley E.M.,					
A Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,					
A Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Brotrier P.,					
A Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,					
A Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,					
A de Pablo S.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,					
A Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,					
A Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Pleischmann W.,					
A Fosler A.E., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,					
A Glodek A., Gobrial J.H., Gu Z., Guan P., Harris M.,					
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,					
A Hostin D., Houston K.A., Howland T.J., Kei Z., Kleinman J.A., Ketchum K.A.,					
A Jalali M., Kalush F., Karpen G.H., Kerec J., Kettman J.A., Kimmelman B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,					
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,					
A Liu X., Mattei B., McIntosh M.P., McPherson D.,					
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherrefi A.,					
A Mount S.M., Moy M., Murphy B., Murphy L., Munty D.M., Nelson D.R.,					
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paciek J.M.,					
A Palazzo M., Pittman G.S., Pan S., Pollard J., Puriv V., Reese M.G.,					
A Rehert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,					
A Shue B.C., Siden-Klamo T., Simpson M., Skupski M.P., Smith T.,					
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,					
A Svirska S.R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,					
A Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T.A., Worley K.C., Wu D., Yang S., Yao Q.A.,					
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,					
A Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,					
A "The genome sequence of Drosophila melanogaster.";					
A Science 287:2185-2195(2000).					
[2]					
X FUNCTION AND SYNTHESIS OF 76-106.					
X MEDLINE=21216780; PubMed=11316500;					
X Coast G.M., Webster S.G., Schlegg K.M., Tobe S.S., Schooley D.A.;					
X "The Drosophila melanogaster homologue of an insect calcitonin-like diuretic peptide stimulates v-ATPase activity in fruit fly Malpighian tubules";					
RESULT 8					
IYAFL-CAEEL	STANDARD;	PRT;	121 AA.		
ID YAFI-LCAEEL					
AC P52880;					
DT 01-OCT-1996 (Rel. 34, Created)					
DT 01-OCT-1996 (Rel. 34, Last sequence update)					
DT 01-OCT-1996 (Rel. 34, Last annotation update)					
DE Hypothetical protein F46C5.1 in chromosome II.					
GN F46C5.1.					
OS Caenorhabditis elegans.					
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderrinae; Caenorhabditis.					
OC Rhabditidae;					
OX NCBI_TaxID:6239;					
RN [1]					
RP SEQUENCE FROM N_A.					
RC STRAIN=Bristol N2;					
RA Thomas K.;					
RL Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.					
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CC DR EMBL; 254281; CAA91048.1; -.					
DR WormPep; F46C5.1; CE03343.					
KW Hypothetical protein; transmembrane.					
FT TRANSMEM 6					
FT SEQUENCE 121 AA; 13440 MW; 477FD9C171CDP01 CRC64;					
OY 1 AAPM 4					

RESULT 9
 VS1_HEVBU STANDARD; PRT; 123 AA.
 ID VS1_HEVBU
 AC P29325;
 DT 01-DEC-1992 (Rel. 24, created)
 DT 01-DEC-1992 (Rel. 24, last sequence update)
 DT 01-FEB-1994 (Rel. 28, last annotation update)
 DE Structural protein 1 (ORF3).
 OS Hepatitis E virus (strain Burma) (HEV), and
 OS Hepatitis E virus (strain Pakistan) (HEV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage;
 OC Hepatitis E-like viruses.
 OX NCBI_TAXID=31767; 33774;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Burma;
 RX MEDLINE=92024057; PubMed=1926770;
 RA Tam C.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
 RA Fry K.E., Reyes G.R.;
 RT "Hepatitis E virus (HEV): molecular cloning and sequencing of the
 full-length viral genome";
 RL Virology 185:120-131(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pakistan;
 RX MEDLINE=921115700; PubMed=1731327;
 RA Tsareva S.U., Emerson S.U., Reyes G.R., Legters L.J.,
 RT "Characterization of a prototype strain of hepatitis E virus";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5563(1992).
 CC -----
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 CC -----
 DR EMBL; M83218; AAA45735.1; -.
 DR EMBL; M80511; AAA45726.1; -.
 DR PIR; BA0778; VHWHE.
 DR Interpro; IPR003384; HEV_ORF2.
 SQ SEQUENCE 123 AA; 127/14 MW; C88BF5D638852A68 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 DR 1111
 Db 7 AAPM 10

RESULT 11
 VS1_HEVMY STANDARD; PRT; 123 AA.
 ID VS1_HEVMY
 AC Q04612;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Structural protein 1 (ORF3).
 OS Hepatitis E virus (strain Myanmar) (HEV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage;
 OC Hepatitis E-like viruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93221573; PubMed=8470371;
 RA Aye T.T., Uchida T., Ma M.Z., Tida F., Shikata T., Ichikawa M.,
 RA Rakhisha T., Winn K.;
 RT "Sequence and gene structure of the hepatitis E virus isolated from
 RT Myanmar";
 RL Virus Genes 7:95-109(1993).
 CC -----
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 CC -----
 DR EMBL; D10330; BAA0173.1; -.
 DR Interpro; IPR003384; HEV_ORF2.
 DR PIR; BA0778; VHWHE.
 SQ SEQUENCE 123 AA; 127/14 MW; FB81143FOB31FF8A4 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4
 DR 1111
 Db 7 AAPM 10

RESULT 10
 VS1_HEVME STANDARD; PRT; 123 AA.
 ID VS1_HEVME
 AC 003499;
 DT 01-OCT-1993 (Rel. 27, Last created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Structural protein 1.
 OS Hepatitis E virus (strain Mexico) (HEV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage;
 OC Hepatitis E-like viruses.
 OX NCBI_TAXID=31768;
 RN [1]
 RP SEQUENCE FROM N.A.

RESULT 12
ACPS_DETRA STANDARD; PRT; 133 AA.
ID ACPS_DETRA STANDARD; PRT; 133 AA.
AC Q9RKR0;
DT 15-JUN-2002 (Rel. 41, created)
DT 15-JUN-2002 (Rel. 41, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN ACPS OR Dr0247;
OS Deinococcus radiodurans.
OC Bacteria; Thermus/deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dossen R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vanathavean J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1."
RL Science 286:1571-1577(1999).
CC -I- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
A to a Ser of an acyl-carrier protein, (By similarity).
CC -I- CATALYTIC ACTIVITY: CoA + apoenzyme + holo-[acyl-carrier protein] = adenosine
3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -I- COFACTOR: Magnesium (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
FAMILY.
CC
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CC
CC EMBL: AEG001885; ARF09829.1; -.
DR TIGR; DS0247; -.
DR InterPro; IPR0042542; ACPS.
DR InterPro; IPR004586; Pantethn_trn.
DR Prodom; PD004282; ACPS; 1.
DR TIGRFAMS; TIGR0056; Pantethn_trn; 1.
KW Complete proteome.
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 56 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 133 AA; 15114 MW; C5E009B9728D120 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 133;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPM 4
OY 1 AAPM 4
Db 86 AAPM 89

RESULT 13
YECC_ECOLI STANDARD; PRT; 142 AA.
AC PA6888;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

RESULT 14
YECC_SALTY STANDARD; PRT; 142 AA.
ID YECC_SALTY
AC Q9RKR6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yecc.
GN YECC OR USP5 OR SIM1927;
OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20052996; PubMed=10586519;
 RA Yanagihara S., Iyoda S., Ohnishi K., Iino T., Kutsukake K.;
 RT "structure and transcriptional control of the flagellar master operon
 of *Salmonella typhimurium*";
 RL Genes Genet. Syst. 74:105-111(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LIT2 / SGSC112 / ATCC 700720;
 RX MEDLINE=21534908; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvane E.,
 RA Raver E., Sun H., Flores L., Miller W., Stokenek T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LIT2";
 RL Nature 413:852-856(2001).
 CC -!- SIMILARITY: BELONGS TO THE UFF0022 (USPA) FAMILY.

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 or send an email to license@isb-sib.ch).
 CC -!-
 DR EMBL; D43601; BAA83131; -.
 DR EMBL; AE00786; AA120843; 1; -.
 DR STYGene; SG????; YEGC.
 DR InterPro; IPR00001; USP.
 DR Pfam; PF00582; USP; 1.
 KW HYPothetical protein; Complete proteome.
 SQ SEQUENCE 142 AA; 15/98 MW: F39ABEB55B1777C2 CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy |||||
 Db 50 AAPM 4
 Db 50 AAPM 53

RESULT 15
 VEGA_SHEEP STANDARD: PRT; 146 AA.
 ID VEGA_SHEEP
 AC P50412;
 DT 01-OCT-1996 (Rel. 34, created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE vascular endothelial growth factor A precursor (VEGF-A) (vascular
 permeability factor) (VPF).
 DE VEGF OR VEGFA.
 OS Ovis aries (Sheep).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bovidae; Cervidae; Ovis.
 OX NCBI_TaxID=9440;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9711798; PubMed=8958842;
 RA Reimer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
 RA Reynolds L.P., Moor R.M.,
 RT "Characterization and expression of vascular endothelial growth
 factor (VEGF) in the ovine corpus luteum.;"
 RL J. Reprod. Fertil. 108:157-165(1996).

RESULT 16
 NAPB_RHOSH STANDARD: PRT; 154 AA.
 ID NAPB_RHOSH
 AC P53177;
 DT 01-NOV-1997 (Rel. 35, created)
 DT 16-OCT-2001 (Rel. 35, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE diheme cytochrome c napB precursor.
 GN NAPB
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Rhodobacter.
 OX NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC 11023 / 2.4.1 / NCIB 8253 / DSM 158;
 RX MEDLINE=95332666; PubMed=8730872;
 RA Reyes F., Rodan M.D., Klipp W., Castillo F., Moreno-Vivian C.;
 RT "isolation of periplasmic nitrate reductase genes from Rhodobacter
 sphaeroides DSM 158: structural and functional differences among
 RT prokaryotic nitrate reductases";
 RL Mol. Microbiol. 19:1307-1318(1996).
 CC -!- FUNCTION: SMALL SUBUNIT OF THE PERIPLASMIC NITRATE REDUCTASE.
 CC (NAP). ONLY EXPRESSED AT HIGH LEVELS DURING AEROBIC GROWTH. NAPAB
 CC COMPLEX RECEIVES ELECTRONS FROM THE MEMBRANE-ANCHORED TETRAIME
 RL NAPC PROTEIN, THUS ALLOWING ELECTRON FLOW BETWEEN MEMBRANE AND

PERIPLASM. ESSENTIAL FUNCTION FOR NITRATE ASSIMILATION AND MAY HAVE A ROLE IN ANAEROBIC METABOLISM. CC
 SUBUNIT: HETERO-DIMER OF A CATALYTIC SUBUNIT AND A CYTOCHROME C (BY SIMILARITY). CC
 -!- SUBCELLULAR LOCATION: periplasmic. CC
 -!- INDUCTION: INDUCED BY NITRATE. NOT REPRESSED BY AMMONIUM OR OXYGEN. CC
 -!- PTM: BINDS TWO HEME GROUPS PER MOLECULE (BY SIMILARITY). CC
 -!- SIMILARITY: STRONG, TO OTHER BACTERIAL NAPB. CC
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 EMBL; Z46806; -; NOT_ANNOTATED_CDS. DR
 InterPro; IPR00335; Cytc_heme_bind. DR
 PROSITE; PS00190; CYTOCHROME_C; 2. DR
 Electron transport; Heme; Periplasmic; Signal. FT
 SIGNAL 1 24 FT
 CHAIN 25 154 FT
 MOD_RES 25 25 FT
 BINDING 82 82 FT
 BINDING 85 85 FT
 METAL 86 86 FT
 BINDING 122 122 FT
 BINDING 125 125 FT
 METAL 126 126 FT
 SEQUENCE 154 AA: 16908 MW: 63CE7404A5864977 CRC64: SQ

Query Match? 100.0%: Score 20; DB 1; Length 154;
 Best Local Similarity 100.0%; Prod. No. 1.8e+02; Length 154;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT
 Qy 1 AAPM 4 Db 95 AAPM 98 RT

RESULT 17 RN
 BCCP_ECOLI RP
 ID BCCP_ECOLI STANDARD: PRT: 156 AA. RX
 AC P02905; RA
 DT 21-JUL-1986 (Rel. 01, Created) RA
 DT 01-JUL-1989 (Rel. 11, Last sequence update) RA
 DT 15-JUN-2002 (Rel. 41, Last annotation update) RA
 DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP). RA
 GN FABE OR B225 OR Z4615 OR ECS4127. RA
 OS Escherichia coli and RA
 Escherichia coli O157:H7. RA
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; RA
 NCBI_Taxid=562, 83334; RN [1]
 SEQUENCE FROM N.A. RA
 STRAIN=K12; RC
 MEDLINE:89282408; PubMed=2660106; RN [3]
 MURAMATSU S., Mizuno T.; RX
 "Nucleotide sequence of the fabE gene and flanking regions containing RT
 a bent DNA sequence of Escherichia coli.", Nucleic Acids Res. 17,3982-3982(1989). RL
 [2] RN
 SEQUENCE FROM N.A. RX
 MEDLINE:9212819; PubMed=1370469; RA
 Li, S.-J., Cronan J.E. Jr.; RA
 "The gene encoding the biotin carboxylase subunit of Escherichia coli acetyl-CoA carboxylase.", J. Biol. Chem. 267:855-863(1992). RL
 J. Biol. Chem. 267:855-863(1992). RX

SEQUENCE FROM N.A. RN [3]
 MEDLINE:90126231; PubMed=2575489; RP
 Allix, J.-H.; RX
 "A rapid procedure for cloning genes from lambda libraries by complementation of *E. coli* defective mutants: application to the fabE region of the *E. coli* chromosome.", DNA 8:779-789(1989). RA
 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Colombo-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; RA
 "The complete genome sequence of *Escherichia coli* K-12.", Science 277:1453-1474(1997). RL
 SEQUENCE FROM N.A. RN [4]
 STRAIN=K12 / MG1655; RX
 MEDLINE:97426617; PubMed=9278503; RA
 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; RA
 "The complete genome sequence of *Escherichia coli* K-12.", Science 277:1453-1474(1997). RN [5]
 SEQUENCE FROM N.A. RX
 STRAIN=O157:H7 / EDL933 / ATCC 700927; RX
 MEDLINE:21074935; PubMed=11206551; RA
 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobebeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; RA
 "Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.", RT
 Nature 409:529-533(2001). RN [6]
 SEQUENCE FROM N.A. RP
 STRAIN=O157:H7 / RIMD 050952; RX
 MEDLINE:21156231; PubMed=11258796; RA
 Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., RA
 Kuhara S., Shiba T., Hattori M., Shinagawa H.; RA
 "Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12.", RT
 DNA Res. 8:11-22(2001). RL
 SEQUENCE OF 1-25 FROM N.A. RN [8]
 MEDLINE:9312150; PubMed=7678242; RX
 Li, S.-J., Cronan J.E. Jr.; RA
 "Growth rate regulation of *Escherichia coli* acetyl coenzyme A carboxylase, which catalyzes the first committed step of lipid biosynthesis.", J. Bacteriol. 175:332-340(1993). RN [9]
 SEQUENCE OF 75-156. RP
 MEDLINE:7187896; PubMed=324999; RX
 Sutton M.R., Fall R.R., Nervi A.M., Alberts A.W., Vagelos P.R., RA
 Bradshaw R.A.; RA
 "Amino acid sequence of *Escherichia coli* biotin carboxyl carrier protein (9100).", J. Biol. Chem. 252:3934-3940(1977). RN [10]
 SEQUENCE OF 133-156 FROM N.A. RP
 STRAIN=K12; RX
 MEDLINE:92052166; PubMed=1882920; RA
 Kondo H., Shiratsuchi K., Yoshimoto T., Masuda T., Kitazono A., Tsuru D., Arai M., Sekiguchi M., Tanabe T.; RA
 "Acetyl-CoA carboxylase from *Escherichia coli*: gene organization and nucleotide sequence of the biotin carboxylase subunit.", Proc. Natl. Acad. Sci. U.S.A. 88:9730-9733(1991). RN [11]
 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 77-156. RP
 MEDLINE=96363677; PubMed=847466;

RA Atappilly F.K.; Hendrickson W.A.;
 RT "structure of the biotinyl domain of acetyl-coenzyme A carboxylase
 determined by MAD phasing";
 RL STRUCTURE 3:1407-1419(1995);
 RN [112]
 RP STRUCTURE BY NMR OF 70-156.
 RX PDBID=90060761; PubMed=9398256;
 RA Yao X.; Wei D.; Soden C. Jr.; Summers M.F.; Beckett D.; Chapman-Smith A.;
 RT Structure of the carboxy-terminal fragment of the apo-biotin
 carboxyl carrier subunit of Escherichia coli acetyl-CoA
 RT Biochemistry 36:15089-15100(1997).
 RN [113]
 RP STRUCTURE BY NMR OF 77-156.
 RX MEDLINE=99130195; PubMed=10213607;
 RA Roberts E.L.; Shu N.; Howard M.J.; Broadhurst R.W.; Chapman-Smith A.;
 Wallace J.C.; Morris T.; Cronan J.E. Jr.; Perham R.N.;
 RT "solution structures of apo and holo biotinyl domains from acetyl-
 coenzyme A carboxylase of Escherichia coli determined by triple-
 resonance nuclear magnetic resonance spectroscopy.";
 RL Biochemistry 38:5015-5033(1999).
 CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
 CARBOXYLIC COMPLEX. FIRST, BIOTIN CARBOXYLASE CATALYZES THE
 CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
 CC COENZYME A CARBOXYL GROUP TO FORM MALONYL-COA.
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC -!- SUBUNIT: HOMODIMER.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X14825; CAA32933; 1; -.
 DR EMBL; M32214; AAA23744; 1; -.
 DR EMBL; M32214; AAA23744; 1; -.
 DR EMBL; M7446; ; NOT_ANNOTATED_CDS.
 DR EMBL; M83198; AAA23745; 1; -.
 DR EMBL; U18987; AAAS58058; 1; -.
 DR EMBL; AE000404; AAC76287; 1; -.
 DR EMBL; AE00553; AAQ58383; 1; -.
 DR EMBL; A002564; BAB3750; 1; -.
 DR EMBL; S52932; ARB24892; 1; -.
 DR PIR; A033402; BBBC9.
 DR PIR; A33643; ARB24892.
 DR PIR; JS0686; JS0686.
 DR PIR; PS0272; PS0272.
 DR PIR; C40637; C40637.
 DR PDB; 1BDO; O1-AUG-96.
 DR PDB; 2BDO; 27-APR-99.
 DR PDB; 3BDO; 26-APR-99.
 DR PDB; 1A6X; 14-OCT-98.
 DR SWISS-2DPAGE; P02905; COLI.
 DR Ecogene; EG102149; AccCoA_biotinCC.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR PIR; PF00364; biotin_lipoyl; 1.
 DR PRINTS; PRO1071; ACOBIOPTINC.
 DR TIGRFAMS; TIGR00531; BCCP; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 KW Fatty acid biosynthesis; Biotin; 3D-structure; Complete proteome.
 FT BINDING 122 122 BIOTIN.
 FT CONFLICT 113 113 D -> N (IN REF. 3).
 SQ SEQUENCE 156 AA; 1687 MW; 05FFDCB912A683A3 CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 19 BFR_RHOCA

ID BFR_RHCA STANDARD; PRT; 161 AA.
 AC 059738;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Bacterioferritin (BFR).
 GN BFR.
 OS Rhodobacter capsulatus (*Rhodopseudomonas capsulata*).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Rhodobacter.
 OX NCBI_TAXID=1061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 938 / 37b4;
 RX MEDLINE=9627593; PubMed=8674981;
 RA Pentof C.N., Ringeling P.L., Davy S.L., Moore G.R., McEwan A.G.,
 RA Spiro S.;
 RT "isolation, characterisation and expression of the bacterioferritin gene of Rhodobacter capsulatus.";
 RL MEDLINE=139143-148(1995).
 CC -!- FUNCTION: May perform analogous functions in iron detoxification and storage to that of animal ferritins (BY SIMILARITY).
 CC -!- SUBUNIT: OLIGOMER OF 24 IDENTICAL SUBUNITS (BY SIMILARITY).
 CC -!- MISCELLANEOUS: Bacterioferritin contains protoheme IX in addition to the non-heme iron core.
 CC -!- SIMILARITY: BELONGS TO THE BACTERIOFERRITIN FAMILY.
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 CC
 CC EMBL: Z44247; CAA01017.1; -.
 DR HSSP; P11056; IBCF.
 DR InterPro; IPR002024; Bacterioferritin.
 DR Pfam; PF01334; Bacteriofer; 1.
 DR PRINTS; PR00001; BACFERRITIN.
 DR PRODOM; PD02269; Bacterioferritin; 1.
 DR TIGRFAMS; TIGR00754; bfr; 1.
 DR PROSITE; PS00549; BACTERIOFERRITIN; 1.
 DR KW Iron storage; Heme; METAL.
 FT SEQUENCE 161 AA: 18172 MW: 98534C8C531EC709 CRC64;
 Query Match 100.0% Score 20; DB 1; Length 161;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 154 AAPM 157

RESULT 20
 RL10_CHIPN ID RL10_CHIPN STANDARD; PRT; 170 AA.
 AC 0959A2; 09J0B8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L10.
 GN RPLJ OR RL10 OR CP0079 OR CP0696.
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydaceae; Chlamydophila.
 OX NCBI_TAXID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mopn / Niig;
 RX MEDLINE=2010255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Heidelberg J.F., Berry K., Bass S., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Wedman J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., Debay R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
 RA "Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.", Nucleic Acids Res. 28:3311-3314 (2000).
 RC SEQUENCE FROM N.A.
 RX MEDLINE=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuwara S., Nakayawa T.;
 RA "Comparison of whole genome sequences of *Chlamydia pneumoniae* J138 from Japan and CWL029 from USA.", Nucleic Acids Res. 28:3311-3314 (2000).
 CC -!- SIMILARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 DR EMBL: A800153; AAD1832.1; -.
 DR EMBL; AE002228; AAF38504.1; -.
 DR PHC1-2DPAGE; O9Z9A2; -.
 DR TIGR; CP0696; -.
 DR InterPro; IPR00190; Ribosomal_L10.
 DR InterPro; IPR002363; Ribosomal_L10eub.
 DR Pfam; PF00466; Ribosomal_L10; 1.
 DR PROSITE; PS01109; RIBOSOMAL_L10; 1.
 DR KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 170 AA: 184249 MW: 148263C17E062632 CRC64;
 Query Match 100.0% Score 20; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 142 AAPM 145

RESULT 21
 RL10_CHIMU ID RL10_CHIMU STANDARD; PRT; 172 AA.
 AC 09P78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L10.
 GN RPLJ OR TC0591.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydaceae; Chlamydia.
 OX NCBI_TAXID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mopn / Niig;
 RX MEDLINE=2010255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Heidelberg J.F., Berry K., Bass S., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Bodson R., Salzberg S.L., RA Gwin M., Nelson W., Debroy R., Kolony J., McCarty G., Salzberg S.L., Eisen J., Fraser C.M., "Genomic sequences of Chlamydia trachomatis MOMP and Chlamydia RT pneumoniae AR99"; Nucleic Acids Res. 28:11397-11406(2000).

CC -- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL: AE002328; AAPM39423; 1; --.

CC TIGR: TC0591; IPR001790; Ribosomal L10. Interpro: IPR002363; Ribosomal_L10eub. DR Pfam: PF00466; RIBOSOMAL_L10; 1. DR PROSITE: PS01109; RIBOSOMAL_L10; 1. KW ribosomal protein; Complete proteome; SEQUENCE 172 AA; 1817 MW; 9579AE1d42268483 CRC64;

Query Match 100%; Score 20; DB 1; Length 172; Best Local Similarity 100%; Pred. No. 2e+02; Indels 0; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Qy 1 AAPM 4 Db 142 AAPM 145

RESULT 22

RULJ_CHLTR	STANDARD;	PRT;	172 AA.
ID RULJ_CHLTR			
AC O84311;			
DT 20-MAY-2000 (Rel. 39, Created)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE 50S ribosomal protein L10.			
GN RULJ OR RULJ OR C1317.			
OS Chlamydia trachomatis.			
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.			
OX NCBI_TAXID=813; RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=D/W-3/C/X;			
RX MEDLINE=95000809; PUBMED=9784136;			
RA Stephens R.S., Kalmus S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W., "Genomic sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis," Science 262:755-759(1998).			
CC -- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.			
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CC EMBL: AE001304; AAC67910; 1; --.			
CC PF00466; RIBOSOMAL_L10eub.			
DR Interpro: IPR001790; Ribosomal_L10eub.			
DR Pfam: PF00466; RIBOSOMAL_L10; 1.			
DR PROSITE: PS01109; RIBOSOMAL_L10; 1.			
KW Ribosomal protein; Complete proteome.			

RESULT 23

VEGA_BOVIN	STANDARD;	PRT;	190 AA.
ID VEGA_BOVIN			
AC P15691;			
DT 01-APR-1990 (Rel. 14, Created)			
DT 01-APR-1990 (Rel. 14, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DT vascular endothelial growth factor A precursor (VEGFA) (Vascular permeability factor) (VPF).			
DE VEGF OR VEGFA.			
OS Bos taurus (Bovine).			
OC Mammary; Gutierrez; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovine; Bos.			
OX NCBI_TAXID=9913;			
RN [1]			
RP SEQUENCE FROM N.A. AND SEQUENCE OF 27-47.			
RX MEDLINE=90069688; PUBMED=2479986;			
RA Leung D.W., Cachianes G., Kiang W.-J., Goeddel D.V., Ferrara N.; Lau K., Crisp T., Fiddes J.C.; Abraham J.A.; "vascular endothelial growth factor is a secreted angiogenic mitogen.";			
RT Science 246:1306-1309(1999).			
RT [2]			
RP SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).			
RX MEDLINE=90121625; PUBMED=2610687;			
RA Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J., Lau K., Crisp T., Fiddes J.C.; Abraham J.A.; "vascular endothelial growth factor: a new member of the Platelet-derived growth factor gene family";			
RT Biochem. Biophys. Res. Commun. 165:1198-1206(1989).			
RN [3]			
RP SEQUENCE OF 27-31.			
RX MEDLINE=89386596; PUBMED=2735925;			
RA Ferrara N., Henzel W.J.; "Pituitary follicular cells secrete a novel heparin-binding growth factor specific for vascular endothelial cells";			
RT Biochem. Biophys. Res. Commun. 161:831-838(1989);			
RL -- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and proliferation of endothelial cell growth. It induces endothelial cell induces permeabilization of blood vessels. It binds to the VEGFR1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).			
CC -- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer.			
CC -- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).			
CC -- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are produced by alternative splicing.			
CC -- SIMILARITY: BELONGS TO THE PGF/VEGF FAMILY OF GROWTH FACTORS.			
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CC EMBL: M32976; AAA30502; 1; --.			
CC EMBL: M31836; AAA30504; 1; --.			

DR EMBL; M33750; AAA30805.1; -.

DR PIR; A33255; A33255.

DR HSSP; P15692; IVGH.

DR InterPro; IPR000072; PD_growth_factor.

DR Pfam; PF00341; PDGF_1.

DR ProDom; P001629; PD_growth_factor; 1.

DR SMART; SM00141; PDGF_1.

DR PROSITE; PS00249; PDGF_1.

DR PROSITE; PS50278; PDGF_2; 1.

KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;

KW Heparin-binding; Alternative splicing; Multigene family.

FT SIGNAL 1 26 VASCULAR ENDOTHELIAL GROWTH FACTOR A.

FT CHAIN 27 190 BY SIMILARITY.

FT DISULFID 51 93 BY SIMILARITY.

FT DISULFID 82 127 BY SIMILARITY.

FT DISULFID 86 129 BY SIMILARITY.

FT DISULFID 76 75 INTERCHAIN (BY SIMILARITY).

FT DISULFID 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 100 100 MISSING (IN ISOFORM BETA).

FT VARSPLIC 139 183 R -> K (IN ISOFORM BETA).

FT VARSPLIC 184 184 EDBF903946E24789 CRC64;

SQ SEQUENCE 190 AA; 22310 MW; EDBF903946E24789 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 190;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4

Db 26 AAPM 29

RESULT 24

ID VEGA_HORSE STANDARD; PRT; 190 AA.

AC Q9GR0; 09GL52; 09GL52;

DT 15-JUN-2002 (Rel. 41, created)

DT 15-JUN-2002 (Rel. 41, last sequence update)

DE Vascular endothelial growth factor A precursor (VEGF-A) (vascular permeability factor) (VEGF).

GN VEGF OR VEGFA.

OS Equus caballus (Horse).

OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus;

NCBI_TAXID=9796;

RN SEQUENCE FROM N.A.

RA Mura N., Misumi K., Kawahara K., Nakashima M., Fukumitsu S., Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H., "Cloning of cDNA and high-level expression of equine vascular endothelial growth factor (VEGF)."; Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).

CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PLGF (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).

CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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DR EMBL; AB053350; BAB20890.1; -.

DR HSSP; P15692; IVGH.

DR InterPro; IPR000072; PD_growth_factor.

DR Pfam; PF00341; PDGF_1.

DR ProDom; P001629; PD_growth_factor; 1.

DR SMART; SM00141; PDGF_1.

DR PROSITE; PS00249; PDGF_1.

DR PROSITE; PS50278; PDGF_2; 1.

KW Multigene; Angiogenesis; Growth factor; Glycoprotein; Signal;

KW Heparin-binding; Alternative splicing; Multigene family.

FT SIGNAL 1 26 VASCULAR ENDOTHELIAL GROWTH FACTOR A.

FT CHAIN 27 190 BY SIMILARITY.

FT DISULFID 51 93 BY SIMILARITY.

FT DISULFID 82 127 BY SIMILARITY.

FT DISULFID 86 129 BY SIMILARITY.

FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).

FT DISULFID 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 190 AA; 22312 MW; 8729E161439EF87 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 190;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4

Db 26 AAPM 29

RESULT 25

ID VEGA_PIG STANDARD; PRT; 190 AA.

AC P4951; 09GL52; 09GL52;

DT 01-FEB-1996 (Rel. 33, created)

DT 01-FEB-1996 (Rel. 33, last sequence update)

DE Vascular endothelial growth factor A precursor (VEGF-A) (vascular permeability factor) (VEGF).

GN VEGF OR VEGFA.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

NCBI_TAXID=9823;

RN [1] RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RA MEDLINE:95141284; PubMed=7841203;

RA Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.; "Nucleotide sequence and expression of the porcine vascular endothelial growth factor.".

RL Biochim. Biophys. Acta 1260:235-238(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Leg.T., Carty J.M.; "PCR cloning of porcine cardiac vascular endothelial growth factor gene.";

RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).

CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PLGF (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).

CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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CC EMBL; X81380; CAA51143.1; -.

CC DR EMBL; AF318502; AAC333004.1; -.

CC DR HSSP; P15692; IVGH.

CC DR InterPro; IPR000072; PP_growth_factor.

CC DR Pfam; PF00341; PDGF; 1.

CC DR Prodrom; PDD01629; PD_growth_factor; 1.

CC DR SMART; SM00141; PDGF; 1.

CC DR PROSITE; PS00249; PDGF; 1.

CC KW PROSTATE; PS50278; PDGF; 2; 1.

CC KW MitoGen; Angiogenesis; Growth factor; Glycoprotein; Signal;

CC KW Heparin-binding; Multigene family.

CC FT SIGNAL 1

CC FT CHAIN 27 190

CC FT DISULFID 51 93

CC FT DISULFID 82 127

CC FT DISULFID 76 76

CC FT DISULFID 85 85

CC FT CARBOHYD 100 100

CC FT CONFLICT 102 102

CC SQ SEQUENCE 190 AA; 2266 MW; 04D40BB0D7913047F CRC64;

Query Match 100.0%; Score 20; DB 1; Length 190;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 1 AAPM 4

Db 26 AAPM 29

RESULT 26

CBP2_ARATH ID CBP2_ARATH STANDARD; PRT; 191 AA.

AC P301187; AC DT 01-APR-1993 (Rel. 25, created)

AC DT 01-APR-1993 (Rel. 25, last sequence update)

AC DT 15-OCT-2001 (Rel. 40, last annotation update)

DE 22 kDa calmodulin-like calcium-binding protein (CBP2-22).

GN AT2G41090 OR TAK9.14.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia; TISSUE=leaf;

RX MEDLINE=93183626; PubMed=8507824;

RA Ling V.; Zielinski R.E.;

RT "Isolation of an Arabidopsis cDNA sequence encoding a 22 kDa calcium-binding protein (CBP2-22) related to calmodulin.";

RL Plant Mol. Biol. 22:207-214(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083487; PubMed=10617197;

RA Lin X.; Kaul S.; Rounseville S.D.; Shea T.P.; Benito M.-I.; Town C.D.;

RA Fuji J.Y.; Mason T.M.; Bowman C.L.; Barnstead M.E.; Feldblum T.V.;

RA Bell C.R.; Keckhun K.A.; Lee J.J.; Ronning C.M.; Koo H.L.;

RA Moffat K.S.; Cronin L.A.; Pai G.; Van Aken S.; Umayan L.,

RA Tallon L.J.; Gill J.B.; Adams M.D.; Carrera A.J.; Creasy T.H.;

RA Goodman H.M.; Somerville C.R.; Copenhaver G.P.; Preuss D.;

RA Nierman W.C.; White O.; Eisen J.A.; Salzberg S.L.; Fraser C.M.;

RA Venette J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";

RT Nature 402:761-768(1999).

CC ! TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN LEAVES.

CC ! SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

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CC !

CC DR EMBL; Z12136; CAA78124.1; -.

CC DR EMBL; AC004261; AAC12002.1; -.

CC DR PIR; S25125; S25125.

CC DR PIR; S35188; S35188.

CC DR HSSP; P2593; 1CDM.

CC DR InterrPro; IPR002048; EF-hand.

CC DR Pfam; PF00036; eifhand; 4.

CC DR Prodrom; PDD00012; EF-hand; 2.

CC DR PROSITE; PS00054; EFH; 4.

CC DR PROSITE; PS00018; EF_HAND; 4.

CC DR Calcium-binding; Repeat.

CC FT CA_BIND 21 32

CC FT CA_BIND 57 68

CC FT CA_BIND 91 102

CC FT CA_BIND 127 138

CC SQ SEQUENCE 191 AA; 21727 MW; 571F40CIE64370AB CRC64;

Query Match 100.0%; Score 20; DB 1; Length 191;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAPM 4

Db 175 AAPM 178

RESULT 27

ACD2_CLOPE ID ACD2_CLOPE STANDARD; PRT; 198 AA.

AC 08XM99; AC DT 15-JUN-2002 (Rel. 41, created)

AC DT 15-JUN-2002 (Rel. 41, last sequence update)

AC DT 15-JUN-2002 (Rel. 41, last annotation update)

DE Putative acyl carrier protein phosphodiesterase 2 (EC 3.1.4.14) (ACP DE Phosphodiesterase 2).

GN CPE0191.

OS Clostridium perfringens

OC bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium; Clostridium.

OX NCBI_TaxID=1502;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=13 / Type A;

RX Pubmed=11192842;

RA Shimizu T.; Ontani K.; Hirakawa H.; Oshshima K.; Yamashita A.,

RA Siba T.; Ogawara N.; Hattori M.; Kubara S.; Hayashi H.;

RT "Complete genome sequence of Clostridium perfringens, an anaerobic RT flesh-eater.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

CC FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of CC the phosphopantetheine prosthetic group from ACP (By similarity).

CC -!- CATALYTIC ACTIVITY: Holo-acyl-carrier protein + H(2)O = 4'-CC phosphopantetheine + apo-[acyl]-carrier protein].

CC ! SIMILARITY: BELONGS TO THE ACPD FAMILY.

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CC -----
DR EMBL; AP003188; BAR80497.1; -;
KW Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 198 AA; 22835 MW; 1BPE0B6B2EB1C3 CRC64;

Query Match	Best Local Similarity	Score	Pred.	No.	Mismatches	Indels	Gaps
Matches 4;	Similarity 100.0%;	Score 20;	DB 1;	Length 198;			
Conservative 0;	Pred. No. 2.3e+02;			Mismatches 0;			
Indels 0;							
Gaps 0;							

Qy 1 AAPM 4
Db 89 AAPM 92

RESULT 28
ACPD_ECO57 STANDARD; PRT: 200 AA.
ID ACPD_ECO57 STANDARD; PRT: 200 AA.
AC Q8X9S9;
DT 15-JUN-2002 (Rel. 41, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP)
GN ACPD OR 22315 OR EG52014.
OS Escherichia coli 0157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia;
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / EDL933 / ARCC 700927;
RX MEDLINE=21150231; PubMed=12258796;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohemorrhagic Escherichia coli 0157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / RIMD 0509952;
RX MEDLINE=21150231; PubMed=12258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Otsukai H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kubara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res 8:11-22(2001).
RL Res 8:11-22(2001).
CC -I- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of
the phosphopantetheine prosthetic group from ACP. Its
physiological function is not clear (By similarity).
CC -I- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H₂O = 4'-
CC Phosphopantetheine + apo-[acyl-carrier protein].
CC -I- SIMILARITY: BELONGS TO THE ACPD FAMILY.

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or send an email to license@isb-sib.ch).

DR AP005365; AAG56367.1; -.
DR AP00257; BAB35437.1; -.
KW Hydrolase; Complete proteome.
FT INT_MET 0 BY SIMILARITY.
SQ SEQUENCE 200 AA; 21514 MW; 5672782FF940FFCE CRC64;

Query Match 100.0%; Score 20; DB 1; Length 200;

Best Local Similarity	Score	Pred.	No.	Mismatches	Indels	Gaps
Matches 4;	Similarity 100.0%;	Score 20;	DB 1;	Length 198;		
Conservative 0;	Pred. No. 2.3e+02;			Mismatches 0;		
Indels 0;						
Gaps 0;						

Qy 1 AAPM 4
Db 92 AAPM 95

RESULT 29
ACPD_ECOLI STANDARD; PRT: 200 AA.
ID ACPD_ECOLI STANDARD; PRT: 200 AA.
AC P4107; P77143; Q93V21;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP)
DE Phosphodiesterase (EC 3.1.4.14) (ACP)
GN ACPD OR B1412.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Kitakawa M., Kasai H., Baba T., Honjo A., Isono K.;
"NUCLEOTIDE SEQUENCE OF THE REPLICATION TERMINUS REGION OF ESCHERICHIA COLI";
RT Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RL [2]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kasimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Micobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura T., Nashimura H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
RA Takeimoto K., Takeuchi Y., Wada C., Yamamoto Y., Horituchi T.,
RT "A 57-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
RN [4]
RP SEQUENCE OF 1-143 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=95206938; PubMed=7899078;
RA Moriya H., Kasai H., Isono K.;
RT "Cloning and characterization of the hrpa gene in the terc region of
Escherichia coli that is highly similar to the DEAH family RNA
helicase genes of Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 23:595-598(1995).
RN [5]
RP SEQUENCE OF 1-15, AND CHARACTERIZATION.
RX MEDLINE=90368607; PubMed=2168383;
RA Fischl A.S., Kennedy E.P.,
"Isolation and properties of acyl carrier protein phosphodiesterase
of Escherichia coli.";
RL J. Bacteriol. 172:5445-5449(1990).
CC -I- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of
the phosphopantetheine prosthetic group from ACP. Its
physiological function is not clear.
CC -I- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H₂O = 4'-
phosphopantetheine + apo-[acyl-carrier protein].

CC -!- SIMILARITY: BELONGS TO THE ACPC FAMILY.

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CC EMBL: D85031; BAA25408_1; -.

DR EMBL; AE000238; AAC74494_1; -.

DR EMBL; D97670; BAA15282_1; -.

DR EMBL; D90779; BAA15241_1; -.

DR EMBL; D42105; BAA1684_1; -.

DR EMBL; EG12695; acpc; -.

KW Hydrolase; Complete proteome.

FT INIT_MET 0

FT CONFLICT 22 34 DYFVEQWREKHS A-> ITLLNNGAKSTRP (IN REF 1 AND 4).

FT SEQ 200 AA; 21526 MW; E26A182AED432BC8 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 200;

Best Local Similarity 100.0%; Pred. No. 2; 3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 92 AAPM 95

RESULT 30

ACPD_SALTY STANDARD: PRT; 200 AA.

ID Q8AFP4; (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP)

DE Phosphodiesterase).

GN ACPO OR STM642 OR STY1427.

OS Salmonella typhimurium, and

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBL_TaxID-602, 601;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=S. typhimurium; STRAIN=LTH / SGSC1412 / ATCC 700720;

RX MEDLINE=21534946; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvanev E., Ryan E., Sun H., Flores L., Miller W., Stoenkirk T., Khan M., Waterston R., Wilson R.K.;

RT "complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2";

RL Nature 413:852-856(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=S. typhi; STRAIN=CT18;

RX MEDLINE=21334947; PubMed=11677608;

RA Parkhill J., Dougan G., James D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Mungall G., Holden M.T.G., Barrell B.G., Brooks D., Bentley S.D., Brooks S.D., Cerdano-Tarraga A.M., Baker S., Basham D., Bentley D., Cronin A., Davies R.M., Davis P., Dougan G., Chillingworth T., Durbin R., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moulis S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; RT "Genome sequence of *Yersinia pestis*, the causative agent of plague";

RL Nature 413:523-527(2001).

CC -!- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP. Its physiological function is not clear (By similarity).

CC -!- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)O = 4/- phosphopantetheine + apo-[acyl-carrier protein].

CC -!- SIMILARITY: BELONGS TO THE ACPC FAMILY.

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DR EMBL: AJ414152; CAC91120.1; -.
 KW Hydrolase; Complete proteome.
 FT INIT_MEI 0 BY SIMILARITY.
 SEQUENCE 200 AA; 21468 MW; 0512BFS28000808F CRC64;
 SQ Best Local Similarity 100.0%; Score 20; DB 1; Length 200;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS
 QY 1 AAPM 4
 |||||
 Db 92 AAPM 95

RESULT 32
 ACD3_PSEAE STANDARD; PRT; 213 AA.
 AC 09H217; DT 15-JUN-2002 (Rel. 41, created)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Putative acyl carrier protein phosphodiesterase 3 (EC 3.1.4.14) (ACP
 DE phosphodiesterase 3).
 GN PA3223.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]-
 SEQUENCE FROM N.A.
 RC STRAIN=AVCC 15692 / PAOL;
 RX MEDLINE=200437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 RA Hickey M.J., Brinkman F.S.L., Hurlage W.O., Kovalek D.J., Lagrou M.,
 RA Gabber R.L., Golty L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brady L.L., Coulter S.N., Folger K.R., Kas A., Harbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen T.T.,
 RA Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAOL, an
 RT opportunistic pathogen." Nature 406:959-960(2000).
 CC Nature 406:959-960(2000).
 CC -- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of
 CC the phosphopantetheine prosthetic group from ACP (BY similarity).
 CC -- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H₂O = 4,-
 CC phosphopantetheine + apo-[acyl-carrier protein].
 CC -- SIMILARITY: BELONGS TO THE ACPD FAMILY.
 CC
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 CC
 DR EMBL: AE004745; AAC06611.1; -.
 DR HYPOTHETICAL protein; Hydrolase; Complete proteome.
 SQ SEQUENCE 213 AA; 23898 MW; DBE4B84DFD627E7B CRC64;

Query Match 100.0%; Score 20; DB 1; Length 213;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS
 QY 1 AAPM 4
 |||||
 Db 93 AAPM 96

RESULT 33
 VEGA_CANFA STANDARD; PRT; 2114 AA.
 ID VEGA_CANFA
 AC 09MV3; 09XSF5; 09XSF4; 09XSF3;
 DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
 DE permeability factor) (VPF).
 GN VEGF OR VEGFA.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]-
 RP SEQUENCE FROM N.A. (ISOFORM VEGF188).
 RX MEDLINE=20125516; PubMed=10661877;
 RA Schiedecker P., Weiglhofer W., Suarez S., Kaser-Hotz B., Steiner R.,
 RA Ballmer-Hofen K., Jaussi R.;
 RT "Vascular endothelial growth factor (VEGF) and its receptors in tumor-
 bearing dogs".
 RL Biol. Chem. 300:1449-1454(1999).
 RN [2]-
 RP SEQUENCE FROM N.A. (ISOFORMS VEGF188; VEGF-182 AND VEGF-164).
 RC TISSUE Heart;
 RA JinDing L., Roque R.S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
 CC proliferation, promotes cell migration, inhibits apoptosis, and
 CC induces permeabilization of blood vessels. It binds to the
 CC VEGFR1/FT1-1 and VEGFR2/Kdr receptors and to heparan sulfate and
 CC heparin. (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
 CC with PIGF (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 CC to the extracellular matrix unless released by heparin (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms: VEGF188 (shown here),
 CC VEGF182 and VEGF164; are produced by alternative splicing.
 CC -!- SIMILARITY: BELONGS TO THE PGF/VEG FAMILY OF GROWTH FACTORS.
 CC ---
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 CC ---
 DR EMBL: AJ133758; CAB2426.1; -.
 DR EMBL: AF133259; AAD29653.1; -.
 DR EMBL: AF133248; AAD29682.1; -.
 DR HSSP: P15692; LVGH.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00341; PDGF; 1.
 DR ProDom: PD001629; PD_growth_factor; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
 KW Heparin-binding; Alternative splicing; Multigene family.
 FT SIGNAL 1 BY SIMILARITY.
 FT CHAIN 27 214 BY SIMILARITY.
 FT VASCULAR ENDOTHELIAL GROWTH FACTOR A.
 FT DISULFID 51 93 BY SIMILARITY.
 FT DISULFID 82 127 BY SIMILARITY.
 FT DISULFID 86 129 BY SIMILARITY.
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 100 100 N-LINKED GLCNAC. (POTENTIAL).
 FT VARSPLIC 140 140 K -> N (IN ISOFORM VEGF-164).
 FT VARSPLIC 141 164 MISSING (IN ISOFORM VEGF-164).
 FT VARSPLIC 159 164 MISSING (IN ISOFORM VEGF-182).
 FT CONFLICT 143 143 I -> V (IN REF. 2).
 FT CONFLICT 161 161 P -> S (IN REF. 2).
 SQ SEQUENCE 214 AA; 25175 MW; OAC98015844B27 CRC64;

Query Match	100.0%	Score 20;	DB 1;	Length 214;	CC
Best Local Similarity	100.0%	Pred. No.	2.4e+02;	Mismatches	0;
Matches	4;	Conservative	0;	Indels	0;
OY	1 AAPM 4			Gaps	0;
Db	26 AAPM 29				
RESULT	34				
RS5_DROME					
ID	RS5_DROME	STANDARD;	PRT;	228 AA.	CC
AC	Q24186; Q9YX78;				CC
DT	01-NOV-1997 (Rel. 35, created)				CC
DT	01-NOV-1997 (Rel. 35, last sequence update)				CC
DT	16-OCT-2001 (Rel. 40, last annotation update)				CC
DE	40S ribosomal protein S55				CC
GN	RS5 OR M(1)15 OR CG8922.				CC
OS	Drosophila melanogaster (Fruit fly)				CC
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				CC
OC	Insecta; Neoptera; Endopterygota; Diptera; Brachycera;				CC
OC	Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.				CC
OX	NEBI_TAXID:7227;				CC
RN	[1]				CC
RP	SEQUENCE FROM N.A.				CC
RX	MEDLINE-#7032939; Pubmed=8878687;				CC
RA	Markin K.S., Dalmat J., Hawley R.S.;				CC
RT	*Cloning of the Drosophila melanogaster meiotic recombination gene				CC
RT	meal-218: a genetic and molecular analysis of interval 15E.;				CC
RL	Genetics 144:215-228(1996).				CC
RN	[1-2]				CC
RP	SEQUENCE FROM N.A.				CC
RC	STRAIN-Berkeley;				CC
RX	MEDLINE-#20156006; Pubmed=10731132;				CC
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				CC
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				CC
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				CC
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				CC
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,				CC
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,				CC
RA	Abrial J.F., Agbayani A., An H.-J., Andrews C., Baldwin D.,				CC
RA	Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				CC
RA	Benson K.Y., Benos P.V., Berman B.P., Bhendari D., Bolshkov S.,				CC
RA	Borkova D., Borchan M.R., Bouk J., Brokstein P., Brottier P.,				CC
RA	Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				CC
RA	Cherry J.M., Cowley S., Dahake C., Davenport L.B., Davies P.,				CC
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew T., Dietz S.M.,				CC
RA	Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunker B.C., Dunn P.,				CC
RA	Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				CC
RA	Frolier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,				CC
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				CC
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				CC
RA	Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,				CC
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				CC
RA	Kimmel B.E., Koira C.D., Kraft C.D., Kravitz S., Kulp D., Lai Z.,				CC
RA	Lasko P., Lee Y., Levinsky A.A., Li J., Li Z., Liang Y., Lin X.,				CC
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,				CC
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherf A.,				CC
RA	Mount S.M., Moy M., Murphy B., Murphy L., Mizny D.M., Nelson D.L.,				CC
RA	Nelson D.R., Nelson K.A., Nixon K., Nusslein-Davidson D.R., Pacelli J.M.,				CC
RA	Pala M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				CC
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,				CC
RA	Schue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,				CC
RA	Spirer E., Spradling A.C., Stapleton M., Strong R., Sun E.,				CC
RA	Svorayas R., Tector C., Turner R., Venter J., Wang A.-H., Wang X.,				CC
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,				CC
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,				CC
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,				CC
RA	Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,				CC
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,				CC
RT	*The genome sequence of Drosophila melanogaster.;				CC
RT	Science 287:2185-2195(2000).				CC
RL	-- SIMILARITY: BELONGS TO THE STP FAMILY OF RIBOSOMAL PROTEINS.				CC
CC	--				CC
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CC	or send an email to license@ish.sib.ch).				CC
CC	--				CC
DR	EMBL: U048394; AAB61633; 1; -.				CC
DR	DRBSP: P22744; IHUS				CC
DR	EMBL: AE003504; AAP48700; 1; -.				CC
DR	PF000290; RPS5				CC
DR	PF000235; Ribosomal_S7				CC
DR	InterPro: IPR000235; Ribosomal_S7; 1.				CC
DR	ProDom: PD000817; Ribosomal_S7; 1.				CC
DR	TIGRFAMs: TIGR01028; S7_S5_EA; 1.				CC
DR	PROSITE: PS00052; RIBOSOMAL_S7; 1.				CC
KW	Ribosomal protein.				CC
SO	SEQUENCE 228 AA; 25434 MW; 9206B1DBFE470C4C CRC64;				CC
Query Match	100.0%	Score 20;	DB 1;	Length 228;	CC
Best Local Similarity	100.0%	Pred. No.	2.6e+02;	Mismatches	0;
Matches	4;	Conservative	0;	Indels	0;
OY	1 AAPM 4			Gaps	0;
Db	185 AAPM 188				CC
Query Match	100.0%	Score 20;	DB 1;	Length 229;	CC
Best Local Similarity	100.0%	Pred. No.	2.6e+02;	Mismatches	0;
Matches	4;	Conservative	0;	Indels	0;
OY	1 AAPM 4			Gaps	0;
Db	16 AAPM 19				CC
RESULT	35				CC
VMAT_VSVSJ					CC
ID	VMAT_VSVSJ STANDARD;	PRT;	229 AA.		CC
AC	P03519;				CC
DT	21-JUL-1986 (Rel. 01, Created)				CC
DT	21-JUL-1986 (Rel. 01, Last sequence update)				CC
DT	01-NOV-1990 (Rel. 16, Last annotation update)				CC
DE	Matrix protein.				CC
GN	Vesicular stomatitis virus (strain San Juan); Vesicular stomatitis virus (strain San Juan); Mononegavirales; Viruses; ssRNA negative-strand viruses; Mononegavirales; OC				CC
OC	Rhabdoviridae; Vesiculovirus.				CC
OX	NC_001285;				CC
RN	[1]				CC
RP	SEQUENCE FROM N.A.				CC
RX	MEDLINE-#8201068; Pubmed=6268840;				CC
RA	Rose J.K., Gallione C.J.;				CC
RA	RT Nucleotide sequence of the mRNA's encoding the vesicular stomatitis virus G and M proteins determined from cDNA clones containing the complete coding regions.;				CC
RT	RT J. Virol. 39:519-528(1981);				CC
RL					CC
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CC	--				CC
DR	EMBL: J02428; AAA818369; 1; -.				CC
DR	DRBSP: A04111; MFVN.				CC
KW	Matrix Protein; Envelope protein.				CC
SO	SEQUENCE 229 AA; 20694 MW; C89E2ACAA4365B847 CRC64;				CC
Query Match	100.0%	Score 20;	DB 1;	Length 229;	CC
Best Local Similarity	100.0%	Pred. No.	2.6e+02;	Mismatches	0;
Matches	4;	Conservative	0;	Indels	0;
OY	1 AAPM 4			Gaps	0;
Db	185 AAPM 188				CC

RESULT 36
 YXHK_CAEEL STANDARD; PRT; 229 AA.
 CC
 ID YXHK_CAEEL STANDARD;
 AC Q20728;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein F53F4..3 in chromosome V.
 GN F53F4..3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis.
 NCBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Barlow K.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: CONTAINS 1 CAP-GLY DOMAIN.
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 CC
 EMBL: Z77663; CABD121..1; -.
 DR Wormpep; F53F4..3; CE1058.
 DR InterPro; IPR000938; CAP-GLY.
 DR Pfam; PF01302; CAP-GLY_1.
 DR PROSITE; PS00845; CAP-GLY_1; 1.
 DR PROSITE; PS00245; CAP-GLY_2; 1.
 KW Hypothetical protein; Cytoskeleton; Microtubules.
 FT DOMAIN 170 212 CAP-GLY.
 SEQUENCE 229 AA: 25440 MW: C465365DAE378A0F CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 |||||
 Db 128 AAPM 131
 RESULT 37
 YROL_CAEEL STANDARD; PRT; 231 AA.
 AC Q10014;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein T25E4..1 in chromosome II precursor.
 GN T25E4..1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis.
 NCBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Johnsson D.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: STRONG, TO C.ELEGANS D2095..6.
 CC
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 CC
 DR EMBL; U23411; AAC46730; 2; -.
 DR Wormpep; T25E4..1; CE28493.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 231 HYPOTHETICAL PROTEIN T55E4..1.
 SQ SEQUENCE 231 AA: 24613 MW: 8832AF97C3F7BB08 CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 231;
 best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 |||||
 Db 84 AAPM 87
 RESULT 38
 ID VEGA_HUMAN STANDARD; PRT; 232 AA.
 AC P15692; Q16889; O60720; O75875; Q9U23; Q9H1W8; Q9H1W8;
 AC Q9H1W5;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Vasculular endothelial growth factor (VEGF-A) (Vascular
 DE permeability factor) (VPF).
 GN VEGF OR VEGA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS VEGF189 AND VEGF165).
 RX MEDLINE:9006608; PubMed=2479986;
 RA Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
 RT "vascular endothelial growth factor A precursor (VEGF-A) (Vascular
 RT mitogen);",
 RL Science 246:1306-1309(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE.
 RX MEDLINE:90059609; PubMed=2479987;
 RA Keck P.J., Hauser S.D., Krivil G., Sanzo K., Warren T., Feder J.,
 RA Connolly D.T.;
 RT "vascular permeability factor, an endothelial cell mitogen related to
 RT pOF";
 RL Science 246:1309-1312(1989).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF189).
 RX MEDLINE:91268072; PubMed=111045;
 RA Fischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
 RA Fiddes J.C., Abramham J.A.;
 RT "The human gene for vascular endothelial growth factor. Multiple
 RT protein forms are encoded through alternative exon splicing.",
 RL J. Biol. Chem. 266:11947-11954(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF206).
 RX MEDLINE:92188017; PubMed=1791831;
 RA Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;
 RT "The vascular endothelial growth factor family: identification of a
 RT fourth molecular species and characterization of alternative splicing
 RT of RNA.",
 RL Mol. Endocrinol. 5:1806-1814(1991).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
 RX MEDLINE:92231879; PubMed=1567395;

- RA Weinodel K., Marme D., Welch H.A.;
RT "AIDS-associated Kaposi's sarcoma cells in culture express vascular
endothelial growth factor.";
RL Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
- RN [6]
- RP SEQUENCE FROM N.A. (ISOFORM VEGF145).
RX MEDLINE=97207275; PubMed=9054410;
RA Poltorak Z., Cohen T., Sivan R., Kandelis Y., Spira G., Vlodavsky I.,
RA Kashet E., Neufeld G.;
"VEGF145, a secreted vascular endothelial growth factor isoform that
binds to extracellular matrix.";
RT J. Biol. Chem. 272:7151-7158(1997).
RN [7]
- RP SEQUENCE FROM N.A. (ISOFORM VEGF183).
RC TISSUE-RIDLEY;
RX MEDLINE=99096474; PubMed=9878851;
RA Lei J., Jiang A., Pei D.;
"Identification and characterization of a new splicing variant of
vascular endothelial growth factor: VEGF183.";
RT Biochim. Biophys. Acta 1443:400-406(1998).
RN [8]
- RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
RC TISSUE-BREAST;
RX MEDLINE=98119755; PubMed=9450968;
RA Claffey K.P., Shih S.-C., Mullen A., Dziennis S., Cusick J.L.,
RA Abrams K.R., Lee S.W., Detmar M.;
"Identification of a human VPF/ESF 3' untranslated region mediating
hypoxia-induced mRNA stability";
RT Mol. Biol. Cell 9:469-481(1998).
RN [9]
- RP SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183).
RC TISSUE-Retina;
RX MEDLINE=99165303; PubMed=10067980;
RA Jingjing L., Xue Y., Ararwal N., Roque R.S.;
RT "Human Muller cells express VEGF183, a novel spliced variant of
vascular endothelial growth factor";
RL Invest. Ophthalmol. Vis. Sci. 40:752-759(1999).
RN [10]
- RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
RC TISSUE-Hemangioperitoneum;
RA Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.;
RT "Human cDNA for the vascular endothelial growth factor isoform
VEGF165.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [11]
- RP SEQUENCE FROM N.A. (ISOFORM VEGF148).
RC TISSUE-Renal glomerulus;
RX MEDLINE=99394945; PubMed=10464055;
RA Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W.,
RA Harper S.J.;
RT "Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA
and receptor mRNA expression in human glomeruli, and the
identification of VEGF148 mRNA, a novel truncated splice variant.";
RT Clin. Sci. 97:303-312(1999).
RN [12]
- RP SEQUENCE FROM N.A. (ISOFORM VEGF121).
RA Satco J.D., Whitney R.G.;
RT "Human cDNA for vascular endothelial growth factor isoform VEGF121.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [13]
- RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [14]
- RP SEQUENCE OF 23-232 FROM N.A. (VEGF165).
RA Rieder M.J., Arnett T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [15]
- RP PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX MEDLINE=90062112; PubMed=2584205;
RA Connolly D.T., Olander J.V., Hevelelman D., Nelson R., Monsell R.,
RA Siegel N., Haymore B.L., Leingruber R., Feder J.;
- RT "Human vascular permeability factor. Isolation from U937 cells.";
RL J. Biol. Chem. 264:20017-20024(1989).
RN [16]
- RP SEQUENCE OF 27-41.
RX MEDLINE=93145946; PubMed=7678805;
RA Kochs D., Marme D., Hug H., Welch H.A.;
"Synthesis and assembly of functionally active human vascular
endothelial growth factor homodimers in insect cells.";
RL Eur. J. Biochem. 211:19-26(1993).
RN [17]
- RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
de Vos A.M.;
RT "Vascular endothelial growth factor: crystal structure and functional
mapping of the kinase domain receptor binding site.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN [18]
- RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX MEDLINE=98035035; PubMed=95211807;
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
"The crystal structure of vascular endothelial growth factor (VEGF)
refined to 1.93-A resolution: multiple copy flexibility and receptor
binding.";
RL Structure 5:1325-1338(1997).
RN [19]
- RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX MEDLINE=99119204; PubMed=9322112;
RA Westmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
Fairbrother W.J., Keenan C.H., Meng G., de Vos A.M.;
"Crystal structure of the complex between VEGF and a receptor-blocking
peptide.";
RL Biochemistry 37:17765-17772(1998).
RN [20]
- RP STRUCTURE BY NMR OF 34-135.
RX MEDLINE=9477915; PubMed=9336848;
RA Fairbrother W.J., Champé M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "1H, 13C, and 15N backbone assignment and secondary structure of the
receptor-binding domain of vascular endothelial growth factor.";
RL Protein Sci. 6:2250-2260(1997).
RN [21]
- RP STRUCTURE BY NMR OF 137-215.
RX MEDLINE=98298440; PubMed=9334701;
RA Fairbrother W.J., Champé M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "Solution structure of the heparin-binding domain of vascular
endothelial growth factor.";
RL Structure 6:637-648(1998).
RN [22]
- RP FUNCTION.
RX MEDLINE=21320570; PubMed=11427521;
RA Murphy J.F., Fitzgerald D.J.;
RT "Vascular endothelial growth factor induces cyclooxygenase-dependent
proliferation of endothelial cells via the VEGF-2 receptor.";
RL FASEB J. 15:1657-1659(2001).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and
induces permeabilization of blood vessels. It binds to the
VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and
heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
with PIGF (By similarity).
CC -1- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.
CC VEGF165 is more basic, has heparin-binding properties and,
although a significant proportion remains cell-associated, most is
freely secreted. VEGF189 is very basic; it is cell-associated
after secretion and is bound avidly by heparin and the
extracellular matrix, although it may be released as a soluble
form by heparin, heparinase or plasmin.
CC -1- ALTERNATIVE PRODUCTS: 7 isoforms; VEGF206 (shown here), VEGF189,

CC VEGF183, VEGF165/VEGF, VEGF148, VEGF145 and VEGF121; may be produced by alternative splicing.

CC -!- TISSUE SPECIFICITY: The VEGF189, VEGF-165 and VEGF-121 isoforms are widely expressed, whereas the VEGF206 and VEGF-145 are uncommon.

CC -!- INDUCTION: Regulated by growth factors, cytokines, gonadotropins, nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.

Query Match 100.0%; Score 20; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; DT 13-AUG-1987 (Rel. 05, Last sequence update)
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DE 01-Nov-1995 (Rel. 32, Last annotation update)

Qy 1 AAPM 4
Db 26 AAPM 29

RESULT 39

YV26_MYCNU STANDARD: PRT; 232 AA.

ID YV26_MYCNU
AC Q50702
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical PPE family protein Rv3426.
GN Rv3426 OR MRCY78 OR 03C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales; Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID:1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN="H37Rv";
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutten S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; RT deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. ";
RT Nature 393:537-544(1998).
RL Nature 393:537-544(1998).
CC -!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.

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ID VMAT_VSVIG STANDARD: PRT; 237 AA.

AC P04876;
DR P04876; 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 01-Nov-1995 (Rel. 32, Last annotation update)

M. Vesicular stomatitis virus (serotype Indiana / strain Glasgow).
OS Vesicular stomatitis virus (serotype Indiana / strain Glasgow).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11278;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86142630; PubMed=3005478;
RA Vandepol S.B., Holland J.J.;
RT "Evolution of vesicular stomatitis virus in athymic nude mice: mutations associated with natural killer cell selection.";
RL J. Virol. 57:441-451(1986).
RN [2]
RP SEQUENCE OF 1-229 FROM N.A.
RX MEDLINE=86068892; PubMed=2999421;
RA Gopalakrishna Y., Lenard J.;
RT "Sequence alterations in temperature-sensitive M-protein mutants (complementation group III) of vesicular stomatitis virus.";
RL J. Virol. 56:655-659(1985).
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DR EMBL; X04452; CAM28051.1; -.
DR EMBL; M11754; AAA4844.1; -.
DR P04876; M8VNGG.
KW Matrix protein; Envelope protein.

FT CONFLICT 32 32 S -> N (IN REF. 2).
FT CONFLICT 64 64 S -> F (IN REF. 2).
FT CONFLICT 215 215 E -> K (IN REF. 2).
FT CONFLICT 228 228 S -> F (IN REF. 2).
SQ SEQUENCE 237 AA: 26824 MW; C1DF0CF71510959D CRC64;

Query Match 100.0%; Score 20; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; DT 13-AUG-1987 (Rel. 05, Last sequence update)
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DE 01-Nov-1995 (Rel. 32, Last annotation update)

Qy 1 AAPM 4
Db 185 AAPM 188

SEQUENCE 232 AA; 23872 MW; D76512D49EB272C6 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; DT 13-AUG-1987 (Rel. 05, Last sequence update)
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DE 01-Nov-1995 (Rel. 32, Last annotation update)

Qy 1 AAPM 4
Db 163 AAPM 166

RESULT 40
VMAT_VSVIG

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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 6, 2002, 13:25:09 ; Search time 19.5556 seconds
 (without alignments)
 .42.146 Million cell updates/sec

title:	US_10-033-526-2
Perfect score:	20
Sequence:	1 AAPM 4
Scoring table:	BLOSUM62
Gapop:	10.0 , Gapext: 0.5
searched:	671580 seqs, 206047115 residues
total number of hits satisfying chosen parameters:	671580
Minimum DB seq length:	0
Maximum DB seq length:	200000000
post-processing:	Minimum Match 0%
Maximum Match 100%	
Listing first 45 summaries	

Database :

- 1: SPREMBL_21; *
- 2: sp_archeab; *
- 3: sp_bacteria; *
- 4: sp_human; *
- 5: sp_invertebrate; *
- 6: sp_mammal; *
- 7: sp_minic; *
- 8: sp_organelle; *
- 9: sp_phage; *
- 10: sp_plant; *
- 11: sp_rabbit; *
- 12: sp_rat; *
- 13: sp_vertebrate; *
- 14: sp_unclassified; *
- 15: sp_rvirus; *
- 16: sp_bacteriap; *
- 17: sp_archeap; *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	20	10.0	23	10	Q94AM6	Q94am6 arabidopsis
2	20	10.0	30	4	Q96TC2	Q96tc2 homo sapien
3	20	10.0	47	4	Q96NB8	Q96nb8 homo sapien
4	20	10.0	53	12	Q3586	Q3586 hepatitis e
5	20	10.0	53	12	Q3589	Q3589 hepatitis e
6	20	10.0	53	12	Q3592	Q3592 hepatitis e
7	20	10.0	53	12	Q36583	Q36583 hepatitis e
8	20	10.0	53	12	Q36588	Q36588 hepatitis e
9	20	10.0	59	12	Q947U2	Q947u2 hepatitis e
10	20	10.0	61	6	Q97581	Q97581 cantharis dro
11	20	10.0	71	10	Q85666	Q85666 oryza sativa
12	20	10.0	76	6	Q91MK8	Q91mk8 monodelphis
13	20	10.0	76	8	Q96UH7	Q96uh7 salmon salar
14	20	10.0	76	11	Q89946	Q89946 mus musculus
15	20	10.0	77	10	Q85764	Q85764 oryza sativa
16	20	10.0	79	5	Q94188	Q94188 coenorhabdi

RESULTS

ID	094AM6	PRELIMINARY;	PRT:	23 AA.
AC	Q94AM6;			
DT	01-DEC-2001 (TREMBL); 19, created)			
DT	01-DEC-2001 (TREMBL); 19, Last sequence update)			
DT	01-DEC-2001 (TREMBL); 19, Last annotation update)			
DE	Hypothetical 2.8 kDa protein.			
GN	T6L1-23.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Eudicotyledons; core eudicots; Rosidae; eucommiids II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen R., Cheuk R., Hayashizaki Y., Ishii J., Jones T., Kamiya A., Karlin-Neumann G., Kawaji J., Kim C., Koosema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shin P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Eckley J.R., Theologis A.;			
RA	"Full Length cDNA of gene T6L1-23 (not previously annotated).";			
RT	Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AV045928; ANK76602.1; -			
KW	Hypothetical protein.			
SO	SEQUENCE 23 AA; 2756 MW; DFL14370FC0FBF9BC CRC64;			

Query Match Best Local Similarity 100.0%; Score 20; DB 10; Length 23; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPM 4

Db 15 AAPM 18

RESULT 2		RESULT 4	
096TC2	PRELIMINARY;	PRT;	30 AA.
AC 096TC2;		ID 036586	PRELIMINARY;
DT 01-DEC-2001 (TREMBLrel. 19, Created)		AC 036586;	PRT;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)	53 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)		DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)	
DE Brain-derived neurotrophic factor (Fragment)		DE ORF-3 (Fragment)	
GN BDNF 2-5		OS Hepatitis E virus.	
OS Homo sapiens (Human).		OC ssRNA positive-strand viruses, no DNA stage;	
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		OC Hepatitis E-like viruses.	
OX NCBI_TaxID=9606;		OX NCBI_TaxID=12461;	
RN [1]		RN [1]	
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RA Aoyama M., Asai K., Kato T., Miura Y., Kokubo M., Kawai Y.,		RC STRAIN=MOROCCOF12;	
RA Miyachi T., Yokoi T., Tsuiki H.;		RX MEDLINE=7745412; PubMed=9334924;	
RT Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.		RA Chattejee R., Tsarev S., Pillot J., Coursaget P., Emerson S.U.,	
RL EMBL: AB038671; BAB5546.1; -.		RT Purcell R.H.;	
FT NON_TER		RT "African strains of hepatitis E virus that are distinct from Asian	
SQ SEQUENCE 30 AA; 3323 MW; B33237A993FF4BDD0 CRC64;		RL strains."; J. Med. Virol. 53:139-144(1997).	
QY 1 AAPM 4		DR EMBL: AF010418; AA666533.1; -.	
Db 18 AAPM 21		DR InterPro: IPR003384; HEV_ORF2.	
QY 1 AAPM 4		DR Pfam: PF02444; HEV_ORF2; 1.	
Db 7 AAPM 10		FT NON_TER 53 MW; 638F95EEAFF7E62D CRC64;	
QY 1 AAPM 4		SQ SEQUENCE 53 AA; 5405 MW; 638F95EEAFF7E62D CRC64;	
Db 7 AAPM 10		Query Match 100.0%; Score 20; DB 12; Length 53;	
Best Local Similarity 100.0%; Pred. No. 3.8e-02;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Query Match 100.0%; Score 20; DB 12; Length 53;	
Oy 1 AAPM 4		Best Local Similarity 100.0%; Pred. No. 4.3e-02;	
Db 7 AAPM 21		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 3		RESULT 5	
0969NB	PRELIMINARY;	PRT;	47 AA.
ID 0969NB;		ID 036589	PRELIMINARY;
AC 0969NB;		AC 036589;	PRT;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)	53 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)		DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE Brain-derived neurotrophic factor (Fragment);		DE ORF-3 (Fragment)	
GN BDNF 1-5 OR BDNF 3-5 OR BDNF 4-5 OR BDNF 4I-5.		OS Hepatitis E virus.	
OS Homo sapiens (Human);		OC Viruses; ssRNA positive-strand viruses, no DNA stage;	
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		OC Hepatitis E-like viruses.	
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.		OX NCBI_TaxID=12461;	
OX NCBI_TaxID=9606;		RN [1]	
RN SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RA Aoyama M., Asai K., Kato T., Miura Y., Kokubo M., Kawai Y.,		RC STRAIN=MOROCCOF13;	
RA Miyachi T., Yokoi T., Tsuiki H.;		RX MEDLINE=97475612; PubMed=9334924;	
RT "partial sequence of human BDNF mRNA.";		RA Chatterjee R., Tsarev S., Pillot J., Coursaget P., Emerson S.U.,	
RT Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.		RA Purcell R.H.;	
RL [2]		RT "African strains of hepatitis E virus that are distinct from Asian	
RP SEQUENCE FROM N.A.		RT strains."; J. Med. Virol. 53:139-144(1997).	
RA Aoyama M., Asai K., Kato T., Miura Y., Kokubo M., Kawai Y.,		DR EMBL: AB010419; BAB66536.1; -.	
RA Miyachi T., Yokoi T., Tsuiki H.;		DR InterPro: IPR003384; HEV_ORF2.	
RT "partial sequence of human BDNF mRNA.";		DR Pfam: PF02444; HEV_ORF2; 1.	
RT Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.		FT NON_TER 53 MW; 638F95EEAFF7E62D CRC64;	
RL EMBL: AB038670; BAB55454.1; -.		SQ SEQUENCE 53 AA; 5405 MW; 638F95EEAFF7E62D CRC64;	
EMBL: AB038672; BAB5547.1; -.		Query Match 100.0%; Score 20; DB 12; Length 53;	
EMBL: AB038673; BAB5548.1; -.		Best Local Similarity 100.0%; Pred. No. 4.3e-02;	
EMBL: AB038674; BAB5549.1; -.		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
FT NON_TER 47 MW; 5076 MW; A9D3DC22639759B1 CRC64;		Query Match 100.0%; Score 20; DB 12; Length 53;	
FT NON_TER 47 MW; 5076 MW; A9D3DC22639759B1 CRC64;		Best Local Similarity 100.0%; Pred. No. 4.3e-02;	
QY 1 AAPM 4		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db 7 AAPM 10		QY 1 AAPM 4	
18 AAPM 21		Db 7 AAPM 10	

036592
ID O36592; PRELIMINARY; PRT; 53 AA.
AC O36592;
DT 01-JAN-1998 (TREMBUREL. 05, Created)
DT 01-JAN-1998 (TREMBUREL. 05, Last sequence update)
DE ORF-3 (Fragment).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage;
OC Hepatitis E-like viruses.
OX NCBI_Taxid=12461;
RN [1]
RP SQUENCE FROM N.A.
RC STRAIN=MOROCCOF23;
RX MEDLINE=9745412; PubMed=9334924;
RA Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emerson S.U.,
RA Purcell R.H.;
RT "African strains of hepatitis E virus that are distinct from Asian
strains.";
RL J. Med. Virol. 53:139-144(1997).
DR EMBL; AF010420; AAB66591; -.
DR InterPro; IPR003384; HEV_ORF2.
DR Pfam; PF02444; HEV_ORF2; 1.
FT NON_TER 53
SQ SQUENCE 53 AA: 5405 MW: 638FF95EEAFF7E62D CRC64;
Query Match 100.0%; Score 20; DB 12; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;
QY 1 AAPM 4
Db 7 AAPM 10

RESULT 7
036583
ID O36583; PRELIMINARY; PRT; 53 AA.
AC O36583;
DT 01-JAN-1998 (TREMBUREL. 05, Created)
DT 01-JAN-1998 (TREMBUREL. 05, Last sequence update)
DT 01-DEC-2001 (TREMBUREL. 19, Last annotation update)
DE ORF-3 (Fragment).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage;
OC Hepatitis E-like viruses.
OX NCBI_Taxid=12461;
RN [1]
RP SQUENCE FROM N.A.
RC STRAIN=KIRGIZIA;
RX MEDLINE=97475412; PubMed=9334924;
RA Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emerson S.U.,
RA Purcell R.H.;
RT "African strains of hepatitis E virus that are distinct from Asian
strains.";
RL J. Med. Virol. 53:139-144(1997).
DR EMBL; AF010417; AAB66590; 1; -.
DR InterPro; IPR003384; HEV_ORF2.
DR Pfam; PF02444; HEV_ORF2; 1.
FT NON_TER 53
SQ SQUENCE 53 AA: 5405 MW: 638FF95EEAFF7E62D CRC64;
Query Match 100.0%; Score 20; DB 12; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;
QY 1 AAPM 4
Db 7 AAPM 10

RESULT 9
09W7U2
ID 09W7U2; PRELIMINARY; PRT; 59 AA.
AC 09W7U2;
DT 01-NOV-1999 (TREMBUREL. 12, Created)
DT 01-OCT-2001 (TREMBUREL. 18, Last annotation update)
DE ORF-3 (Fragment).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage;
OC Hepatitis E-like viruses.
OX NCBI_Taxid=12461;
RN [1]
RP SQUENCE FROM N.A.
RC STRAIN=M/ALGERIA, AND T3;
RX MEDLINE=98071272; PubMed=9407381;
RA van Cuylck-Gaudre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA Cohen S.J., Coudil J.D., Buisson Y., Coursaget P., Warren R.L.,
RA Longer C.F.;
RT "Characterization of hepatitis E virus (HEV) from Algeria and Chad by
partial genome sequence.";
RL J. Med. Virol. 53:340-347(1997).
DR EMBL; AF001276; AAB94812; 1; -.
DR InterPro; IPR003384; HEV_ORF2.
DR Pfam; PF02444; HEV_ORF2; 1.
FT NON_TER 59
SQ SQUENCE 59 AA: 5906 MW: AC9B75C5F23E338F CRC64;
Query Match 100.0%; Score 20; DB 12; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;
QY 1 AAPM 4
Db 7 AAPM 10

RESULT 8
036598

Q9T8B1 PRELIMINARY; PRT; 61 AA.
 ID Q9T8B1; AC 002709; ID 09T8B1; AC 002709; PRELIMINARY; PRT; 76 AA.
 DT 01-MAY-2000 (TREMBrel. 13, Created) DT 01-JUL-1997 (TREMBrel. 04, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update) DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMBrel. 15, Last annotation update) DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Glycerol ester HYDROLAS (EC 3.1.1.3) (Fragments). DE Brain-derived neurotrophic factor (Fragment).
 OS Camelus dromedarius (Dromedary) (Arabian camel); BDNF
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OC NCBI_TaxID=9838; OX NCBI_TaxID=13616;
 RN [1] RN [1]
 RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
 RX MEDLINE=94297034; PubMed=8025121; RX Vischer H.A.;
 RA Mejidou H., Reinbolt J., Gargouri Y.; RA "BDNF is expressed at the crush-site after spinal cord-lesion in
 RT "Dromedary pancreatic lipase: purification and structural properties." RT neoratal opossum (*Monodelphis domestica*).";
 RL Biochim. Biophys. Acta 1213:119-126(1994). RL Submitted (MAR-1997) to the EMBL/CeGenBank/DDJB databases.
 DR HSSP; P29183; IHPPL. DR EMBL; U95024; AAB5633.1; -.
 FT NON_TER 1 FT NON_TER 1
 FT NON_CONS 20 FT NON_TER 76
 FT NON_CONS 46 FT NON_TER 76
 FT NON_TER 61 FT NON_TER 76
 SQ SEQUENCE 61 AA; 6593 MW; DFA187455BAD5F2 CRC64; SQ SEQUENCE 76 AA; 8421 MW; 37C9EDEDBR076259 CRC64;
 Query Match 100.0%; Score 20; DB 6; Length 61; Query Match 100.0%; Score 20; DB 6; Length 76;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0; Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4 Qy 1 AAPM 4
 Db 29 AAPM 32 Db 9 AAPM 12

RESULT 11 RESULT 13
 ID Q8SE66 PRELIMINARY; PRT; 71 AA. ID 003382 PRELIMINARY; PRT; 76 AA.
 AC 003382; AC 003382; PRELIMINARY; PRT; 76 AA.
 DT 01-JUL-1997 (TREMBrel. 04, Created) DT 01-JUL-1997 (TREMBrel. 04, Created)
 .DT 01-JUN-2002 (TREMBrel. 21, Last sequence update) DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update) DE NADH dehydrogenase subunit 4L (Fragment).
 DE Hypothetical 7.3 kDa protein. OS *Salmo salar* (Atlantic salmon).
 GN OSINBB0024B15.9. OG Mitochondrion.
 OS *Oryza sativa* (Japonica cultivar-group). OG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC *Eukaryota*; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Actinopterygii; Neopterygii; Teleostei; Buteleoste; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; RN NCBI_TaxID=39947; RN [1]
 OX NCBI_TaxID=8030; RN [1]
 RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
 RC STRAIN=N.C. NIPPONARE; RC STRAIN=SHIBETSU SALMON PARK;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., RA Oohara I., Sawano K., Okazaki T.
 RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., RA "Mitochondrial DNA sequence analysis of the masu salmon phylogeny in
 RA Tsitrin T., Riggs F., Hsiao J., Zisman V., Blunt S., Pai G., the genus *Oncorhynchus*,"; RT Mol. Phylogenetic Evol. 7:71-78(1997).
 RA VanAken S.E., Utterback T.R., Feldblum T.V., Kalb E., Quackenbush J., DR EMBL; DB4148; BA20160.1; -.
 RA Salzberg S.L., White O., Fraser C.M.; DR InterPro; IPR001133; Oxidored4L.
 RT "Oryza sativa chromosome 3 BAC OSJNB0024B16 genomic sequence."; DR InterPro; IPR003214; Oxidored4L.
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. DR Pfam; PP00420; oxidored_92; 1.
 DR EMBL; AC093017; AAC183624.1; DR PRODom; PD000359; Oxidred4L; 1.
 KW Hypothetical protein. KW Mitochondrion.
 SQ SEQUENCE 71 AA; 7299 MW; F50CD01F81C7D659 CRC64; FT NON_TER 76
 RX MEDLINE=9715563; PubMed=9007022; RX SEQUENCE 76 AA; 8093 MW; E0A2B08AF297F56 CRC64;
 RA Oohara I., Sawano K., Okazaki T. RA "Mitochondrial DNA sequence analysis of the masu salmon phylogeny in
 RT the genus *Oncorhynchus*,"; RT Mol. Phylogenetic Evol. 7:71-78(1997).
 RL DR EMBL; DB4148; BA20160.1; -.
 DR InterPro; IPR001133; Oxidored4L.
 DR InterPro; IPR003214; Oxidored4L.
 DR Pfam; PP00420; oxidored_92; 1.
 DR PRODom; PD000359; Oxidred4L; 1.
 DR Mitochondrion.
 FT NON_TER 76
 SQ SEQUENCE 76 AA; 8093 MW; E0A2B08AF297F56 CRC64;
 Query Match 100.0%; Score 20; DB 8; Length 76; Query Match 100.0%; Score 20; DB 8; Length 76;
 Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0; Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4 Qy 1 AAPM 4
 Db 16 AAPM 19 Db 58 AAPM 61

RESULT 12 RESULT 14
 ID 002709 PRELIMINARY; PRT; 76 AA.
 AC 002709; AC 002709; PRELIMINARY; PRT; 76 AA.
 DT 01-JUL-1997 (TREMBrel. 04, Created) DT 01-JUL-1997 (TREMBrel. 04, Created)
 DT 01-JUL-1997 (TREMBrel. 04, Last sequence update) DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)
 DE BDNF
 OS *Monodelphis domestica* (Short-tailed grey opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
 OC NCBI_TaxID=13616;
 RN RN [1]
 RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
 RX Vischer H.A.; RX Vischer H.A.;
 RT "BDNF is expressed at the crush-site after spinal cord-lesion in RT "BDNF is expressed at the crush-site after spinal cord-lesion in
 RL neoratal opossum (*Monodelphis domestica*)."; RL neoratal opossum (*Monodelphis domestica*).";
 DR EMBL; U95024; AAB5633.1; -. DR EMBL; U95024; AAB5633.1; -.
 FT NON_TER 1 FT NON_TER 1
 FT NON_TER 76 FT NON_TER 76
 SQ SEQUENCE 76 AA; 8421 MW; 37C9EDEDBR076259 CRC64; SQ SEQUENCE 76 AA; 8421 MW; 37C9EDEDBR076259 CRC64;
 Query Match 100.0%; Score 20; DB 6; Length 76; Query Match 100.0%; Score 20; DB 6; Length 76;
 Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0; Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4 Qy 1 AAPM 4
 Db 9 AAPM 12 Db 58 AAPM 61

RESULT 13 RESULT 14
 ID 002709 PRELIMINARY; PRT; 76 AA.
 AC 002709; AC 002709; PRELIMINARY; PRT; 76 AA.
 DT 01-JUL-1997 (TREMBrel. 04, Created) DT 01-JUL-1997 (TREMBrel. 04, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update) DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DE NADH dehydrogenase subunit 4L (Fragment).
 OS *Salmo salar* (Atlantic salmon).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteleoste; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OC NCBI_TaxID=8030; RN [1]
 RN [1]
 RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
 RC STRAIN=SHIBETSU SALMON PARK;
 RA MEDLINE=9715563; PubMed=9007022;
 RA Oohara I., Sawano K., Okazaki T.
 RA "Mitochondrial DNA sequence analysis of the masu salmon phylogeny in
 RA the genus *Oncorhynchus*,"; RT Mol. Phylogenetic Evol. 7:71-78(1997).
 RA TSitrin T., Riggs F., Hsiao J., Zisman V., Blunt S., Pai G., DR EMBL; DB4148; BA20160.1; -.
 RA VanAken S.E., Utterback T.R., Feldblum T.V., Kalb E., Quackenbush J., DR InterPro; IPR001133; Oxidored4L.
 RA Salzberg S.L., White O., Fraser C.M.; DR InterPro; IPR003214; Oxidored4L.
 RT "Oryza sativa chromosome 3 BAC OSJNB0024B16 genomic sequence."; DR Pfam; PP00420; oxidored_92; 1.
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. DR PRODom; PD000359; Oxidred4L; 1.
 DR EMBL; AC093017; AAC183624.1; DR Mitochondrion.
 KW Hypothetical protein. KW Mitochondrion.
 SQ SEQUENCE 71 AA; 7299 MW; F50CD01F81C7D659 CRC64;
 Query Match 100.0%; Score 20; DB 8; Length 76; Query Match 100.0%; Score 20; DB 8; Length 76;
 Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0; Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4 Qy 1 AAPM 4
 Db 58 AAPM 61 Db 58 AAPM 61

ID	OB8946	PRELIMINARY;	PRY;	76 AA.	DT	01-FEB-1997 (TREMBLrel. 02; Last sequence update)	
AC	OB8946;				DT	01-DEC-2001 (TREMBLrel. 19; Last annotation update)	
DT	01-NOV-1998 (TREMBLrel. 08; Last sequence update)				DE	F22H10.3 protein.	
DT	01-NOV-1998 (TREMBLrel. 08; Last annotation update)				GN	F22H10.3.	
DT	Artisense product of high-affinity glutamate transporter EAAC1 and DE				OS	Caenorhabditis elegans.	
DE	EAAC2.				OC	Mammalia: Metazoa: Chromadorea: Rhabditida: Rhabditoidea: GN	
GN	ASCL1.				OC	Rhabditidae: Pelerinae; Caenorhabditis.	
OS	Mus musculus (Mouse).				OX	NCBI_Taxid=6239;	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				RN	[1]	
OC	Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.				RP	SEQUENCE FROM N.A.	
OX	NCBI_Taxid=10090;				RC	STRAIN=BRISTOL N2;	
RN	[1]				RX	MEDLINE=94150718; Pubmed=7906398;	
RP	SEQUENCE FROM N.A.				RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,	
RC	STRAIN=BALB/C; TISSUE=BRAIN;				RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton J.,	
RA	Jin X., Peng J., Fei J., Guo L.; "natural antisense mRNA transcript of meAC1 and meAC2 from neonatal mouse brain, complete cds."				RA	Croxton M., Dear S., Du Z., Durbin R., Favello A., Fulton J.,	
RT	neonatal mouse brain, complete cds."				RA	Gardner A., Green P., Hawkins R., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latrellie P.,	
RL	Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.				RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Parcy C., Riffen L., Roopra A., Saunders D., Shawnee M., Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaughn M., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,	
DR	EMBL: AF087578; AAC11495.1; -; DDAC6EBECD5029F7 CRC64;				RA	Watson A., Weinstock L., Wilkison-Sproat J., Wohldman P., elegans.";	
SQ	SEQUENCE 76 AA; 7857 MW;				RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.	
Query Match	100.0%; Score 20; DB 11; Length 76;				RL	Nature 368:32-38(1994).	
Best Local Similarity	100.0%; Pred. No. 6e+02; 0; Mismatches 4; Conservative 0; Matches 0; Indels 0; Gaps 0;				RN	[2]	
QY	1 AAPM 4				RP	SEQUENCE FROM N.A.	
Db	1111 AAPM 44				RC	STRAIN=BRISTOL N2;	
RESULT 15					RA	Langston, Y., Hawkins J.;	
QB8744	PRELIMINARY;	PRY;	77 AA.		RT	"The sequence of C. elegans cosmid F22H10.;"	
ID	QB8744;				RL	Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.	
AC					RN	[3]	
DT	01-JUN-2002 (TREMBLrel. 21; Last sequence update)				RP	SEQUENCE FROM N.A.	
DT	01-JUN-2002 (TREMBLrel. 21; Last annotation update)				RC	STRAIN=BRISTOL N2;	
DE	Hypothetical, 8.1 kDa protein.				RA	Waterston R.;	
GN	OSONBA0057L21.13.				RL	Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.	
OS	Oryza sativa (Rice).				DR	EMBL: U70845; AAC09098.1; -.	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				SQ	SEQUENCE 79 AA; 8863 MW;	
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				Query Match	100.0%; Score 20; DB 5; Length 79;	
OC	Embryoflora; Oryzeae; Oryza.				Best Local Similarity	100.0%; Pred. No. 6.2e+02; 0; Mismatches 4; Conservative 0; Matches 0; Indels 0; Gaps 0;	
QX	NCBI_Taxid=4530;				QY	1 AAPM 4	
RN	[1]				Db	1111 AAPM 50	
RP	SEQUENCE FROM N.A.						
RC	STRAIN=CV; NIPPONBARE;						
RA	Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitirin T., Riggs F., Hsiao M., Zisman V., Blunt S., Pai G., Vanaken S.E., Utterback T.R., Fieldlyum T.V., Kalb E., Quackenbush J., Salzberg S.L., White O., Fraser C.M.; "Oryza sativa chromosome 10 BAC OSJN1a0057L21 genomic sequence.";				RESULT 17		
RT	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.				ID	Q91MLO	
RL	DR	EMBL: AC087599; AAC11492.1; -.			ID	Q91MLO	
KW	Hypothetical protein.				AC	Q91MLO;	
SQ	SEQUENCE 77 AA; 8068 MW;	doCB87D68C03FD03 CRC64;			PRELIMINARY;	PRY;	
QY	1 AAPM 4				RT	01-DEC-2001 (TREMBLrel. 19; Last sequence update)	
Db	1111 AAPM 40				DT	01-DEC-2001 (TREMBLrel. 19; Last annotation update)	
RESULT 16					DT	01-DEC-2001 (TREMBLrel. 19; Last annotation update)	
QY	1 AAPM 4				DE	Major core protein (Fragment).	
Db	1111 AAPM 40				OS	Virovirus sp.-RVA.	
Query Match	100.0%; Score 20; DB 10; Length 77;				OC	Virovirus; dsRNA viruses; Reoviridae; unclassified Reoviridae.	
Best Local Similarity	100.0%; Pred. No. 6e+02; 0; Mismatches 4; Conservative 0; Matches 0; Indels 0; Gaps 0;				QX	NCBI_Taxid=165101;	
RP	SEQUENCE FROM N.A.				RN	[1]	
RC	STRAIN=RVA;				RP	SEQUENCE FROM N.A.	
RX	Medline=2131868; Pubmed=11425715;				RC	STRAIN=RVA;	
RA	Spigner M.I., Di Giovanni G.D.; "Detection and identification of mammalian reoviruses in surface water by combined cell culture and reverse transcription-pcr.";				RA	Appl. Environ. Microbiol. 67:3016-3020(2001).	
RT	by combined cell culture and reverse transcription-pcr.";				RL	DR	EMBL: AF325764; AAC11927.1; -.
RT	Detection and identification of mammalian reoviruses in surface water by combined cell culture and reverse transcription-pcr.";				FT	NON_TER 1	
RT	by combined cell culture and reverse transcription-pcr.";				FT	NON_TER 83	
RT	Appl. Environ. Microbiol. 67:3016-3020(2001).				SQ	SEQUENCE 83 AA; 9794 MW;	
RT	DR	EMBL: AF325764; AAC11927.1; -.			Query Match	100.0%; Score 20; DB 12; Length 83;	
RT	EMBL: AF325764; AAC11927.1; -.						
RT	NON_TER 1						
RT	NON_TER 83						
RT	SEQUENCE 83 AA; 9794 MW;						
RT	74CD2CCF29B3D50 CRC64;						

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE EBSI protein (Putative transcriptional regulator protein).

RN [2]

GN EBSI OR RB1058 OR SMB20935.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OG Plasmid pSymb (megaplasmid 2).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OX Rhizobiaceae; Sinorhizobium.

NB! TAXID=382;

RP SEQUENCE FROM N.A.

RC STRAIN=RCR001 / SU47;

RX MEDLINE=9613389; PubMed=8544814;

RA Becker A., Kuester H., Niehaus K., Puehler A.;

RT "extension of the Rhizobium meliloti succinoglycan biosynthesis gene cluster: identification of the exsA gene encoding an ABC transporter protein, and the exsB gene which probably codes for a . . .";

RL Mol. Gen. Genet. 249:487-497(1995).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=RCR2011 / SU47;

RA York G.M., Walker G.C.;

RT The Rhizobium meliloti exoK gene and prsD/prsE/exsH genes are components of independent degradative pathways which contribute to RT production of low-molecular-weight succinoglycan.;"

RL Mol. Microbiol. 25:117-134(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=RCR001 / SU47;

RA Becker A.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=1021; PLASMID=pSymb (MEGAPLASMID 2);

RX MEDLINE=21396508; PubMed=11481431;

RA Finan T.M., Weidner S., Wong K., Buurmester J., Chain P., Golding B., Puehler A., Cowie A., Gouzy J., Verhoefter F.J., Hernandez Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;

RT "The complete sequence of the 1.683-kb pSymbB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

DR EMBL; AJ225361; CAM12534.1; -.

DR AL605645; CAC49458.1; -.

DR Interpro; IPR001387; HTH_3.

DR PF01381; HTH_3; 1.

DR SMART; SM00530; HTH_XRE_1.

KW Plasmid; Hypothetical protein; Complete proteome.

SQ SEQUENCE 83 AA; 8681 MW; 8054E2D00005EFBF CRC64;

Query Match 100.0%; Score 20; DB 16; Length 83;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Mismatches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPM 4

Db 13 AAPM 16

RESULT 23

ID 086845 PRELIMINARY; PRT; 84 AA.

AC 086845; DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Putative 30.9 kDa protein (Fragment).

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteridae; Actinomycetidae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NB! TAXID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3 (2);

RA Palframan W.;

RL Thesis (1998), University of East Anglia, Department of Biological.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=A3 (2);

RX MEDLINE=20402106; PubMed=10931278;

RA Molle V., Buttner M.J.;

RT "Different alleles of the response regulator gene blm arrest Streptomyces coelicolor development at distinct stages.;"

RL Mol. Microbiol. 61:1265-1278(2000).

DR EMBL; AJ010601; CAA09266.1; -.

DR Interpro; IPR001095; IMPDH/GMPRTase.

DR Pfam; PF01574; IMPDH_N_1.

FT NON_TER 84 AA; 84 MW; 43FA1467EBB4ED8F CRC64;

SQ SEQUENCE 84 AA; 9284 MW; 43FA1467EBB4ED8F CRC64;

Query Match 100.0%; Score 20; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

Matches 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4

Db 52 AAPM 55

RESULT 24

ID 0865M7 PRELIMINARY; PRT; 88 AA.

AC 0865M7;

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE AGR_C_597P.

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21608551; PubMed=11743194;

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970); Rhizobiaceae group;

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OX Rhizobiaceae; Rhizobium.

DR NCBITAXID=176299;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L., Ouellette B., Goldman B.S., Cao Y., Askewazi M., Halling C., Mullin L., Houmeli K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F., William C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.,

RT "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.;"

RL Science 294:2223-2228(2001).

DR EMBL; AE007972; AAK86159.1; -.

SQ SEQUENCE 88 AA; 10016 MW; 1919F5932DE43263 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 88;

Best Local Similarity 100.0%; Pred. No. 6.8e+02; Mismatches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPM 4

Db 64 AAPM 67

RESULT 25

ID QDJAL PRELIMINARY; PRT; 89 AA.

AC QDJAL;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE VPI (Fragment).

GN ID.

OS Foot-and-mouth disease virus O.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;

OC Aphthovirus.

OX	NCBI_TAXID=12118;	RN	[1]	SEQUENCE FROM N.A.	RA	Bentley S.D., Chater K.F., Cerdeno-Tarrega A.-M., Challis G.L.,
RP		RA			RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Kissner H.,
RC		RA			RA	Harpfer D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
STRAIN=TUN/1/99;		RA			RA	Cronin D., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA	"Foot-and-mouth disease type O viruses exhibit genetically and	RA			RA	Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RT	geographically distinct evolutionary lineages (topotypes).";	RA			RA	Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutten S.,
RL	Gen. Virol. 82:0 (2001);	RA			RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
DR	EMBL: AJ296323; CAC2166.1; -.	RA			RA	Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
FT	NON_TER.	RA	1		RA	Hopwood D.A.;
FT	NON_TER.	RA	89		RT	"Complete genome sequence of the model actinomycete Streptomyces
SQ	SEQUENCE 89 AA;	RA	9916 MW;	9A9C9AE97A00AF468 CRC64;	RT	coelicolor A3(2).";
		RA			RT	Nature 417:141-147 (2002).
		RA			DR	EMBL: AL133171; CAB61536.2; -.
		KW			KW	Hypothetical protein.
		SEQUENCE	94 AA;	9520 MW;	SEQUENCE	94 AA;
Qy	1 AAPM 4	Db	31 AAPM 34		Qy	1 AAPM 4
RESULT 26		Db	21 AAPM 24		Qy	1 AAPM 4
ID	0960H7	PRELIMINARY;	PRT;	92 AA.	Qy	1 AAPM 4
AC	0960H7				Db	21 AAPM 24
DT	01-DEC-2001 (TREMBLrel. 19, Created)	RESULT 28				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	047762	PRELIMINARY;	PRT;	98 AA.	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	ID	047762	PRELIMINARY;	PRT;	98 AA.
DE	Fructose-1,6-bisphosphate aldolase (Fragment).	AC	047762	PRELIMINARY;	PRT;	98 AA.
OS	Paracoccidioides brasiliensis.	DT	01-JUN-1998 (TREMBLrel. 06, Created)			
OC	Eukaryota; Fungi; Ascomycota; Eurotiomycetes;	DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
OC	Oxygenales; mitosporic Onygenales; Paracoccidioides;	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
OX	NCBI_TAXID=121759;	DE	NADH oxidoreductase subunit 4L.			
RN	[1]	GN	ND4L.			
RP	SEQUENCE FROM N.A.	OS	Myxocystis asiaticus.			
RA	Carmelo L.C., Jesuino R.S.A., Felipe M.S.S., Pereira M.,	OG	Mitochondrion.			
RA	Soares C.M.A.;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomii;			
RT	"The fructose-1,6-bisphosphate aldolase genomic sequence of	OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
RT	Paracoccidioides brasiliensis."	OX	Catostomidae; Myxocystis.			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.	NCBI_TAXID=70543;				
DR	EMBL: AV057387; ALU25625.1; -.	RNA	[1]			
DR	InterPro: IPR00771; F_bp_aldolase.	RP	SEQUENCE FROM N.A.			
DR	pfan: PF01116; F_bp_aldolase; 1.	RX	MEDLINE=21097157; PubMed=11161753;			
DR	Prodom: PD002376; F_bp_aldolase; 1.	RA	Xiao W., Zhang Y., Liu H.;			
FT	NON_TER.	RT	"Molecular Systematics of Xenocyprinae (Teleostei: Cyprinidae): Taxonomy, Biogeography, and Coevolution of a Special Group Restricted			
SQ	SEQUENCE 92 AA;	RT	in East Asia";			
Qy	1 AAPM 4	RNA	Mol. Phylogenet. Evol. 18:163-177 (2001).			
Db	71 AAPM 74	DR	EMBL: AF036180; AAC010088.1; -.			
		DR	InterPro: IPR011133; Oxidored4L.			
		DR	InterPro: IPR03214; Oxidred4L.			
		DR	Pfam: PF00420; oxidored4L.			
		DR	Prodom: PD000359; oxidred4L; 1.			
		KW	Mitochondrion; Ubiquinone.			
		SQ	SEQUENCE 98 AA;	10485 MW;	SQ	SEQUENCE 98 AA;
RESULT 27						
Q9JEG9						
ID	Q9JEG9	PRELIMINARY;	PRT;	94 AA.		
Q9JEG9						
AC	09JEG9					
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE	Hypothetical protein SC00743.					
GN	SC00743 OR SCF81.02C.					
OS	Streptomyces coelicolor.					
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;					
OC	Actinomycetes; Streptomycineae; Streptomycetaceae; Streptomyces.					
OX	NCBI_TAXID=1902;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=FA(2) / M445;					
RESULT 29						
04775						
ID	04775	PRELIMINARY;	PRT;	98 AA.		
AC	04775;					
DT	01-JUN-1998 (TREMBLrel. 06, Created)					
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE	NADH ubiquinone oxidoreductase subunit 4L.					

GN NBL.
 OS Xenocypris fungi.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Xenocypris.
 OX NCBI_TaxID=70547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE=21097357; PubMed=11161753;
 RA Xiao W., Zhang Y., Liu H.
 RT Molecular Systematics of Xenocyprinae (Teleostei: Cyprinidae):
 RT Taxonomy, Biogeography, and Coevolution of a Special Group Restricted
 RT in East Asia.;
 RL Mol. Phylogenet. Evol. 18:163-173 (2001).
 DR EMBL: AF056189; ASN10966.1; -.
 DR InterPro: IPR001133; oxidored4L.
 DR InterPro: IPR003214; oxidored4L.
 DR Pfam: PF00420; oxidored_q2; 1.
 DR ProDom: P000159; Oxidored4L; 1.
 KW Mitochondrion; Ubiquinone.
 SQ SEQUENCE 98 AA; 10543 MW; 0BC09218C5C7565A CRC64;

Query Match 100.0%; Score 20; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02; PRT; 98 AA.
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 Db 58 AAPM 61

RESULT 30
 ID 047781 PRELIMINARY; PRT; 98 AA.
 AC 047781;
 DT 01-JUN-1998 (TREMBL: 06, Created)
 DT 01-JUN-1998 (TREMBL: 06, Last sequence update)
 DT 01-JUN-2002 (TREMBL: 21, Last annotation update)
 DE NADH ubiquinone oxidoreductase subunit 4L.
 GN NBL.
 OG Xenocypris yunnanensis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Xenocypris.
 OX NCBI_TaxID=70549;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MUSCLE;
 RX MEDLINE=21097357; PubMed=11161753;
 RA Xiao W., Zhang Y., Liu H.;
 RT "molecular Systematics of Xenocyprinae (Teleostei: Cyprinidae):
 RT Taxonomy, Biogeography, and Coevolution of a Special Group Restricted
 RT in East Asia.";
 RL Mol. Phylogenet. Evol. 18:163-173 (2001).
 DR EMBL: AF056193; ASN10964.1; -.
 DR InterPro: IPR001133; oxidored4L.
 DR InterPro: IPR003214; oxidored4L.
 DR Pfam: PF00420; oxidored_q2; 1.
 DR ProDom: P000159; Oxidored4L; 1.
 KW Mitochondrion; Ubiquinone.
 SQ SEQUENCE 98 AA; 10679 MW; F2D2265885938A2C CRC64;

Query Match 100.0%; Score 20; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02; PRT; 98 AA.
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 Db 58 AAPM 61

RESULT 31
 ID 09G6S9 PRELIMINARY; PRT; 98 AA.
 AC 09G6S9;
 DT 01-MAR-2001 (TREMBL: 16, Created)
 DT 01-MAR-2001 (TREMBL: 16, Last sequence update)
 DT 01-JUN-2002 (TREMBL: 21, Last annotation update)
 DE NADH dehydrogenase subunit 4L.
 GN Sardinops melanostictus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
 OC Sardinops.
 OX NCBI_TaxID=41197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inoue J.;
 RL Inoue J.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Complete mitochondrial DNA sequence of the Japanese sardine Sardinops
 melanostictus"; Fisheries Sci. 66:924-932(2000).
 DR EMBL: AB02255; BAB1860.1; -.
 DR InterPro: IPR001133; Oxidored4L.
 DR InterPro: IPR003214; Oxidored4L.
 DR Pfam: PF00420; oxidored_q2; 1.
 DR ProDom: P000159; Oxidored4L; 1.
 KW Mitochondrion.
 SQ SEQUENCE 98 AA; 10462 MW; 226D411ECBC4E709 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02; PRT; 98 AA.
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPM 4
 Db 58 AAPM 61

RESULT 32
 ID 09T919 PRELIMINARY; PRT; 98 AA.
 AC 09T919;
 DT 01-MAY-2000 (TREMBL: 13, Created)
 DT 01-MAY-2000 (TREMBL: 13, Last sequence update)
 DT 01-JUN-2002 (TREMBL: 21, Last annotation update)
 DE NADH ubiquinone oxidoreductase subunit 4L.
 GN NBL.
 OG Aristichthys nobilis (bighead carp).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Aristichthys.
 OX NCBI_TaxID=75338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RA Xiao W., Zhang Y.;
 RT "Phylogenetic analysis of the family Cyprinidae (Teleostei, Cypriniformes):
 RT implications for its origination and East Asia biogeography.";
 RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF008319; AF21263.1; -.
 DR InterPro: IPR001133; Oxidored4L.
 DR InterPro: IPR003214; Oxidored4L.
 DR Pfam: PF00420; oxidored_q2; 1.
 DR ProDom: P000159; Oxidored4L; 1.
 KW Mitochondrion; Ubiquinone.
 SQ SEQUENCE 98 AA; 10529 MW; 4434C35DC5D08081 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 58 AAPM 61

RESULT 33

ID Q9T911 PRELIMINARY; PRT; 98 AA.

AC 09T911; DR AF154051; AAF78155_1;
DT 01-MAY-2000 (TREMBUREl. 13, Created) DR InterPro; IPR003214; Oxidored4L.
DT 01-MAY-2000 (TREMBUREl. 13, Last sequence update) DR Pfam; PF00420; Oxidored4L; 1.
DE NADH ubiquinone oxidoreductase subunit 4L. DR ProDom; PD000359; Oxidred4L; 1.
GN ND4L. KW Mitochondrion.
OS Megalobrama pellegrini.

Mitochondrion. R.L. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

OG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; DR EMBL; AF154051; AAF78155_1;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; DR InterPro; IPR003214; Oxidored4L.
OC Cyprinidae; Megalobrama. DR Pfam; PF00420; Oxidored4L; 1.
NCBI_TAXID=77646; [1]

SEQUENCE FROM N.A.

Xiao W., Zhang Y.; R.A. "Phylogenetic analysis of the family Cyprinidae (Teleostei, Cypriniformes) based on complete cytochrome b and ND_{4L}-ND₁ sequences: implications for its origination and East Asia biogeography."; R.T. Submitted (May-1998) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF006835; AF21275_1; DR InterPro; IPR001133; Oxidred4L.
DR InterPro; IPR003214; Oxidred4L.
DR Pfam; PF00420; oxidred4L; 1.
DR ProDom; PD000359; Oxidred4L; 1.
KW Mitochondrion; Ubiquinone. SQ SEQUENCE 98 AA; 10537 MW; 3EB0BDFD3507A6A9 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 58 AAPM 61

RESULT 35

ID 09G322 PRELIMINARY; PRT; 98 AA.

AC 09G322; DR AF154051; AAF78155_1;
DT 01-MAR-2001 (TREMBUREl. 16, Created) DR InterPro; IPR003214; Oxidored4L.
DT 01-JUN-2002 (TREMBUREl. 21, Last annotation update) DR NADH dehydrogenase subunit 4L.
DE NADH-4L. GN NADH-4L.

Cottus bairdii (mottled sculpin). OS Mitochondrion. R.L. Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

OG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; DR EMBL; AF112388; AAG47826_1; OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes; OC Cetodonti; Cottidae; Cottus. DR InterPro; IPR001133; Oxidred4L.
DR InterPro; IPR003214; Oxidred4L.
DR Pfam; PF00420; oxidred4L; 1.
DR ProDom; PD000359; Oxidred4L; 1.
DR Mitochondrion. SQ SEQUENCE 98 AA; 10391 MW; 0766B0BC1563C3C4 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPM 4
Db 58 AAPM 61

RESULT 34

ID Q9M1A1 PRELIMINARY; PRT; 98 AA.

AC 09M1A1; DR AF154051; AAF78155_1;
DT 01-OCT-2000 (TREMBUREl. 15, Created) DR InterPro; IPR003214; Oxidored4L.
DT 01-OCT-2000 (TREMBUREl. 15, Last sequence update) DR NADH dehydrogenase subunit 4L.
DE NADH-4L. GN NADH-4L.

Typhlonectes natans (Rubber eel). OS Mitochondrion. R.L. Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

OG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; DR EMBL; AF154051; AAF78155_1; OC Amphibia; Gymnophiona; Caeciliidae; Typhlonectes. NCBI_TAXID=8456; [1]

SEQUENCE FROM N.A.

MEDLINE=20286752; PubMed=10835397; RX Zardoya R., Meyer A.; DR Mitochondrial Evidence on the Phylogenetic Position of Caecilians RT (Amphibia: Gymnophiona); " R.L. Genetics 155:765-775(2000). RN [2]

SEQUENCE FROM N.A.

R.A. Zardoya R.; DR Mitochondrion; DR InterPro; IPR003214; Oxidred4L. RN [1]

OS Cottus carolinae (banded sculpin). OG Mitochondrion. R.L. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; DR EMBL; AF154051; AAF78155_1; OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes; OC Cottidae; cottidae; cottus. DR InterPro; IPR001133; Oxidred4L.
DR Pfam; PF00420; Oxidred4L; 1. NCBI_TAXID=147209; [1]

RP SEQUENCE FROM N.A.
 RA Nelson S.E., Schwery S.P., Baker R.L., Eckdahl T.T.;
 RT "Identification of *Cottus* Species Using Mitochondrial RFLP Analysis.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF312389; AAC47825.1; -
 DR InterPro; IPR001133; Oxidored4L.
 DR Pfam; PF00420; oxidored92; 1.
 DR Prodom; P000359; Oxidred4L; 1.
 KW Mitochondrion.
 SQ SEQUENCE 98 AA; 10416 MW; 199AAC82E5D3543 CRC64;
 Query Match 100.0%; Score 20; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 7.5e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAPM 4
 Db 58 AAPM 61

RESULT 37
 Q9G3Y6 PRELIMINARY; PRT; 98 AA.
 ID Q9G3Y6
 AC 98G3Y6:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 4L.
 GN NADH-4L
 OS Cottus hypselurus (Ozark sculpin).
 OG Mitochondrion.
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha;
 OC Cottoidei; Cottidae; Cottus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nelson S.E., Schwery S.P., Baker R.L., Eckdahl T.T.;
 RT "Identification of *Cottus* Species Using Mitochondrial RFLP Analysis.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF312390; AAC47832.1; -
 DR InterPro; IPR001133; Oxidored4L.
 DR Pfam; PF00420; oxidored92; 1.
 DR Prodom; P000359; Oxidred4L; 1.
 KW Mitochondrion.
 SQ SEQUENCE 98 AA; 10421 MW; A77A57D79FB7ADE CRC64;
 Query Match 100.0%; Score 20; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 7.5e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAPM 4
 Db 58 AAPM 61

RESULT 38
 Q9G3Y3 PRELIMINARY; PRT; 98 AA.
 ID Q9G3Y3
 AC 98G3Y3:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-JUN-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 4L.
 GN NADH-4L
 OS Cottus cognatus (slimy sculpin).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Butteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;

OC Cottoidei; Cottidae; Cottus.
 OX NCBI_TaxID=147210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inoue J.G., Mita M., Tsukamoto K., Nishida M.;
 RT "A Mitogenomic Perspective on the Basal Teleostean Phylogeny: Resolving the Higher-Level Relationships with Longer DNA Sequences.";
 RL Mol. Phylogenet. Evol. 20:275-285 (2001).
 DR EMBL; AB043025; BAB64365.1; -
 DR InterPro; IPR001133; Oxidored4L.
 DR Pfam; PF00420; oxidored92; 1.
 DR Prodom; P000359; Oxidred4L; 1.
 KW Mitochondrion.
 SQ SEQUENCE 98 AA; 10539 MW; 4D6EABC7754E1753 CRC64;
 Query Match 100.0%; Score 20; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAPM 4
 Db 58 AAPM 61

RESULT 40
 Q94TBL PRELIMINARY; PRT; 98 AA.
 ID Q94TBL
 AC 984TBL:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 4L.
 GN NDAL.

OS Neoscopelus microchir.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Scopelomorpha; Myctophiformes; Neoscopelidae; Neoscopelus.
 OX NCBI_TaxID=143321;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miya M.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21519020; PubMed=11606696;
 RA Miya M., Kawaguchi A., Nishida M.;
 RT "Mitogenomic exploration of higher teleostean phylogenies: A case
 study for moderate-scale evolutionary genomics with 38 newly
 determined complete mitochondrial DNA sequences.";
 RL Mol. Biol. Evol. 18:1993-2009(2001).
 DR EMBL; AP002921; BABY0061_1; -;
 DR InterPro; IPR001133; Oxidored_4L.
 DR InterPro; IPR003214; Oxidred1L.
 DR Pfam; PF004420; oxidored_q2; 1;
 DR Prodom; PD000359; Oxidred4L; 1.
 KW Mitochondrion.
 SQ SEQUENCE 98 AA; 10368 MW; EB8ED12057A684CB CRC64;
 Query Match 100.0%; Score 20; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPM 4
 Db 58 AAPM 61

Search completed: December 6, 2002, 13:30:08
 Job time : 19.556 secs

Copyright (c) 1993 - 2002 Compugen Ltd.	Gencore version 5.1.3	
OM protein - protein search, using sw model		
Run on:	December 6, 2002, 13:19:54 ; Search time 26 Seconds (without alignments) 20.500 Million cell updates/sec	
Title:	US-10-033-526-1	
Perfect score:	21	
Sequence:	1 AAPF 4	
Scoring table:	BLOSUM62	
Scoring table:	Gapop 10.0 , Gapext 0.5	
Searched:	908470 seqs, 133250620 residues	
Total number of hits satisfying chosen parameters:	908470	
Minimum DB seq length:	0	
Maximum DB seq length:	200000000	
Post-processing:	Minimum Match 0%	
Maximum Match 100%		
Listing first 45 summaries		
Database :		
1: /SID52/gcldata/genesed/geneseq/geneseqp-emb1/AA1980.DAT:*	A_Genesed-101002;*	
2: /SID52/gcldata/genesed/geneseqp-emb1/AA1981.DAT:*		
3: /SID52/gcldata/genesed/geneseqp-emb1/AA1982.DAT:*		
4: /SID52/gcldata/genesed/geneseqp-emb1/AA1983.DAT:*		
5: /SID52/gcldata/genesed/geneseqp-emb1/AA1984.DAT:*		
6: /SID52/gcldata/genesed/geneseqp-emb1/AA1985.DAT:*		
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11: /SID52/gcldata/genesed/geneseqp-emb1/AA1991.DAT:*		
12: /SID52/gcldata/genesed/geneseqp-emb1/AA1992.DAT:*		
13: /SID52/gcldata/genesed/geneseqp-emb1/AA1993.DAT:*		
14: /SID52/gcldata/genesed/geneseqp-emb1/AA1994.DAT:*		
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17: /SID52/gcldata/genesed/geneseqp-emb1/AA1997.DAT:*		
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19: /SID52/gcldata/genesed/geneseqp-emb1/AA1999.DAT:*		
20: /SID52/gcldata/genesed/geneseqp-emb1/AA2000.DAT:*		
21: /SID52/gcldata/genesed/geneseqp-emb1/AA2001.DAT:*		
22: /SID52/gcldata/genesed/geneseqp-emb1/AA2002.DAT:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Query	
	Match Length DB ID	
	Description	
1	21 100.0 4 5 AAP40459	N-terminal polyhyd Peptidase substrat Peptide component Ketone analogue pr Cathepsin G inhibi Chromogenic Peptid Cathepsin G inhibi Aminophthalene P Bacillus alkali pr Serine protease in
2	21 100.0 4 11 AAR04102	
3	21 100.0 4 12 AAR0887	
4	21 100.0 4 12 AAR1223	
5	21 100.0 4 13 AAR0964	
6	21 100.0 4 14 AAR4258	
7	21 100.0 4 14 AAR8410	
8	21 100.0 4 14 AAR4109	
9	21 100.0 4 15 AAR2024	
10	21 100.0 4 15 AAR6223	
RESULT	1	
ID	AAP40459 standard; Protein; 4 AA.	
XX		
AC	AAP40459;	
XX		
DT	27-NOV-1991 (first entry)	
XX		
DE	N-terminal Polyhydroxyalkanoyl peptide.	
XX		
KW	Polyhydroxyalkanoyl peptide; protease; peptidase; prodrug.	
XX		
PN	EP126685-A.	
XX		
PD	28-NOV-1985.	
XX		
PF	15-MAY-1984; 84EP-0400984.	
XX		
PR	16-MAY-1983; 83FR-0300051.	
XX		
PA	(CNRS) CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE.	
XX		
PI	Monsigny M, Mayer R;	
XX		
DR	WPI, 1984-296065/48.	
XX		
PT	N-terminal polyhydroxyalkanoyl peptide and aminoacid derivs. - opt. having C-terminal active gps., e.g. chloroquine, are water-soluble antitumour or antiparasitic cpd.s and protease targets.	
PT		
PS	Claim 11; page 15; 20pp; french.	
XX		
CC	The peptide is polyhydroxyalkanoyl-L-Ala-L-Ala-L-Pro-L-Phe-X. X is	

Sequence of intern

Substrate for pept

Substrate for pept

Serine protease-in

Substrate peptide

Substrate for seri

proteinas site of

Synthetic substrat

B. subtilis subtil

Synthetic oligope

Indicator for dete

peptide conjugated

Alkaline protease

Peptidase comprising

Chymotrypsin subst

Subtilisin substra

Cathepsin G peptid

Peptidylprolyl cis

Model substrate pe

Ztryp3 substrate u

Peptide inhibitor

Model peptide subs

Artificial substra

Human peptide #2,

Peptide #2. Unide

CC R2-NH-derived from an aromatic amine, eg P-nitro-aniline, alpha-
 CC or beta-naphthylamine, or it is R3NH derived from an amino drug, eg
 CC daunorubicin or chloroquine, or it is a gp. which may confer
 CC activity, eh H, OH, CH2Cl. When X is the residue of a drug, the
 CC cpd. is a prodrug in which the peptide is the substrate for a
 CC specific protease secreted by the target cell for the active drug,
 CC eg tumour cells or microorganism pathogens, eg plasmodium
 CC falciparum. Due to the polyhydroxy gp., the cpds. are very soluble
 CC in water or buffer soln. and are able to be used at high concn. The
 CC cpds. also allow the detection of proteases and peptidases and
 CC allow easy determination of the best substrate for a particular
 CC protease.

Sequence 4 AA;

SQ

Query Match

Best Local Similarity

Matches

Qy

1 AAPF 4

Db

1 AAPF 4

AC

AAR04012;

XX

AC

AAR04012;

XX

DT

19-Nov-1991 (first entry)

XX

DE

Peptidase substrate analogues having peptidase inhibition activity.

XX

DE

Elastase; plasminogen activator; cathepsin; calpain; enkephalinase;

KW

Angiotensin converting enzyme.

XX

OS

Synthetic.

XX

KEY

Location/Qualifiers

FT

Modified-site

4

/label= "Terminal modified from -COOH to -COCR

/note= "R = alkyl group or -H"

FT

EP363284-A.

XX

PN

PR

XX

DE

11-APR-1990.

XX

PD

06-OCT-1989;

XX

PF

07-OCT-1988;

XX

PR

06-OCT-1989;

XX

(RICH) MERRELL DOW PHARM INC.

PI

Bey P, Angelastro M, Mehdi S;

XX

WPI: 1991-030811/05.

XX

PS

Claim 5; Page 25; 40pp; English.

XX

PT

Novel serine-, carboxylic acid-and metallo-proteinase-inhibitors

XX

PT

- inhibit range of proteinase(s) in treating rheumatoid

XX

PT

arthritis, thrombosis and psoriasis, also is a male contraceptive

XX

CC

This peptide is the R1 gp. of the cpd. of formula: R1NHCH(R2)-

CC

COC(2)CF3. This cpd. is a peptidase substrate analogue and is a

CC

specific enzyme inhibitor for a range of proteases, e.g. serine-,

CC

carboxylic acid-, and metallo-proteases. It is useful in the

CC

treatment of rheumatoid arthritis, thrombosis and psoriasis and is

CC

also used as a male contraceptive. See also AAR10876-83, AAR10886 and

CC

AAR10888.

XX

SQ

Sequence 4 AA;

SQ

Query Match

Best Local Similarity

Matches

Qy

1 AAPF 4

Db

1 AAPF 4

AC

AAR11223;

XX

AC

AAR11223;

XX

DT

24-MAY-1991 (first entry)

XX

DE

Ketone analogue protease inhibitor #2.

XX

KW

protease inhibitor; antiinflammatory agent; hypotensive; analgesic;

KW

antiangiogenesis agent; antidiabetic; antithrombotic.

KW

SQ

Sequence 4 AA;

SQ

Query Match

100.0%; Score 21; DB 11; Length 4;

Best Local Similarity

100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Synthetic.
 XX
 FH Location/Qualifiers
 KEY
 FT Modified-site 1
 FT /label= Methoxysuccinyl-Ala
 FT 4 /label= Phe-carboxyoxalyl
 XX
 PN EP41771-A.
 XX
 PD 20-MAR-1991.
 XX
 PP 11-SEP-1990; 90EP-0117461.
 XX
 PR 11-SEP-1999; 89US-0405491.
 PA (RICH) MERRELL DOW PHARM INC.
 XX
 PT Flynn GA, Bey P;
 XX
 DR wpi; 1991-08180/12.
 XX
 PT New ketone analogue peptidase and isomerase inhibitors - for
 PT inhibition of leukocyte elastase, cathepsin G, thrombin,
 PT chymotrypsin, plasmin etc.
 XX
 PS Claim 5; Page 26; 50pp; English.
 CC This peptide is a specific example of a highly generic protease
 CC inhibitor useful for medical purposes. The peptide analogues include
 CC inhibitors of urokinase, renin, cathepsin D, etc. which can be used
 CC as anti-proliferative agents and abortifacients, hypotensives,
 CC antiinflammatory and antidiemylinating agents, respectively.
 See also ARR11222 and HARI1224-R11238.
 XX
 SQ Sequence 4 AA;

Query	Match	Score	Length
Best Local Similarity	100.0%	DB 12;	4;
Matches	4;	Pred. No.	7.8e+05;
Qy	1 AAPF 4	Mismatches	0;
Db	1 AAPF 4	Indels	0;
		Gaps	0;

RESULT 5
 ARR29964
 ID ARR29964 standard; peptide: 4 AA.
 XX
 AC ARR29964;
 DT 19-APR-1993 (first entry)
 XX
 DE Cathepsin G inhibiting fragment.
 KW Cathepsin G; elastase; connective tissue; degradation; protease;
 KW gout; rheumatoid arthritis; emphysema; ARDS;
 KW adult respiratory distress syndrome; para-phenylene.
 OS Synthetic.
 XX
 FH Location/Qualifiers
 KEY
 FT Modified-site 1
 FT /note= "N-terminal amino acids of the peptides of
 FT ARR29963-64 are pref. linked by
 FT -C(O)-phenylene-C(O)-, esp. wherein the
 FT phenylene is para-phenylene gp."
 FT Modified-site 4
 FT /note= "C-terminal Phe is in keto form, i.e. OH
 FT replaced by CGIM, pref. CF3 or CF2CF3"
 XX
 PN WO9220357-A.

OS Synthetic.
 XX
 FH Location/Qualifiers
 KEY
 FT Modified-site 1
 FT /note= "N-succinyl alanine"
 FT 4 /note= "Phe-p-nitroanilide"
 XX
 PN WO9307276-A.
 XX
 PD 15-APR-1993.
 XX
 PR 07-OCT-1992; 92WO-US08341.
 XX
 PR 08-OCT-1991; 91US-0772087.
 XX

XX
 PD 26-NOV-1992.
 XX
 PR 21-APR-1992; 92WO-US03288.
 XX
 PR 23-MAY-1991; 91US-0704449.
 XX
 PA (RICH) MERRELL DOW PHARM INC.
 PT Angelastro MR, Bey P, Doherty NS, Janusz MJ, Mendi S;
 PT Peet NP;
 XX
 DR wpi; 1992-415461/50.
 XX
 PT New peptide derivs. used as cathepsin G and elastase inhibitors -
 PT for treating gout, rheumatoid arthritis, inflammatory disorders,
 PT emphysema and adult respiratory distress syndrome
 XX
 PS Claim 13-17; Page 52; 53pp; English.
 XX
 CC This sequence is an example of a highly generic formula.
 CC Inhibitors of cathepsin G and elastase for preventing connective
 CC tissue degradation are chemically linked inhibitors of the proteases
 CC elastase (pref. the peptide of ARR29963, or Lys(2CBz)-Pro-Val or
 CC Val-Pro-Val) and cathepsin G (pref. the peptide of ARR29964, or
 CC Val-Pro-Phe or Phe).
 CC The N-terminal amino acids of the peptides of ARR29963-64 are pref.
 CC linked by -C(O)-phenylene-C(O)-, esp. wherein the phenylene is a
 CC para-phenylene gp.
 CC The cdps. have an anti-inflammatory effect useful in the treatment
 CC of gout, rheumatoid arthritis and other inflammatory diseases and
 CC to prevent elastic mediated tissue damage. They can also be used
 CC in the treatment of emphysema and adult respiratory distress syndrome.
 XX
 SQ Sequence 4 AA;

Query	Match	Score	Length
Best Local Similarity	100.0%	DB 13;	4;
Matches	4;	Pred. No.	7.8e+05;
Qy	1 AAPF 4	Mismatches	0;
Db	1 AAPF 4	Indels	0;
		Gaps	0;

RESULT 6
 ARR34258
 ID ARR34258 standard; peptide: 4 AA.
 XX
 AC ARR34258;
 XX
 DT 19-AUG-1993 (first entry)
 XX
 DE Chromogenic peptide substrate for peptidase assay.
 XX
 KW Alkaline protease; detergent; stability.
 OS Synthetic.
 XX
 FH Location/Qualifiers
 KEY
 FT Modified-site 1
 FT /note= "N-succinyl alanine"
 FT 4 /note= "Phe-p-nitroanilide"
 XX
 PN WO9307276-A.
 XX
 PD 15-APR-1993.
 XX
 PR 07-OCT-1992; 92WO-US08341.
 XX
 PR 08-OCT-1991; 91US-0772087.

PA (CHEM-) CHEMGEN CORP.
 PA (VIST-) VISTA CHEMICAL CO.
 XX
 PI Fodge DW, Hsiao H, Lalonde JJ;
 XX
 DR WPI: 1993-134465/16.

PT Alkaline protease produced by bacillus stable in alkaline
 PT conditions - used in detergents and bleaches to decompose
 PT proteinaceous stains

PS Disclosure; Page 8; 58pp; English.

XX The peptide is a chromogenic substrate for use in a peptidase assay
 CC to test the peptidase activity of a novel alkaline protease.
 CC Detergent was found to interfere with the assay by reducing the
 CC protease activity. See also AAR34259-61 and AAR34463-66.

Query	1 AAPF 4	Db	1 AAPF 4
Sequence		Sequence	
Query Match	100.0%; Score 21; DB 14; Length 4;	Query Match	100.0%; Score 21; DB 14; Length 4;
Best Local Similarity	100.0%; Pred. No. 7.8e+05;	Best Local Similarity	100.0%; Pred. No. 7.8e+05;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 AAR38410
 ID AAR38410 standard; Protein; 4 AA.
 XX
 AC AAR38410;
 XX
 DT 29-OCT-1993 (first entry)
 DE Cathepsin G inhibitor peptide #1.
 XX
 KW Inflammatory disease; prevention; rheumatoid arthritis; emphysema;
 KW neutrophil-mediated connective tissue degradation; gout; elastase;
 KW inhibition; adult respiratory distress syndrome.
 XX
 OS Synthetic.

XX
 PH Key Modified-site Location/Qualifiers
 FT 1 /note= "Linked via a linking chain such as
 FT -CO-phenyleneCO- to the N-terminal of a
 FT Cathepsin G inhibiting molecule as described
 FT in AAR38410-11".
 FT
 FT Modified-site 4 /note= "May opt. be modified by COCOR, CF2CF3, CF3,
 FT CHF2, COOR3, CONHR3, CF2CHR, CONHR, H, alkyl,
 FT aryl, aralkyl or COR; where R3 is H, alkyl,
 FT phenyl or benzyl and R is OH or alkoxy"
 XX
 PN ZA9203602-A.
 XX
 PD 24-FEB-1993.
 XX
 PF 18-MAY-1992; 922A-0003602.
 XX
 PR 23-MAY-1991; 91US-0704499.
 XX
 PA (RICH) MERRELL DOW PHARM INC.
 XX
 PT Angelastro MM, Bey P, Doherty NS, Janusz MJ, Mehdi S;
 PT Peet NP;
 XX
 DR WPI: 1993-197380/24.

PT New cathepsin G and elastase inhibitors - prevents connective

PT tissue degradation
 XX
 PS Claim 13-17; Page 52; 55pp; English.

XX
 CC The sequences given in AAR38410-11 are cathepsin G inhibiting peptides
 CC which were produced by standard peptide synthesis methods. In the
 CC context of the invention one of these peptides may be linked via
 CC their N-termini to an elastase inhibiting peptide (see features
 CC table). The peptide conjugates may be used to prevent neutrophil-
 CC mediated connective tissue degradation associated with inflammatory
 CC diseases e.g. gout and rheumatoid arthritis. They may also be used
 CC for preventing elastin-mediated tissue damage in the treatment of
 CC emphysema and adult respiratory distress syndrome.

XX
 Sequence 4 AA;
 SQ Query Match 100.0%; Score 21; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 AAR4109
 ID AAR4109 standard; peptide; 4 AA.
 XX
 AC AAR4109;
 XX
 DT 16-MAY-1994 (first entry)
 XX
 DE Aminonaphthalene propyl sulphamide tetrapeptide.
 XX
 KW chymotrypsin assay; ansa-substrate; detector group.
 XX
 OS Synthetic.

XX
 PH Key Modified-site Location/Qualifiers
 FT 1 /note= "Suc-Ala (Claim 1) or z-Ala (Claim 2)"
 FT
 FT Modified-site 4 /label= OTHER
 FT
 FT /note= "Phe-NH-(1,5-naphthylene)-SO2NH-C3H7"
 XX
 PN SU17171478-A.
 XX
 PD 23-OCT-1992.
 XX
 PF 20-JUL-1990; 90SU-4872552.
 XX
 PR 20-JUL-1990; 90SU-4872552.
 XX
 PA (ALTB-) AS LITH BIOCHEM INST.
 PA (ASMO) AS USSR MOLECULAR GENETICS.
 XX
 PT Nedospasov AA, Palaima AI, Yanchene RA;
 XX
 DR WPI: 1993-358242/45.

XX
 PT Prepn. of new succinyl-alanyl-alanyl-propyl-phenylalanyl-amino-
 PT naphthalen-propyl-sulphamide - for use as ansa-substrate in the
 PT quantitative determin. of chymotrypsin
 XX
 PS Claim 1 and 2; Column 8; 4pp; Russian.

XX
 CC 5-(N-succinyl)-alanyl-alanyl-propyl-phenylalanyl)aminonaphthalene-1-
 CC (N-propyl)sulphamide (Claim 1) and 5-(N-benzoyloxycarbonyl)-alanyl-
 CC (N-propyl)-propyl-phenylalanylaminonaphthalene-1-(N-propyl)sulphamide
 CC (Claim 2) are prepared by initially reacting N-benzoyloxycarbonyl-
 CC phenylalanine with isobutyl chloroformate in tetrahydrofuran

CC followed by reaction with 5-aminonaphthalene-1-(N-propyl)sulphamide.
 CC The new compounds are used as detector groups in quantitative
 CC determination of chymotrypsin.

XX sequence 4 AA;

SQ Query Match 100.0%; Score 21; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAPF 4
 Db 1 AAPF 4
 1 AAPF 4

RESULT 9
 AAR52024 AAR52024 standard; peptide; 4 AA.

ID XX AC AAR46223;
 ID XX DT 04-AUG-1994 (first entry)

AC XX DE Serine protease inhibitor tetrapeptide.
 XX XX Prevention; schistosomiasis; parasite; infection; prevention;
 XX KW parasitic penetration; skin; cercariae; anti-penetrant.

XX OS Synthetic.

XX XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "BG(peptide blocking gp.) attached"
 FT Modified-site 4
 FT /note= "PI(protease inhibitor), other than
 chloromethyl ketone, attached"
 XX XX PN US5284829-A.
 XX PD 08-FEB-1994.
 XX PR 26-NOV-1991; 91US-0798565.
 XX PA (RBGC) UNIV CALIFORNIA.
 XX PI Cohen FE, McKerrow JH;
 DR WPI; 1994-056364/07.
 XX PT Synthetic tetra:peptide(s) with an N-terminal blocking gp. and
 PT C-terminal enzyme inhibitor - can be formulated into soaps and
 PT sprays and used to prevent schistosomal skin penetration
 XX XX PS Disclosure; Page 7; 35pp; English.
 XX CC The sequence is that of a synthetic tetrapeptide serine protease
 CC inhibitor which can be used to prevent schistosome parasite
 CC infection. It may be used in a formulation as a soap, lotion,
 CC cream, spray, etc. to stop parasitic penetration of the skin.
 XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 15; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAPF 4
 Db 1 AAPF 4
 1 AAPF 4

RESULT 11
 AAR53781 AAR53781 standard; Peptide; 4 AA.

ID XX AC AAR3781;
 ID XX DT 29-DEC-1994 (first entry)

DE Sequence of internal fragment of a chromogenic substrate for
 DE cathepsin G.
 XX XX QY 1 AAPF 4
 XX KW Enzyme; cathepsin G; protease; chromogenic substrate.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Suc-Ala

RESULT 10
 AAR46223 AAR46223 standard; peptide; 4 AA.

ID FT

FT Modified-site 4 /note= "Succinyl group"
 FT /label= "Phe-pNA"
 FT /note= "p-nitroanil."
 CPN WO9412637-A-
 XX PD 09-JUN-1994.
 XX PR 19-JUL-1999; 89JP-0184738.
 FT PF 06-OCT-1999; 89JP-0260744.
 FT PR 29-DEC-1999; 89JP-0344705.
 XX PR 19-NOV-1993; 93US-0155331.
 XX PT
 XX PA (NOVO) NOVO-NORDISK AS.
 PA (ZYMO) ZYMOGENETICS INC.
 XX PI Foster DC, Norris K, Sprecher CA;
 DR WPI; 1994-200265/24.
 XX
 CC New human Kunitz type protease inhibitor and related DNA - for
 PT treating pancreatic and other disorders involving serine
 PT protease, also new amyloid protein precursor homologues including
 PT the inhibitor in its sequence.
 XX PS Example; Page 63; 70pp; English.
 XX CC Protease inhibitory profiles of the Kunitz inhibitors
 CC were determined for a variety of proteases using
 CC a variety of chromogenic substrates and compared to the inhibitory
 CC activity shown by the Kunitz-type inhibitor domain of the amyloid
 CC protein precursor and bovine aprotinin. The substrate AAR33780
 CC was tested using the protease leukocyte elastase.
 XX SQ Sequence 4 AA;
 XX Query Match 100.0%; Score 21; DB 15; Length 4;
 CC Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 CC Matches 4; Conservative 0; Mismatches 0;
 CC Indels 0; Gaps 0;
 CC Qy 1 AAPF 4
 CC Db 1 AAPF 4
 XX SQ Sequence 4 AA;
 XX Query Match 100.0%; Score 21; DB 16; Length 4;
 ID AAR72876 standard; Peptide; 4 AA.
 XX ID AAR72876
 AC AAR72876;
 XX AC
 XX DT 29-Nov-1995 (first entry)
 DE Substrate for peptidyl prolyl cis trans isomerase alpha.
 KW Escherichia coli; protein conformation; folding; acceleration;
 KW peptidyl prolyl cis trans isomerase alpha;
 KW catalysis; isomerisation; prolyl peptide bond.
 OS Synthetic.
 XX FH Key
 FT Modified-site 1 Location/Qualifiers
 FT /note= "N-succinyl-Ala"
 FT 4 /note= "Phe-MCA (sic)"
 PN EP647713-A.
 XX PD 12-APR-1995.
 XX PR 19-JUL-1990; 90EP-0307914.
 XX PR 19-JUL-1989; 89JP-0184738.
 PR 06-OCT-1989; 89JP-0260244.
 PR 29-DEC-1989; 89JP-0344705.
 XX PA (TOFU) TONEN CORP.
 XX PI Hayano T, Katou S, Maki N, Suzuki M, Takahashi N;
 DR WPI; 1995-140755/19.

Query Match Score 21; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

Qy	Db
1 AAPF 4	1 AAPF 4

RESULT 15
 AAR7196
 ID AAR7196 standard; peptide: 4 AA.
 AC AAR7196;
 XX DT 27-FEB-1996 (first entry)
 XX DE Cell proliferation enzyme proteinase activity substrate peptide #1.
 KW Proteinase; cell growth-stimulating protein; hydrolysis;
 KW macrophage chemotactic action; serine protease inhibitor; wound;
 KW gastric ulcer; leg ulcer; bed sore.
 XX OS Synthetic.

RESULT 14
 AAR7315
 ID AAR7315 standard; Protein: 4 AA.
 XX AC AAR7315;
 XX DR 28-FEB-1996 (first entry)
 DE Porphyromonas gingivalis protease substrate.
 XX KW Protease; periodontal disease; pathogenic microbe; diagnosis;
 KW substrate.
 XX OS Synthetic.

KEY Location/Qualifiers
 FT 1
 FT /label= "Succinyl-Ala"
 FT 4
 FT Modified-site /note= "Modified by 4-methyl-coumaryl-7-amide"
 XX PN EB661293-A2.
 XX PD 05-JUL-1995.
 XX PF 22-DEC-1994; 94EP-0120405.
 XX PR 29-DEC-1993; 93JP-0351225.
 XX PA (SANW) SANWA KAGAKU KENKYUSHO CO.
 XX PI Avaya J, Uesaka H, Watanabe K, Yamaguchi T;
 XX DR WPI; 1995-233274/31.
 XX PT Protein derived from Clostridium perfringens FERM BP-4584 -
 PT stimulates cell proliferation and has macrophage chemotactic action
 XX PN JP07135973-A..
 XX PD 30-MAY-1995.
 XX PF 15-NOV-1993; 93JP-0307084.
 XX PR 15-NOV-1993; 93JP-0307084.
 XX PA (SUNR) SUNMORY LTD.
 XX DR WPI; 1995-227397/30.
 XX PT An enzyme originated from a periodontal disease pathogenic microbe -
 PT and an antibody against the enzyme, for the determination of the
 PT progress and activity of the disease
 PS Example; Page 7, 15pp; Japanese.
 XX CC AAR7315 is a target substrate for a Porphyromonas gingivalis (a
 CC periodontal disease pathogenic microbe) protease. An antibody
 CC raised against the enzyme can be used to diagnose the presence
 CC and progress of a periodontal disease, caused by a pathogenic
 CC microbe.
 XX SQ Sequence 4 AA:
 Query Match Score 21; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

Qy	Db
1 AAPF 4	1 AAPF 4

Db	1 AAPF 4	
RESULT 16		
AAR85709		
ID AAR85709 standard; peptide; 4 AA.		
XX		
AC		
AAW52606;		
XX		
DT 22-JUN-1998 (first entry)		
DE Serine Protease-Inhibiting Peptide with C-terminal phosphonate residue.		
XX		
KW Selective; serine protease inhibitor; trypsin; elastase; chymotrypsin;		
KW antiinflammatory; anticoagulant; antitumour.		
XX		
RESULT 17		
AAW52606		
ID AAW52606 standard; peptide; 4 AA.		
XX		
AC		
AAW52606;		
XX		
DT 22-JUN-1998 (first entry)		
DE Serine Protease-Inhibiting Peptide with C-terminal phosphonate residue.		
XX		
KW Selective; serine protease inhibitor; trypsin; elastase; chymotrypsin;		
KW antiinflammatory; anticoagulant; antitumour.		
XX		
Query Match 100.0%; Score 21; DB 17; Length 4;		
Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;		
Matches 4; Conservative 0; Differ 0; Sequence 4 AA;		
Qy 1 AAPF 4		
Db 1 AAPF 4		
SQ		
Sequence 4 AA:		
XX		
RESULT 18		
AAW30747		
ID AAW30747 standard; Protein; 4 AA.		
XX		
AC		
AAW30747;		
XX		
DT 19-JAN-1998 (first entry)		
DE Substrate peptidase for mutant subtilisin (SAAPP-pna).		
XX		

KW Subtilisin; BPN'; site specific; protease; substrate assisted catalysis;
 KW fusion polypeptide; analogue; variant; mutant; enzyme specificity;
 XX
 OS Synthetic.
 XX
 FH Key Modified-site Location/Qualifiers
 FT 1 /note= "N-terminal succinyl"
 FT Modified-site 4 /note= "Phe-p-nitroanilide"
 XX
 PN US2562136-A.
 XX
 PD 29-JUL-1997.
 XX
 PF 07-JUN-1995; 95US-04988096.
 XX
 PR 04-APR-1983; 89US-0334081.
 PR 29-MAY-1984; 84US-0614491.
 PR 29-MAY-1984; 84US-0614612.
 PR 29-MAY-1984; 84US-0614615.
 PR 01-APR-1986; 840S-0614617.
 PR 30-APR-1986; 86US-0846627.
 PR 06-APR-1987; 87US-0055652.
 PR 01-DEC-1987; 87US-0127134.
 PR 14-JAN-1992; 92US-0823039.
 PR 22-SEP-1994; 94US-028964.
 PR 12-JUL-1993; 93US-0090902.
 PA (GBMV) GENENCOR INT INC.
 XX
 PI Carter PJ, Wells JA.
 XX
 DR WPI; 1997-392947/736.
 XX
 PT Production of recombinant polypeptide(s) - by expression of fusion
 PT polypeptides) with a selected target sequence cleavable by a
 PT subtilisin-related protease
 XX
 PS Example 16; Column 41; 44pp; English.
 XX
 CC This synthetic substrate has been designed to investigate the ability of
 CC the subtilisin BPN' analogue S24c:H64A (see AAW3039) to cleave this
 CC substrate in the presence of imidazole in order to study substrate
 CC assisted catalysis. The specificity of a precursor enzyme is modified by
 CC altering or replacing a catalytically functional amino acid at the
 CC active site, and also through modification of the target substrate. The
 CC target substrate then provides the catalytic activity by interaction
 CC with the variant enzyme i.e. the substrate assists in its own catalytic
 CC conversion to product. This variant subtilisin, where a catalytic His
 CC residue in precursor subtilisin-related protease (wild type) has been
 CC replaced by Ala, is capable of cleaving a fusion polypeptide where the
 CC target cleavage site is composed of a His residue at position P2
 CC (see AAW3073/ for details). The substrate S24c-H64A has no equivalent
 CC residue, however the addition of imidazole has been found to supply
 CC the necessary residue. The *keat* and *km* values for the hydrolysis of
 CC variant S24c:H64A subtilisin increased in the presence of imidazole
 CC whereas the wild-type enzyme remained unaffected.
 XX
 SQ Sequence 4 AA:
 Query Match 100.0%; Score 21; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 DB 1 AAPF 4
 RESULT 19
 RAW24567

ID AAW24567 standard; peptide; 4 AA.
 XX
 AC AAW24567;
 XX
 DT 05-Nov-1997 (first entry)
 XX
 DE Substrate for serine protease.
 XX
 KW Serine protease; N-terminus; Streptomyces griseus; guanidine; pre-soak; cleaning composition; laundry detergent; additive composition; enzyme; dishwasher detergent; drain opener; urea; contact lens cleanser; proteinaceous stain.
 XX
 OS Synthetic.
 XX
 FH Key Modified-site Location/Qualifiers
 FT 1 /note= "succinylated"
 FT Modified-site 4 /note= "para-nitroanilidated"
 XX
 PN US25646028-A.
 XX
 PD 08-JUL-1997.
 XX
 PF 18-JUN-1991; 91US-0718303.
 XX
 PR 18-JUN-1991; 91US-0718303.
 PR 06-NOV-1992; 92US-073343.
 PR 18-AUG-1994; 94US-029294.
 PR 17-OCT-1995; 95US-0544143.
 XX
 PA (CLRX) CLOROX CO.
 XX
 PT Leigh SD;
 XX
 DR WPI; 1997-362936/33.
 XX
 PT Serine protease from Streptomyces griseus ATCC 55178 - with good
 PT stability in presence of urea or guanidine; useful in cleaning
 PT compositions, including laundry and dishwashing detergents
 XX
 PS Claim 4; column 25; 16pp; English.
 XX
 CC This sequence represents a substrate for the serine protease of the
 CC invention. The protease has the N-terminal and C-terminal sequences
 CC represented by AAW4565 and AAW4566 respectively. The serine protease
 CC was isolated from *Streptomyces griseus* variety alkaliphilus No. 33 (ATCC
 55178). The protease has an apparent molecular weight of 19 kD (by
 CC reducing sodium dodecyl sulphate polyacrylamide gel electrophoresis) and
 CC improved stability against urea and guanidine. The serine protease is
 CC specific for the substrate represented by this sequence, but also
 CC recognises the substrates shown in AAW2078-W26096. The protease is
 CC inhibited by phenylmethylsulphonyl fluoride. The serine protease is
 CC useful in liquid or granular cleaning compositions, specifically laundry
 CC detergents or additive compositions. It is also useful in automatic
 CC dishwasher detergents, pre-soaks, drain openers, contact lens cleaners
 CC etc. The protease has better activity against proteinaceous stains than
 CC known enzymes and unusually high stability in the presence of chaotropic
 agents.
 XX
 SQ Sequence 4 AA:
 Query Match 100.0%; Score 21; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 DB 1 AAPF 4
 RESULT 20
 RAW24567

AAW0165
ID AAW0165 standard; Peptide; 4 AA.
XX
AC
XX
DT 26-AUG-1997 (first entry)
XX
DE Proteinase site of a TGF-beta fusion protein.
XX
KW Transforming growth factor-beta fusion protein; wound healing;
XX
artificial skin; surgery recovery time.
XX
OS Synthetic.
XX
PN WO9639430-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US08973.
XX
PR 06-JUN-1995; 95US-0470837.
XX
PA (CHEUNG) CHEUNG D T.
PA (HALL) HALL F L.
PA (NIMMI) NIMMI M E.
PA (TUAN) TUAN T.
PA (WU) WU L.
XX
PI Cheung DT, Hall FL, Nimm M E, Tuan T, Wu L;
XX
DR WPI; 1997-043065/04.
XX
PT Prepn. of transforming growth factor-beta fusion protein - useful to
reduce surgery recovery time and to prepare artificial skin
PS Claim 8; Page 33; 59pp; English.

A novel transforming growth factor-beta (TGF-beta) fusion protein
comprises a purification tag and a TGF active fragment. The present
sequence represents a specifically claimed proteinase site.
Additionally, the fusion protein may comprise proteinase-sensitive
linker sites and binding domain so the protein sequence may contain
some or all of the following elements: purification tag:proteinase
site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes
wound healing, and the fusion protein can be used to reduce surgery
recovery time and in the preparation of artificial skin. The inclusion
of a purification tag facilitates purification of the fusion protein.
The proteinase site is included to permit cleavage and release of the
purification tag after purification if desired. The extracellular
matrix binding site facilitates delivery of the fusion protein to the
desired site of action. Delivery of the TGF-beta to the site to be
treated reduces the amount of TGF-beta required to be administered to
CC treated cells and reduces the amount of TGF-beta required to be administered to
CC which may result in undesirable effects.

XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPF 4
Db 1 AAPF 4

RESULT 21
AAW12810
ID AAW12810 standard; peptide; 4 AA.
XX
AC
XX
DT 21-APR-1997 (first entry)

XX
Sequence 4 AA;
Query Match 100.0%; Score 21; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPF 4
Db 1 AAPF 4

RESULT 22
AAW79700
ID AAW79700 standard; Protein; 4 AA.
XX
AC AAW79700;
XX
DT 25-JAN-1999 (first entry)
XX
DE B. subtilis subtilisin E assay solution peptide.
XX

KW Subtilisin E; mutant; template; in vitro mutagenesis; primer extension.
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 /note= "Modified by presence of succinyl group"
 4
 /note= "Modified by presence of p-nitroanilide"
 XX
 PN WO9842728-A1.
 XX
 PD 01-OCT-1998.
 XX
 PR 25-MAR-1998; 98WO-US05956.
 XX
 PR 04-AUG-1997; 97US-0905359.
 PR 25-MAR-1997; 97US-0041666.
 PR 30-APR-1997; 97US-0045211.
 PR 12-MAY-1997; 97US-0046256.
 XX
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX
 PI Affholter JA, Arnold FH, Giver LJ, Shao Z, Zhao H;
 DR WPI; 1998-542275/46.
 XX
 PT New mutagenised polynucleotide encoding ECB deacetylase enzyme -
 produced by the polymerase-catalysed extension of primers
 XX
 PS Example 6; Page 54; 115pp; English.
 XX
 CC This peptide is used in a novel method for producing double-stranded
 CC mutagenised polynucleotides (PNS) from at least 1 template PN, where the
 CC mutagenised PNS have at least 1 nucleotide which is different from the
 CC same nucleotide in the template PN. The method is useful for the in vitro
 CC mutagenesis and recombination of PNS based on polymerase catalysed
 CC extension of primers. The method can produce full-length genes which are
 CC mutants of the original template PNS, and these genes can be further
 CC amplified and cloned into vectors. The new PNS can be used in DNA-base
 CC computing or for evolving new gene products with improved or new
 CC functions.
 XX
 SQ Sequence 4 AA:
 Query Match 100.0%; Score 21; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 23
 AAW76694 standard; Peptide; 4 AA.
 ID AAW76694;
 AC AAW76694;
 XX
 DT 11-JAN-1999 (first entry)
 DE B. subtilis subtilisin E assay solution peptide.
 KW Subtilisin E; mutant; template; in vitro mutagenesis; primer extension.
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 /note= "Modified by presence of succinyl group"
 4
 /note= "Modified by presence of p-nitroanilide"
 XX
 PN WO9821319-A1.
 XX
 PD 22-MAY-1998.
 XX
 PR 12-NOV-1997; 97WO-US21859.

XX
 PR 15-NOV-1996; 96US-0751070.
 PT - comprises adding reagent composition to the sample containing an
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Damodaran S, Han X;
 XX
 PS WPI; 1998-322335/28.
 DR
 XX
 PT New purified alkaline protease with strong proteolytic activity - is
 PT highly resistant to denaturing agents and may be used in cleaning
 PT compositions
 XX
 Disclosure; Page 9; 50pp; English.
 PS
 XX
 CC The synthetic oligopeptide was used to determine the amidase activity of
 CC protease O. Protease O is a pure alkaline protease composition which is
 CC highly resistant to denaturing agents such as sodium dodecyl sulfate or
 CC urea. It is therefore useful as an additive for detergent and cleaning
 CC compositions, such as dish washing or laundry soap compositions. The
 CC protease can also be used in industrial cleaning such as the cleaning of
 CC ultrafiltration and microfiltration membranes in food and pharmaceutical
 XX
 Sequence 4 AA;
 SQ Query Match 100.0%; Score 21; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 25
 ID AAW5J451
 ID AAW5J451 standard; peptide; 4 AA.
 AC
 XX
 AC AAW5J451;
 DT 02-SEP-1998 (first entry)
 DE Indicator for detection of leukocyte esterase activity in urine.
 XX
 DE Indicator for detection of leukocyte esterase activity in urine.
 KW Urine; indicator; detection; leukocyte esterase; activity;
 KW white blood cell.
 OS Synthetic.
 XX
 FH Key
 FT Modified-site Location/Qualifiers
 FT 1 /note= "Acetyl-, hydrochloride-H-, methoxy-succinyl-suc-",
 FT 4 suc-, gln-, mal- or HB-NH2(CH2)5CO-Ala"
 FT
 FT Modified-site 4 /note= "Phe-nitroanilide"
 PN US5776780-A.
 XX
 PD 07-JUL-1998.
 XX
 PF 12-APR-1996; 96US-0631581.
 XX
 PR 12-APR-1996; 96US-0631581.
 PR 28-MAY-1993; 93US-0068956.
 PR 24-APR-1995; 95US-0429292.
 XX
 PA (CHIM-) CHIMERA RES & CHEM INC.
 XX
 PI Carter JM, Smith JV;
 XX
 DR WPI; 1998-398049/34.

PT Automated measurement of white blood cell esterase activity in urine
 PT - comprises adding reagent composition to the sample containing an
 PT indicator; placing sample in a analyser and comparing absorbance
 PT with a standard measurement
 XX
 PS Claim 11; Column 14; 8pp; English.
 XX
 CC The invention relates to a method for the measurement of white blood
 CC cell esterase activity in urine. It comprises: (i) Placing an aliquot of
 CC the urine in an automated analyser sampling cup; (ii) placing the cup in
 CC a sampling tray with the automated analyser, transferring the urine to a
 CC cuvette and injecting at least one reagent composition in an aqueous
 CC medium into the cuvette, where the reagent composition comprises a
 CC buffer to adjust the pH of the urine to 7.9, an activator and surfactant
 CC selected from benzalkonium chloride, 2,5-dimethylbenzenesulphonic acid
 CC and benzethonium chloride, and an indicator to determine leukocyte
 CC esterase activity in the urine; (iii) reading the aliquot of urine at
 CC specified intervals, in accordance with a preprogrammed code introduced
 CC into the automated analyser, at a preprogrammed monochromatically
 CC specified wavelength, to compare absorbance of the urine sample and
 CC reagent composition complex with that of a standard containing a known
 CC concentration of leukocyte esterase and determining the quantitative
 CC amount of leukocyte esterase in the patient's urine. The method provides
 CC a fully automated method for determining white blood cells in urine. The
 CC method is preferable to the old dipstick method as it reduces consumable
 CC material and labour costs. It also offers increased accuracy, sensitivity
 CC and reduction of interference by substances which affected prior art
 CC tests. The present sequence represents a specifically claimed indicator.
 XX
 Sequence 4 AA;
 SQ Query Match 100.0%; Score 21; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 26
 ID AAW5I610
 ID AAW5I610 standard; peptide; 4 AA.
 AC
 XX
 AC AAW5I610;
 DT 03-SEP-1998 (first entry)
 XX
 DE Peptide conjugated to Lipid for use in liposomal drug delivery.
 XX
 KW Liposome; conjugate; drug delivery; peptidase-secreting cell;
 KW tumour; diagnosis; therapy.
 OS Synthetic.
 XX
 PN WO9816240-A1.
 XX
 PD 23-APR-1998.
 PF 15-OCT-1997; 97WO-US18538.
 XX
 PR 15-OCT-1996; 96US-0027544.
 XX
 PA (LIPO) LIPOSOME CO INC.
 XX
 PI Ali S, Caballilly D, Erukulla RK, Franklin JC;
 PI Janoff AS, Meers PR, Pak C;
 XX
 DR WPI; 1998-261025/23.
 XX
 PT New peptide-lipid conjugates are incorporated into liposome(s) - to
 PT selectively destabilise the liposome(s) in the vicinity of target
 peptide-secreting cells, e.g., tumour cells; useful in diagnosis

OS	Unidentified.	FT	Modified site 1	1
XX		FT	/note= "succinylated"	4
PN	W0955137-A1.	FT		
XX		FT	/note= "Arg is C-terminally modified to	
PD	10-DEC-1998.	FT	Arg-p-nitroanilide"	
XX		XX		
PF	02-JUN-1998;	XX	WO20047578-A1.	
XX	98WO-US11189.	PD	17-AUG-2000.	
PR	03-JUN-1997;	XX	97US-0860452.	
XX		PF	11-AUG-1999;	99WO-US18065.
	(HALL/)	XX		
PA	HALL F L.	PR	09-FEB-1999;	99US-0247062.
(HAB/)	HAN B	XX		
PA	(NIMI/)	XX		
(SHOR/)	NIMI M E.	PA		
PA	(SHOR/)	PA	(THRE-)	3-DIMENSIONAL PHARM INC.
(WUUL/)	SHORS E C.	XX		
PA	WU L.	PI	Marugan JJ;	
XX		PI		
PI	Hall FL,	XX		
PI	Han B,	XX		
PI	Nimni ME,	XX		
PI	Shors EC,	XX		
DR	Wu Li;	XX		
XX		XX		
WPI;	1999-059875/05.	DR		
XX		WPI;	2000-558186/51.	
CC	New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth	XX		
CC	The present peptide represents a proteinase site used in the creation of the bone morphogenetic fusion proteins of the invention. The bone morphogenetic fusion protein may contain some or all of the following elements: a purification tag, a proteinase site, an ECM/bone binding site, a second proteinase site, and a bone morphogenetic active fragment. The fusion proteins of the invention also includes proteins that have transforming growth factor beta active fragments instead of bone morphogenetic protein active fragments. The bone morphogenetic fusion proteins can be used for enhancing wound healing or bone growth.	XX		
PS	Claim 8; Page 34; 64pp; English.	XX		
XX		XX		
CC	PT	PT	New heterocaryl amidines, methylamidines and guanidines, useful for treating e.g. benign prostatic hypertrophy, adult respiratory distress syndrome, wound healing, gout and rheumatoid arthritis	
CC	PT	PT	Example 292; Page 27; 326pp; English.	
CC	PS	XX	The present invention describes heterocaryl amidines, methylamidines and guanidines (I) and their solvates, hydrates and salts. (I) can have cytostatic, antipsoriatic, antigout, noctropic, neuroprotective, antiinflammatory, vulnerary, antirheumatic, antiarticular, antiarteriosclerotic, antiparkinsonian and vasotrophic activities. (I) are inhibitors of proteases selected from leukocyte neutrophil elastase, chymotrypsin, trypsin, pancreatic elastase, cathepsin G, thrombin, urokinase, factor Xa, Plasmin, thermolysin, C-1 esterase, C-3 convertase, aerasin, thrombin, kallikreins, and pepsin, especially trypsin, chymotrypsin, plasmin or urokinase. (I) can be used for treating benign prostatic hypertrophy, prostatic carcinoma, tumour metastasis, restenosis or psoriasis, adult respiratory distress syndrome, wound healing, gout, rheumatoid arthritis, reperfusion damage, atherosclerosis, neoplasia, metastasis, emphysema, Alzheimer's disease, pancreatitis, or Parkinson's disease. The present sequence represents an enzyme substrate peptide which is used in an example from the present invention for the in vitro inhibition of purified enzymes.	
CC	SQ	XX		
XX	Sequence 4 AA;	XX		
XX		XX		
Query Match	100.0%	Score 21;	DB 20;	Length 4;
Best Local Similarity	100.0%	Pred. No.	7.8e+05;	
Matches	4;	Conservative	0;	Mismatches 0;
Qy	1 AAPF 4	Indels	0;	Gaps 0;
Db	1 AAPF 4	SQ	Sequence 4 AA;	
XX		XX		
RESULT 30		Query Match	100.0%	Score 21;
AAB2074		Best Local Similarity	100.0%	DB 21;
AAAS2074	standard; peptide; 4 AA.	Matches	4;	Length 4;
ID		Conservative	0;	Mismatches 0;
AC	AAB2074;	Indels	0;	Gaps 0;
XX		Qy	1 AAPF 4	
XX		AC	1 AAPF 4	
XX		DB	1 AAPF 4	
DT	21-DEC-2000 (first entry)			
XX				
DE	Chymotrypsin enzyme substrate peptide sequence.			
XX				
KW	Heteroaryl amidine; methylanidine; guanidine; protease inhibitor; enzyme substrate; serine protease; chymotrypsin; trypsin; plasmin; urokinase; cytostatic; antipsoriatic; antigout; nootropic; vulnerary; neuroprotective; antiinflammatory; antirheumatic; antiarthritic; antiarteriosclerotic; antiparkinsonian; vasoactive; restenosis; benign prostatic hypertrophy; prostatic carcinoma; tumour metastasis; psoriasis; adult respiratory distress syndrome; wound healing; gout; rheumatoid arthritis; reperfusion damage; atherosclerosis; neoplasia; metastasis; emphysema; Alzheimer's disease; pancreatitis; Parkinson's disease.			
XX				
OS	Synthetic.			
XX				
FH	Key		Location/Qualifiers	

FT Modified-site 1
 FT /note= "Conjugated to succinyl moiety"
 FT Modified-site 4
 FT /note= "Conjugated to p-nitroaniline (PNA)"
 XX PN JP2000116377-A.
 XX
 PD 25-APR-2000.
 XX
 PF 08-OCT-1998; 98JP-0303263.
 PR 08-OCT-1998; 98JP-0303263.
 XX PA (AMAN) AMANO PHARM KK.
 XX DR WPI; 2000-369402/32.
 XX PT A new serine protease and its preparation, used clinically in blood
 PT coagulation, hypertension and anti-inflammation -
 PS Example 3; Page 5; 9pp; Japanese.
 XX
 CC The invention relates to a novel serine protease from *Trichoderma* sp.
 CC No. 9064. The N-terminus of this protease is given in AAB03085. The novel
 CC protease has trypsin-like activity, specifically cleaving peptide chains
 CC on the carbonyl side of a basic amino acid (e.g., arginine or lysine).
 CC It has a pH optimum of 7-8, and is stable between pH 5 and pH 10. It has
 CC a temperature optimum of approximately 40 degrees Celsius, and is stable
 CC between 40 and 50 degrees Celsius. The invention also relates to a
 CC method for the preparation of the novel serine protease and the use of
 CC the protease in protein degradation. The enzyme has coagulant, the use of
 CC hypertensive and anti-inflammatory effects. It may also be used in the
 CC preparation of leather, for raw silk treatment and for the preparation of
 CC protein hydrolysate. Sequences AAB03090-B03094 represent tetrapeptides
 CC used in the determination of the activity of the novel protease.
 XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 1 1 1 1
 Db 1 AAPF 4

RESULT 32
 AAB01922
 ID AAB01922 standard; peptide; 4 AA.
 AC AAB01922;
 XX DT 18-SEP-2000 (first entry)
 DE Synthetic peptide substrate peptide.
 XX KW Peptidyl prolyl cis-trans isomerase; PPIase; hepatitis B surface antigen;
 KW Hsag; hepatitis B virus; HBV; granulisation; immunoassay;
 KW substrate peptide.
 XX OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminus is conjugated to a succinyl moiety"
 FT /note= "C-terminus is conjugated to a p-nitroanilide"
 XX PN JP2000105234-A.
 XX PR 14-AUG-1998; 98US-0134472.
 PD 11-APR-2000.

XX PF 29-SEP-1998; 98JP-0275008.
 XX PR 29-SEP-1998; 98JP-0275008.
 XX PA (SEKI) SURIKU CHEM IND CO LTD.
 PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 XX DR WPI; 2000-334401/29.
 XX PT Preparation of small granules of Hepatitis B surface antigen, used in
 PT manufacture of immunoassay reagent, by simultaneous granulating and
 PT cis-trans isomerase reaction of antigen -
 PS Disclosure; Page 5; 14pp; Japanese.
 XX CC The invention relates to the preparation of small granules of hepatitis
 CC B surface antigen (HBsAg) by granulating the antigen with a surfactant,
 CC subjected to cis-trans prolyl isomerisation by contacting it with a
 CC peptidyl prolyl cis-trans isomerase (PPIase). The small granulated HBsAg
 CC is used in the manufacture of a hepatitis B virus (HBV) immunoassay
 CC reagent. Small granules comprising activated HBsAg, an enzyme labelled
 CC can be used in a highly sensitive HBV immunoassay. The present
 CC sequence represents a PPIase synthetic substrate peptide referred to in
 CC the disclosure of the invention.
 XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 1 1 1 1
 Db 1 AAPF 4

RESULT 33
 AAY91025
 ID AAY91025 standard; peptide; 4 AA.
 XX AC AAY91025;
 XX DT 06-SEP-2000 (first entry)
 XX DE Model substrate peptide sequence.
 KW Carboxylic acid; isostere; heterocyclic compound; vision disorder;
 KW memory disorder; ophthalmological; nootropic; rotamase inhibitor;
 KW peptidylprolyl isomerase inhibitor; visual impairment; orbital disorder;
 KW lacrimal apparatus; eyelid; conjunctiva; cornea; cataract; uveal tract;
 KW retina; optic nerve; visual pathway; free radical induced eye disorder;
 KW immunologically-mediated eye disorder; ophthalmologic disorder.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "succinylated"
 FT Modified-site 4
 FT /note= "Phe is C-terminally modified to
 Phe-p-nitroanilide"
 XX PN WO200009102-A2.
 XX PD 24-FEB-2000.
 XX PR 12-AUG-1999; 99WO-US18230.
 XX PR 14-AUG-1998; 98US-0134472.

PA	(GUILFORD) GUILFORD PHARM INC.	PR	13-OCT-1998; 98DK-0001301.
PT	Ross DT, Sauer H, Hamilton GS, Steiner JP;	PR	04-OCT-1999; 99DK-0001418.
DR	WPI; 2000-2241156/19.	XX	
XX		PA	(NOVO) NOVO-NORDISK AS.
PT	Treating a vision disorder or enhancing memory by administration of N-heterocyclic ring compound including a direct or indirect carboxyl substituent -	XX	
PT	substituent -	DR	WPI; 2000-329163/28.
PS	Disclosure; Page 37; 99pp; English.	XX	
CC	The present invention describes N-heterocyclic ring compounds containing carboxylic acid or carboxylic acid isostere attached to 2-carbon of N-heterocyclic ring useful for treating vision disorders or enhancing memory performance. The compounds have ophthalmological and nootropic activities and are peptidyl/prolyl isomerase and rotamase inhibitors.	CC	New modified polypeptides having an attached polymer for reducing immune responses, useful in e.g. detergents, cleaning products, skin care products, food or feed products, textile products or pharmaceuticals -
CC	Methods from the present invention are useful for treating vision disorders such as visual impairments, orbital disorders, disorders of the lacrimal apparatus, disorders of the eyelids, disorders of the conjunctiva, disorders of the cornea, cataract, disorders of the uveal tract, disorders of the retina, disorders of the optic nerve or visual pathways, free radical induced eye disorders and diseases, immunologically-mediated eye disorders and disorders, eye injuries and symptoms and complications of eye disease, eye disorder or eye injury. The methods are also useful for improving naturally-occurring vision, in the absence of any ophthalmologic disorder, disease or injury. The compositions are additionally useful for treating memory impairment or differentiated memory performance in an animal. The compounds may be differentiated from the non-immunosuppressive compounds used to treat vision disorders by their novel small molecule structure and their lack of general, systemic effects. The present sequence represents a model substrate peptide sequence which is used in the exemplification of the present invention.	CC	Example 5; Page 49; 108pp; English.
CC	Sequence 4 AA;	XX	The invention relates to proteins with reduced immunogenicity, having one or more modified amino acids, where the alpha-carbon atoms of the amino acids are located less than 15 Angstroms from a ligand bound to the protein. The modification may entail substitution of the endogenous residue for a non-endogenous residue and/or attachment of polymeric molecules such as carbohydrates or branched polyethylene glycols to the amino acid residues. The residue to be modified is identified from the 3-dimensional structure of the protein determined, for example, by X-ray crystallography or NMR. A wide variety of enzymes may be modified according to the invention, including proteases (especially subtilisins), carbohydrates (such as amylase), isomerases, transferases and oxidoreductases. The modified proteins of the invention may be used for reducing the allergenicity of industrial products (i.e., those which are not intended to enter the circulatory system). The proteins may be used in cleaning agents (such as laundry products, dish-washing products, or hard surface cleaning products), skin-care products, textile treatments products (e.g., bleaching agents) and food products. The modified polypeptides can also be used for reducing the immunogenicity of pharmaceuticals. The modified proteins have reduced immunogenicity or allergenicity while maintaining a high percentage of activity. The present sequence represents a synthetic peptide substrate used in assays to determine the activities of modified proteases of the invention.
QY	Query Match 100.0%; Score 21; DB 21; Length 4;	CC	
QY	Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	
SQ	Sequence 4 AA;	XX	
Db	1 AAPF 4	XX	
RESULT 34		XX	
AC	AY97813	XX	
ID	AY97813 standard; protein; 4 AA.	XX	
AC	AY97813;	XX	
DT	21-AUG-2000 (first entry)	XX	
DE	Protease peptide substrate.	XX	
XX		XX	
XX		XX	
KW	Protease substrate; immunogenicity; allergenicity; industrial product; pharmaceutical; hypoallergenic.	XX	
XX		XX	
OS	Synthetic.	XX	
XX		XX	
FH	Key Location/Qualifiers	XX	
FT	Modified-site 1 /note= "Conjugated to a succinyl moiety"	XX	
FT	Modified-site 4 /note= "Conjugated to a nitro-anilide moiety"	XX	
PN	WO200022103-A1.	XX	
XX		XX	
PD	20-APR-2000.	XX	
PF	12-OCT-1999; 99WO-DK00542.	XX	
FT	Modified-site 1 /note= "Suc-Ala"	XX	

FT /note= "Phe-pNA"
 XX
 PN WO200005204-A1.
 XX
 PD 03-FEB-2000.
 XX
 PR 16-JUL-1999; 99WO-JP03864.
 XX
 PR 23-JUL-1998; 98JP-0207540.
 XX (SHIO) SHIONOGI & CO LTD.
 XX
 PT Denaka M., Kii M., Nakajima M;
 XX
 DR WPI; 2000-195090/17.
 XX
 PT Chymase inhibitors containing N-substituted azetidinone compounds,
 useful for treating, e.g. inflammation and asthma -
 XX
 PS Disclosure; Page 150; 173pp; Japanese.
 XX
 CC The invention relates to new chymase inhibitors containing an
 CC N-substituted azetidinone compound or derivative. This sequence
 CC represents an example of such an inhibitor. The inhibitors are useful
 CC for treating inflammation, allergies, and circulation disorders,
 CC including scarring, and keloid formation, post-surgical restenosis, myocardi
 CC chronic inflammation, fibrosis, rheumatism,
 CC asthma, dermatitis, arthritis, psoriasis, hepatic sclerosis,
 CC conjunctivitis, Crohn's disease,
 CC heart failure, peripheral circulation disease, diabetic and non-diabetic
 CC kidney damage, stroke, arteriosclerosis. The inhibitors may also be
 CC used as immunomodulators.
 XX
 Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; MisMatches 0; Del 0; Gap 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 36
 ID AAY76808
 XX AAY76808 standard; peptide; 4 AA.
 AC AAY76808;
 XX
 DT 26-APR-2000 (first entry)
 XX
 DE Chymotrypsin substrate peptide.
 XX
 KW Proteolytic enzyme; inhibitor; substrate; aminoquinidine; pyrazine;
 KW hydrazinoamidine; alkoxyaminamide; alkoxymannamide; viral infection;
 KW thrombotic disease; ischaemia; stroke; cancer; restenosis; septic shock;
 KW myocardial infarction; disseminated intramuscular coagulopathy; sepsis;
 KW unstable angina; coronary artery bypass; hip replacement; haemodialysis;
 KW adult respiratory distress syndrome; rheumatoid arthritis; induration;
 KW ulcerative colitis; metastasis; hypercoagulability; Alzheimer's disease;
 KW Down's syndrome; fibrin formation; wound healing; inflammation; therapy;
 KW Chymotrypsin.
 XX
 OS Synthetic.
 XX
 PH Location/Qualifiers
 FT Key
 FT Modified-site 1 /note= "N-succinyl-Ala"
 FT
 FT Modified-site 4 /note= "Phe-p-nitroanilide"
 FT
 XX
 PN WO9954416-A1.
 XX

XX 16-DEC-1999.
 XX
 PD 11-JUN-1999; 99WO-US13228.
 XX
 PR 11-JUN-1998; 98US-0088989.
 XX
 PA (TIRE-) 3-DIMENSIONAL PHARM INC.
 PA (LUTT-) LU T.
 PA (TOMC/) TOMCZUK B. F.
 PA (MARK/) MARKOTAN T P.
 XX
 PT Lu T., Tomczuk BE, Markotan TP;
 XX
 DR WPI; 2000-147091/13.
 XX
 PT Pyrazinone compounds used as potent thrombin (protease) inhibitors -
 XX
 PS Example 36; Page 78; 112pp; English.
 XX
 CC This sequence represents a peptide substrate for chymotrypsin.
 CC The invention relates to aminoguanidine (hydrazinoamidine) and
 CC alkoxyaminidine (alkoxymannamide) pyrazinones that function as
 CC proteolytic enzyme inhibitors. A pharmaceutical composition containing
 CC the pyrazinone is used to treat thrombotic diseases associated with
 CC ischaemia, viral infections, stroke, cancer, restenosis, myocardial
 CC infarction, disseminated intramuscular coagulopathy which occurs during
 CC septic shock, unstable angina, disseminated intramuscular coagulation
 CC caused by trauma, coronary artery bypass, hip replacement, thrombolytic
 CC therapy, sepsis, haemodialysis, adult respiratory distress syndrome,
 CC rheumatoid arthritis, ulcerative colitis, induration, metastasis,
 CC hypercoagulability during chemotherapy, Alzheimer's disease, Down's
 CC syndrome, fibrin formation in the eye, wound healing, or inflammation in
 CC a mammal.
 XX
 Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; MisMatches 0; Del 0; Gap 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 37
 ID AAY78789
 XX AAY78789 standard; peptide; 4 AA.
 AC AAY78789;
 XX
 DE 09-MAY-2000 (first entry)
 XX
 DE Subtilisin substrate peptide.
 KW Subtilisin substrate; chemically modified mutant protein; anti-microbial;
 KW subtilisin substrate; chiral resolution; regioselective acetylation;
 KW pharmaceutical; diagnostic agent; cleaning composition; brewing;
 KW textile treatment.
 XX
 OS Synthetic.
 XX
 PH Location/Qualifiers
 FT Key
 FT Modified-site 1 /note= "Succinyl-Ala"
 FT
 FT Modified-site 4 /note= "Phe-p-nitroanilide"
 FT
 XX
 PN WO200001712-A2.
 XX
 PD 13-JAN-2000.

PF 02-JUL-1999; 99WO-US15138.
 XX
 PR 02-JUL-1998; 98US-0091687.
 XX
 PR 28-APR-1999; 99US-0131446.
 XX
 PA (GEMV) GENENCOR INT INC.
 XX
 PI Jones JB, Davis BG;
 XX
 DR WPI; 2000-170995/15.

PT New chemically modified mutant proteins, particularly proteases, for e.g. peptide synthesis -
 XX
 PS Example 2; Page 33; 86pp; English.

CC This sequence represents a subtilisin peptide substrate. The peptide is used in a procedure for the modification of subtilisin *Bacillus lentinus* mutants. Subtilisin mutants are used in the invention which relates to a chemically modified mutant protein which includes a Cys residue which replaces another amino acid in a precursor, that has been subsequently modified by reaction with a glycosylated thiosulfonate. The chemically modified mutant proteins have altered functional properties, e.g. solubility; cell-cell signalling; catalytic biological or pharmacological activities, also sites critical for immunological or allergic responses, or proteolytic degradation, can be masked. They may be used to determine structure-function relationships, also e.g.:
 CC (a) to alter the catalytic activity of enzymes;
 CC (b) to improve suitability for use in vaccines;
 CC (c) to reduce allergenicity;
 CC (d) to improve solubility (e.g. to facilitate recovery or formulation), or to improve stability against proteolysis.
 CC A particular application is to modify subtilisins so that they have reduced amidase and increased esterase activities, making them useful in chiral resolution; regioselective acylation; and synthesis of peptides or glycoproteins, but more generally modified proteins of the invention may also be used as pharmaceutical or diagnostic agents, or in cleaning compositions, textile treatment, modification of foods or feeds, brewing or starch processing, as anti-microbials and in personal care

XX Sequence 4 AA;

SQ Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 1 AAPF 4

RESULT 38
 AAY9452 standard; peptide; 4 AA.

ID AAY9452
 XX AC AAY9452;
 XX DT 23-MAR-2000 (first entry)
 DE Peptidylprolyl cis-trans isomerase (PPRase) peptide.
 XX KW Peptidylprolyl cis-trans isomerase; PPRase; protein stabilising;
 XX KW protein inactivation inhibitor.
 OS Methanococcus voltae.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-succinyl-Ala"
 FT Modified-site 4
 FT /note= "Phe-p-nitroanilide"
 XX PN JP11302297-A.
 XX PD 02-NOV-1999.
 XX PF 16-APR-1998; 98JP-0105953.
 XX PR 16-APR-1998; 98JP-0105953.
 XX PA (SEIKI) SEKISUI CHEM IND CO LTD.
 PA (KATIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 XX DR WPI; 2000-075343/07.

PT Novel polypeptide sequences used as proteinase inhibitors -
 XX
 PS Disclosure; Page 13; 85pp; English.

CC The invention relates to a new class of proteinase inhibitors called disulfide core proteinase inhibitors (Zdscl) and provides murine and human Zdscl polypeptides. The disulfide core proteins are proteinase inhibitors used for the treatment of acute pancreatitis, various stages of shock syndrome, hypofibrinolytic hemorrhage and myocardial infarction. Antagonists of the polypeptides can be used as research reagents for characterizing sites of ligand-receptor interaction. Antibodies against the proteins may be used for tagging cells that express the protein, for detecting the protein, and for screening expression libraries. Polynucleotides encoding the polypeptides can be used in gene therapy applications where it is desired to increase or inhibit the protein activity.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 1 AAPF 4

RESULT 39
 AAY59632 standard; peptide; 4 AA.

ID AAY59632
 XX AC AAY59632;
 XX DT 23-MAR-2000 (first entry)
 DE Peptidylprolyl cis-trans isomerase (PPRase) peptide.
 XX KW Peptidylprolyl cis-trans isomerase; PPRase; protein stabilising;
 XX KW protein inactivation inhibitor.
 OS Methanococcus voltae.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-succinyl-Ala"
 FT Modified-site 4
 FT /note= "Phe-p-nitroanilide"
 XX PN JP11302297-A.
 XX PD 02-NOV-1999.
 XX PF 16-APR-1998; 98JP-0105953.
 XX PR 16-APR-1998; 98JP-0105953.
 XX PA (SEIKI) SEKISUI CHEM IND CO LTD.
 PA (KATIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 XX DR WPI; 2000-075343/07.

PT A method for stabilisation of a protein - using peptidylprolyl
 PT cis-trans isomerase from a Methanococcus genus microbe
 XX
 PS Disclosure; Page 3; 7pp; Japanese.
 XX
 CC This sequence is a peptide fragment of Methanococcus voltae
 CC peptidylprolyl cis-trans isomerase (PPIase). The peptide is used in the
 CC invention which relates to a method for the stabilisation of a protein.
 CC In the method, the PPIase is prepared from a Methanococcus genus microbe.
 CC or is expressed from DNA prepared from a Methanococcus genus microbe. The
 CC PPIase is present in a solution that is used to inhibit inactivation of a
 CC protein present in the solution. The method is useful for stabilising a
 CC protein. The method is versatile and does not require the use of a high
 CC energy substance such as ATP.
 XX
 SQ Sequence 4 AA:
 Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4

RESULT 40
 AAU07699
 ID AAU07699 standard; Peptide; 4 AA.
 XX
 AC AAU07699;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE ztryp3 substrate used in serine protease activity assay.
 XX
 KW Human; Ztryp3; serine protease; asthma; vascular function; inflammation;
 KW gene therapy; stroke; testicular function; spermatogenesis; haemostatic;
 KW mass spectrometry; circular dichroism; X-ray crystallography;
 KW nuclear magnetic resonance spectroscopy; antiasthmatic; antiinflammatory;
 KW cerebroprotective.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Location/Qualifiers
 KEY
 FT Modified-site 1
 FT /note= "Suc-Ala"
 FT Modified-site 4
 FT /note= "Phe-DNA"
 XX
 PN WO200166711-A2.
 XX
 PD 13-SEP-2001.
 XX
 PP 28-FEB-2001; 2001WO-US06432.
 XX
 PR 03-MAR-2000; 2000US-0516387.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Conklin DC;
 XX
 DR
 WPI; 2001-589946/66.
 XX
 PT Novel ztryp3 polypeptides and polynucleotides useful in the treatment
 PT of asthma, vascular disorders including stroke, inflammation and
 PT testicular function -
 XX
 PS Disclosure; Page 39; 82pp; English.
 XX
 CC The invention relates to an isolated human ztryp3 polypeptide, a member
 CC of the serine protease family. Ztryp3 polypeptides and their associated

CC polynucleotides are useful in diagnosis, therapy and industry and are
 CC used as targets for identifying modulators, preferably inhibitors of
 CC serine protease activity. The sequences are useful in the treatment of
 CC asthma, vascular function such as stroke, inflammation and testicular
 CC function (by modulating spermatogenesis). Ztryp3 proteins can be used for
 CC identifying peptide cleavage sites and for coupling amino and carboxy
 CC terminal tags. The polypeptides are also useful to teach analytical
 CC skills such as mass spectrometry, circular dichroism, X-ray
 CC crystallography and nuclear magnetic resonance spectroscopy. This
 CC sequence represents a Ztryp3 substrate used in serine protease activity
 CC assays.
 XX
 SQ Sequence 4 AA:
 Query Match 100.0%; Score 21; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4

Search completed: December 6, 2002, 13:28:01
 Job time : 26 secs

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On protein - protein search, using sw model

Run on: December 6, 2002, 13:26:14 ; Search time 9.33333 seconds
(without alignments) updates/sec
12.610 Million cell

Title: US-10-033-526-1
Perfect score: 21
Sequence: 1AAPP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

- 1: Issued_Patents_AA;*
- 2: /cggn2_6/podata/1/1aa/5A_COMBO.pep;*
- 3: /cggn2_6/podata/1/1aa/5B_COMBO.pep;*
- 4: /cggn2_6/podata/1/1aa/6A_COMBO.pep;*
- 5: /cggn2_6/podata/1/1aa/PCMS_COMBO.pep;*
- 6: /cggn2_6/podata/1/1aa/backfile1.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4	1 US-07-973-335-1
2	21	100.0	4	1 US-08-155-331-19
3	21	100.0	4	1 US-08-004-645C-2
4	21	100.0	4	1 US-08-463-456-5
5	21	100.0	4	1 US-08-282-860-1
6	21	100.0	4	1 US-08-407-006-6
7	21	100.0	4	1 US-07-890-422B-28
8	21	100.0	4	1 US-08-276-936B-2
9	21	100.0	4	1 US-08-341-820B-2
10	21	100.0	4	1 US-08-544-143B-3
11	21	100.0	4	1 US-08-370-202A-9
12	21	100.0	4	1 US-08-437-029-5
13	21	100.0	4	1 US-08-424-022-19
14	21	100.0	4	1 US-08-434-534-10
15	21	100.0	4	1 US-08-434-959-3
16	21	100.0	4	1 US-08-434-959-4
17	21	100.0	4	1 US-08-434-959-5
18	21	100.0	4	1 US-08-430-959-6
19	21	100.0	4	1 US-08-460-348B-56
20	21	100.0	4	1 US-08-067-180B-2
21	21	100.0	4	1 US-08-390-028B-56
22	21	100.0	4	1 US-08-470-837-3
23	21	100.0	4	1 US-08-722-268B-2
24	21	100.0	4	1 US-08-501-265B-56
25	21	100.0	4	1 US-08-439-005-10
26	21	100.0	4	1 US-08-575E-2
27	21	100.0	4	1 US-08-424-017B-19

ALIGNMENTS

RESULT 1
US-07-973-335-1
; Sequence 1, Application US/07973335
; Patent No. 538547

GENERAL INFORMATION:
APPLICANT: Kennedy and Szubaj
TITLE OF INVENTION: No. 538547e1 Bowman-Birk Inhibitor
NUMBER OF INVENTIONS: Product For Use As An Anticarcinogenesis Agent

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESS: Mackiewicz & No. 538547ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,335
FILING DATE: 19921102
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 824,719
FILING DATE: January 17, 1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 579,155
FILING DATE: September 6, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: USPC-0003

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-973-335-1

Query Match Similarity 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
Db 1 AAPF 4

RESULT 2
US-08-155_331-19
Sequence 19, Application US/08155331
; Patent No. 5,419,311

GENERAL INFORMATION:
APPLICANT: Foster, Donald C
APPLICANT: Sprecher, Cindy
APPLICANT: No.-5441931rs, Kield
TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,331
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-684
REFERENCE/DOCKET NUMBER: 92-21C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
SEQUENCE FOR SEQ ID NO: 19:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLogy: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /label= ALA-1
OTHER INFORMATION: /note= "Amino terminal alanine residue is capped
OTHER INFORMATION: with a succinyl group"

RESULT 2
US-08-155_331-19
Sequence 19, Application US/08155331
; Patent No. 5,419,311

GENERAL INFORMATION:
APPLICANT: Gunter Fischer & Gerhard Kllerz
APPLICANT: Gunter Fischer et al. c/o G. P. Katona
TITLE OF INVENTION: Cyclosporine Assay
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gunter Fischer et al. c/o G. P. Katona
STREET: 230 Park Avenue, Room 2200
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10169

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: conf. to PatentIn Release #1.0, ver.#1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/004,643C
FILING DATE: 12-January 1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 703,590
FILING DATE: 20 May 1991
APPLICATION NUMBER: 398,092
FILING DATE: 24 August 1989
APPLICATION NUMBER: DD WP 601 F/319 577W
FILING DATE: 07 September 1988

ATTORNEY/AGENT INFORMATION:
NAME: Katona, Gabriel P.
REGISTRATION NUMBER: 20,829
REFERENCE/DOCKET NUMBER: 691-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-5377
TELEFAX: (212)986-6126
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

RESULT 4
US-08-462-456-5
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
Db 1 AAPF 4

RESULT 4
US-08-462-456-5
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
Db 1 AAPF 4

RESULT 3

ADRESSEE: Marion Merrell Dow Inc.
STREET: 2110 East Galbraith Rd.
CITY: Cincinnati P. O. Box 156300

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Giblin, James A.
REGISTRATION NUMBER: 25772
REFERENCE/DOCKET NUMBER: MSB-7214
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)705-7910
TELEFAX: (510)705-7904
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS: single strand
MOLECULE TYPE:
DESCRIPTION: peptide

FEATURE:
NAME/KEY: Modified Peptide used for enzyme activity assay
OTHER INFORMATION: Peptide is modified with n-terminal p-nitroanilide group

PUBLICATION INFORMATION:
AUTHORS: Targman, C. W.
TITLE: A Sensitive New Substrate for Chymotrypsin
JOURNAL: Analytical Biochemistry
VOLUME: 99
PAGES: 316-329

DATE: 01-NOV-1979
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4

US-08-282-860-1
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

QY	1 AAPF 4
Db	1 AAPF 4

RESULT 5
US-08-282-860-1
Sequence 1, Application US/08282860
; Patent No. 5561108
; GENERAL INFORMATION:
; APPLICANT: Tsay, Grace C.
; APPLICANT: Cheung, Neal K. H.
; APPLICANT: Bentenourt, Jeffrey D.
; TITLE OF INVENTION: Preparation of Alpha-1 Antichymotrypsin
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; FILING DATE: 07-29-94
; APPLICATION NUMBER: US/08/282, 860
; FILING DATE: 07-29-94
; CLASSIFICATION: 514

US-08-407-000-6
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

QY	1 AAPF 4
Db	1 AAPF 4

RESULT 6
US-08-407-000-6
Sequence 6, Application US/08407000
; Patent No. 5578324
; GENERAL INFORMATION:
; APPLICANT: Dohi, Masahiko
; APPLICANT: Nishibe, Yoshihisa
; APPLICANT: Makino, Yuki
; APPLICANT: Suzuki, Yoshiki
; TITLE OF INVENTION: PEPTIDE PROTEINACOUS DRUG NASAL
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGIRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; FILING DATE: 22-MAR-1995
; APPLICATION NUMBER: US/08/407, 000
; PRIOR APPLICATION DATA:
; APPLICANT NUMBER: PCT/JP94/01257
; FILING DATE: 29-JUL-1994
; APPLICATION NUMBER: JP-A-5-206922

FILING DATE: 30-JUL-1993
 APPLICATION NUMBER: JPA 5-235841
 FILING DATE: 30-AUG-1993
 APPLICATION NUMBER: JP-A-6-1644
 FILING DATE: 12-JAN-1994
 INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-407-000-6
 Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 AAPF 4
 Db 1 AAPF 4

RESULT 7
 US-07-890-422B-28

Sequence 28 Application US/07890422B
 Patent No. 5602102

GENERAL INFORMATION:
 APPLICANT: THIELE, DWAIN L.

APPLICANT: LIPSKY, PETER E.

APPLICANT: MCGUIRE, MICHAEL J.

TITLE OF INVENTION: Dipeptidyl Peptidase-I

TITLE OF INVENTION: Inhibitors and Uses Thereof

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P. O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,936A

FILING DATE: July 19, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 221,078

FILING DATE: March 31, 1994

APPLICATION NUMBER: 221,171

FILING DATE: March 31, 1994

APPLICATION NUMBER: 005,908

FILING DATE: January 15, 1993

APPLICATION NUMBER: 735,335

FILING DATE: July 24, 1991

ATTORNEY/AGENT INFORMATION:

NAME: MAYFIELD, DENISE L.

REGISTRATION NUMBER: 33,732

REFERENCE/DOCKET NUMBER: UTSD-296/MAY

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4

TYPE: Amino Acid

TOPOLOGY: Linear

RESULT 8
 US-08-276-936A-2
 Sequence 2, Application US/08276936A
 Patent No. 5612194

GENERAL INFORMATION:
 APPLICANT: Harvey Rubin, Barry Cooperman, No. 5612194man Schechter,
 APPLICANT: Michael Plotkin, Zhi Wang
 TIME OF INVENTION: Methods of Producing Effective
 TIME OF INVENTION: Recombinant Serine Protease Inhibitors and Uses of These
 TIME OF INVENTION: Inhibitors

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jane Massey Licata, Esq.
 STREET: 210 Lake Drive East, Suite 201
 CITY: Cherry Hill
 STATE: NJ
 COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/276,936A

FILING DATE: July 19, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 221,078

FILING DATE: March 31, 1994

APPLICATION NUMBER: 221,171

FILING DATE: March 31, 1994

APPLICATION NUMBER: 005,908

FILING DATE: January 15, 1993

APPLICATION NUMBER: 735,335

FILING DATE: July 24, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: PENN-0027

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4

TYPE: Amino Acid

TOPOLOGY: Linear

RESULT 9
 US-08-276-936A-2

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TYPE: AMINO ACID

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

US-07-890-422B-28

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acid residues

TOPOLOGY: linear

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/345.820B

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-345-820B-2

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4

Db 1 AAPF 4

RESULT 10

US-08-54-143A-3

Sequence 3, Application US/08544143A

PATENT NO.: 564028

GENERAL INFORMATION:

APPLICANT: Leigh, Scott D.

TITLE OF INVENTION: NOVEL ALKALINE PROTEASE AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majeski, Parsons, Siebert & Hsue

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: U.S.A.

ZIP: 94111-4121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/397,602A

FILING DATE: 02 MAR 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jaeschke, Wayne C.

REGISTRATION NUMBER: 21,062

REFERENCE/DOCKET NUMBER: D8969/M4828

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 832-2200

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "N-SUCCINYL"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /note= "P-NITROANILIDE"

US-08-397-602A-9

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4

Db 1 AAPF 4

RESULT 12

US-08-37-029-5

Sequence 5, Application US/08437029

PATENT NO.: 5688107

GENERAL INFORMATION:

APPLICANT: Miller, Edward J.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Elastase

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

US-08-397-602A-9

RESULT 11

US-08-397-602A-9

STATE: California
COUNTRY: USA
ZIP: 94105

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,029
FILING DATE: 08 May 95
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 017066-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

S-08-437-029-5

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Y 1 AAPF 4
| | |
b 1 AAPF 4

RESULT 13
S-08-437-023-19
Sequence 19, Application US/08424022
Patient No. 5677146
GENERAL INFORMATION:
APPLICANT: Foster, Donald C
APPLICANT: Sprecher, Cindy
APPLICANT: Kjeld, 567716ris
TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,022
FILING DATE: 02-DEC-1992
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/985,692
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-684
REFERENCE/DOCKET NUMBER: 92-21C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322

RESULT 14
US-08-439-534-10
Sequence 10, Application US/08439534
Patient No. 5719041
GENERAL INFORMATION:
APPLICANT: Lazarus, Robert A.
APPLICANT: Dennis, Mark S.
APPLICANT: Ulmer, Jana S.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING
TITLE OF INVENTION: ECOIN AND HOMOLOGS THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,534
FILING DATE: 11-MAY-1995
CLASSIFICATION: 35
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/319501
FILING DATE: 04-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/121004
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0859C1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9801
TELEFAX: 415/952-9801
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPF 4
 Db 1 AAPF 4

RESULT 15
 US-08-434-959-3 Application US/08434959
 Sequence 3, Application US/08434959
 ; Patent No. 5736520

GENERAL INFORMATION:
 APPLICANT: Bey, Philippe
 APPLICANT: Angelastro, Michael R
 APPLICANT: Mehdì, Shujahath
 TITLE OF INVENTION: No. 5736520el Peptidase Inhibitors
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marion Merrell Dow Inc.
 STREET: 2110 East Galbraith Rd.
 CITY: Cincinnati P. O. Box 156300
 STATE: Ohio
 COUNTRY: USA
 ZIP: 45215-6300

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434-959
 FILING DATE:
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/750,439
 FILING DATE: 20-AUG-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/454,803
 FILING DATE: 21-DEC-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/439,201
 FILING DATE: 20-NOV-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/416,817
 FILING DATE: 04-OCT-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/254,762
 FILING DATE: 07-OCT-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Nesbitt, Stephen L
 REGISTRATION NUMBER: 28,981
 REFERENCE/DOCKET NUMBER: M01368F US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (513) 948-7965
 TELEFAX: (513) 948-7961
 TELEX: 214320

TELEFAX: 214320
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-434-959-3

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPF 4
 Db 1 AAPF 4

RESULT 16
 US-08-134-959-4 Application US/08434959
 Sequence 4, Application US/08434959
 ; Patent No. 5736520

GENERAL INFORMATION:
 APPLICANT: Bey, Philippe
 APPLICANT: Angelastro, Michael R
 TITLE OF INVENTION: No. 5736520el Peptidase Inhibitors
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marion Merrell Dow Inc.
 STREET: 2110 East Galbraith Rd.
 CITY: Cincinnati P. O. Box 156300
 STATE: Ohio
 COUNTRY: USA
 ZIP: 45215-6300

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434,959
 FILING DATE:
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/750,439
 FILING DATE: 20-AUG-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/454,803
 FILING DATE: 21-DEC-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/439,201
 FILING DATE: 20-NOV-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/416,817
 FILING DATE: 04-OCT-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/254,762
 FILING DATE: 07-OCT-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Nesbitt, Stephen L
 REGISTRATION NUMBER: 28,981
 REFERENCE/DOCKET NUMBER: M01368F US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (513) 948-7965
 TELEFAX: (513) 948-7961
 TELEX: 214320

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-434-959-4

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPF 4
 Db 1 AAPF 4

RESULT 17
 US-08-434-959-5
 Sequence 5, Application US/08434959
 ; Patent No. 5736520
 ; GENERAL INFORMATION:
 ; APPLICANT: Bey, Philippe
 ; APPLICANT: Angelastro, Michael R
 ; TITLE OF INVENTION: No. 5736520e1 Peptidase Inhibitors
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marion Merrell Dow Inc.
 ; STREET: 2110 East Galbraith Rd.
 ; CITY: Cincinnati P. O. Box 156300
 ; STATE: Ohio
 ; COUNTRY: USA
 ; ZIP: 45215-6300

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434, 959
 FILING DATE: 20-AUG-1991
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/750, 439
 FILING DATE: 21-DEC-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/439, 201
 FILING DATE: 20-NOV-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/416, 817
 FILING DATE: 04-OCT-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/254, 762
 FILING DATE: 07-OCT-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Nesbitt, Stephen L
 REGISTRATION NUMBER: 28,981
 REFERENCE/DOCKET NUMBER: M01368F US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (513) 948-7965
 TELEFAX: (513) 948-7961
 TELEX: 214320

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ; US-08-434-959-5

Query Match 100.0% Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; US-08-434-959-5

RESULT 18
 US-08-434-959-6
 Sequence 6, Application US/08434959
 ; Patent No. 5736520
 ; GENERAL INFORMATION:
 ; APPLICANT: Bey, Philippe
 ; APPLICANT: Angelastro, Michael R
 ; TITLE OF INVENTION: SUBTILISIN VARIANT CAPABLE OF CLEAVING
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco

QY 1 AAPF 4
 QY 1 AAPF 4
 Db 1 AAPF 4
 ; US-08-434-959-6
 ; Sequence 55, Application US/08460343B
 ; Patent No. 5741664
 ; GENERAL INFORMATION:
 ; APPLICANT: Marcus D. Ballinger and James A. Wells
 ; TITLE OF INVENTION: SUBTILISIN VARIANT CAPABLE OF CLEAVING
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco

STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,343B
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/398028
 FILING DATE: 03-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0936C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-8328
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
; US-08-460-343B-56

RESULT 20
 US-08-067-180B-2
 ; Sequence 2, Application US/08067180B
 ; Patent No. 5750650
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKANISHI, Koichiro
 ; APPLICANT: NOMURA, Keiichi
 ; APPLICANT: TAJIMA, Kyoko
 ; APPLICANT: HIRATANI, Hajime
 ; APPLICANT: KATO, Kazuo
 TITLE OF INVENTION: FIBRINOLYTIC PROTEIN AND PRODUCTION
 TITLE OF INVENTION: METHOD THEREOF
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burgess, Ryan and Wayne
 STREET: 370 Lexington Avenue, Suite 2105
 CITY: NEW YORK
 STATE: UNITED STATES OF AMERICA
 ZIP: 100-17
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5 1/4 INCH DISKETTE
 COMPUTER: PC S LIMITED SYSTEM 200
 OPERATING SYSTEM: DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/067,180B
 FILING DATE: 24 - MAY 1993
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/618,494
 FILING DATE: 27 - NOVEMBER 1990
 ATTORNEY/AGENT INFORMATION:
 NAME: WATNE, MILTON J
 REGISTRATION NUMBER: 17,906

RESULT 21
 US-08-398-028B-56
 ; Sequence 56, Application US/08398028B
 ; Patent No. 57506285
 ; GENERAL INFORMATION:
 ; APPLICANT: MARCUS D. Ballinger and James A. Wells
 TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING
 TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/398,028B
 FILING DATE: 03-Mar-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0936
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-8328
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
; US-08-398-028B-56

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; pred. No. 2e+05; 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 1 AAPF 4
 Db 1 AAPF 4

RESULT 22
 US-08-370-837-3
 ; Sequence 3, Application US/08470837

Patent No. 5800811
GENERAL INFORMATION:

APPLICANT: Nimm, Marcel E.

APPLICANT: Hall, Frederick L.

APPLICANT: Tuen, Tai-Lan

APPLICANT: Wu, Lingtao

APPLICANT: Cheung, David T.

TITLE OF INVENTION: Transforming Growth Factor B Fusion

TITLE OF INVENTION: and

TITLE OF INVENTION: Their Use in Wound Healing

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 11150 Santa Monica Boulevard, Suite 400

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90025-3395

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,837

FILING DATE: July 24, 1991

APPLICATION NUMBER: 221,171

FILING DATE: March 31, 1994

APPLICATION NUMBER: 005,908

FILING DATE: January 15, 1993

APPLICATION NUMBER: 735,335

FILING DATE: July 24, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Sharp, Janice A.

REGISTRATION NUMBER: 34,051

REFERENCE/DOCKET NUMBER: 30630-1US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 310-445-1140

TELEFAX: 310-445-9031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-470-837-3

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 1 AAPF 4

RESULT 23

US-08-722-268-2

Sequence 2, Application US/08722268

Patent No. 5827662

GENERAL INFORMATION:

APPLICANT: Harvey Rubin, Barry Cooperman, No. 5827662man Schecter,

APPLICANT: Michael Plotkin, Zhi Wang

APPLICANT: Recombinant Serine Protease Inhibitors and Uses of These

TITLE OF INVENTION: Methods of Producing Effective

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jane Massey Licata, Esq.

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM 486

APPLICATION NUMBER: 08-398028

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kubinec, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0936P1

TELECOMMUNICATION INFORMATION:

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/722-268

FILING DATE: December 18, 1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 276,936

FILING DATE: July 19, 1994

APPLICATION NUMBER: 221,078

FILING DATE: March 31, 1994

APPLICATION NUMBER: 221,171

FILING DATE: March 31, 1994

APPLICATION NUMBER: 005,908

FILING DATE: January 15, 1993

APPLICATION NUMBER: 735,335

FILING DATE: July 24, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: PENN-0107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-722-268-2

Query Match Score 21; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4

Db 1 AAPF 4

RESULT 24

US-08-504-265B-56

Sequence 56, Application US/08504265B

Patent No. 5837516

GENERAL INFORMATION:

APPLICANT: Marcus D. Ballinger and James A. Wells

APPLICANT: Genentech, Inc.

ADDRESS: 1 DNA Way

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

GENERAL INFORMATION:

APPLICANT: Michael Plotkin, Zhi Wang

APPLICANT: Recombinant Serine Protease Inhibitors and Uses of These

TITLE OF INVENTION: Methods of Producing Effective

NUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

GENERAL INFORMATION:

APPLICANT: Harvey Rubin, Barry Cooperman, No. 5827662man Schecter,

APPLICANT: Michael Plotkin, Zhi Wang

APPLICANT: Recombinant Serine Protease Inhibitors and Uses of These

TITLE OF INVENTION: Methods of Producing Effective

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jane Massey Licata, Esq.

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

TELEPHONE: 650/225-8228
 TELEFAX: 650/952-9811
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
; US-08-504-265B-56

RESULT 25
 US-08-439-005-10
 Sequence 10, Application US/08439005
 Patent No. 5843895
 GENERAL INFORMATION:
 APPLICANT: Lazarus, Robert A.
 APPLICANT: Dennis, Mark S.
 APPLICANT: Ulmer, Jana S.
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING
 TITLE OF INVENTION: ECOTIN AND HOMOLOGS THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94090

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/439,005
 FILING DATE: 11 MAY 1995
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/319501
 FILING DATE: 04-OCT-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/121004
 FILING DATE: 14-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0859C1D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
; US-08-439-005-10

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 111
 Db 1 AAPF 4
 111
 1 AAPF 4

RESULT 26
 US-08-698-575E-2
 Sequence 2, Application US/08698575E
 Patent No. 5874585
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS USEFUL AS
 INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL ELASTASE
 NUMBER OF SEQUENCES: 4
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/698,575E
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/345,820
 FILING DATE:
 INFORMATION FOR SEQ ID NO: 2:
 QY 1 AAPF 4
 111
 Db 1 AAPF 4
 111
 1 AAPF 4

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 111
 Db 1 AAPF 4
 111
 1 AAPF 4

RESULT 27
 US-08-424-017B-19
 Sequence 19, Application US/08424017B
 Patent No. 5935854
 GENERAL INFORMATION:
 APPLICANT: Foster, Donald C
 APPLICANT: Sprecher, Cindy
 APPLICANT: No. 5935854, Kjeld
 TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
 TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 4225 Roosevelt Way, N.E.
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,017B
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/155,331
 FILING DATE:
 APPLICATION NUMBER: US 07/985,692
 FILING DATE: 02-DEC-1992

S618PAK

ATTORNEY/AGENT INFORMATION:
 NAME: Parker, Gary E
 REGISTRATION NUMBER: 31-684
 REFERENCE/DOCKET NUMBER: 92-21C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-547-8080 ext 322
 TELEFAX: 206-548-2329
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..4
 OTHER INFORMATION: /label= ALA-1
 OTHER INFORMATION: /note= "Amino terminal alanine residue is capped with a succinyl group."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..4
 OTHER INFORMATION: /label= Phe-4
 OTHER INFORMATION: /note= "Carboxy-terminal phenylalanine residue is capped with p-nitroanil..."
 US-08-424-017B-19
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 28
 US-08-751-070B-4
 Sequence 4, Application US/08751070B
 ; Patent No. 597659
 GENERAL INFORMATION:
 APPLICANT: Damodaran, Srinivasan
 TITLE OF INVENTION: DETERGENT-STABLE MICROBIAL PROTEASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DeWitt Ross & Stevens S.C.
 STREET: 8000 Excelsior Drive, Suite 401
 CITY: Madison
 STATE: Wisconsin
 COUNTRY: U.S.A.
 ZIP: 53717-1914
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/751.070B
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sara, Charles S.
 REGISTRATION NUMBER: 30-492
 REFERENCE/DOCKET NUMBER: 09820.028
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-831-2100
 TELEFAX: 608-831-2106
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 FEATURE:
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-751-070B-4
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 29
 US-09-069-823-2
 Sequence 2, Application US/09069823
 ; Patent No. 6037325
 GENERAL INFORMATION:
 APPLICANT: Gyokes, Albert C.
 APPLICANT: Spruce, Lyle W.
 TITLE OF INVENTION: SUBSTITUTED HETERO CYCLIC COMPOUNDS
 TITLE OF INVENTION: USEFUL AS INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL ELASTASE
 FILE REFERENCE: 20774_24087
 CURRENT APPLICATION NUMBER: US/09/069,823
 CURRENT FILING DATE: 1998-04-30
 EARLIER APPLICATION NUMBER: 08/345,820
 EARLIER FILING DATE: 1995-11-21
 EARLIER APPLICATION NUMBER: 08/698,575
 EARLIER FILING DATE: 1996-08-15
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 4
 TYPE: PRY
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Tetrapeptide
 ; US-09-069-823-2
 Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 1 AAPF 4
 RESULT 30
 US-09-076-460-1
 Sequence 1, Application US/09076460
 ; Patent No. 6080564
 GENERAL INFORMATION:
 APPLICANT: Laustsen, Mads
 APPLICANT: Nielsen, Stig
 TITLE OF INVENTION: Selective Inactivation of Aspergillus
 TITLE OF INVENTION: Proteases (As Amended)
 FILE REFERENCE: 4609_20-US
 CURRENT APPLICATION NUMBER: US/09/076,460
 CURRENT FILING DATE: 1998-05-12
 EARLIER APPLICATION NUMBER: 1392/95
 EARLIER FILING DATE: 1995-12-07
 EARLIER APPLICATION NUMBER: PCT/DK96/00489
 EARLIER FILING DATE: 1996-11-25
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRY
 ORGANISM: Artificial Sequence
 FEATURE:

; OTHER INFORMATION: substrate
; US-09-076-460-1

; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1).(1)

; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.

; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Jainoff, Andrew S
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using Peptidase-Cleavable Fusogenic Phospholipids
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; US-08-950-618-3

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indexes 0;

Qy 1 AAPF 4
Db 1 AAPF 4

RESULT 32
US-08-950-618-18

; Sequence 18, Application US/0895061B
; Patent No. 6087325

; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.

; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Jainoff, Andrew S
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using Peptidase-Cleavable Fusogenic Phospholipids
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1).(1)

; OTHER INFORMATION: N-terminal carboxy sugar group
; US-08-950-618-31

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indexes 0;

Qy 1 AAPF 4
Db 1 AAPF 4

RESULT 34
US-09-120-365-101

; Sequence 101, Application US/09120365
; Patent No. 6103514

; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/09/120,365
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown

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; FEATURE: OTHER INFORMATION: Description of Unknown Organism: substrate
; US-09-120-365-101
; Query Match 100 0%; Score 21; DB 3; Length 4;
; Best Local Similarity 100 0%; Pred. No. 2e+05; Length 4;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 AAPF 4
; Db 1 AAPF 4
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukkila, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; TITLE OF INVENTION: Delivery Using Same
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; US-09-168-010-3

RESULT 35
US-08-319-501-10
; Sequence 10, Application US/08319501
; Patent No. 6113896
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Dennis, Mark S.
; APPLICANT: Ulmer, Jana S.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING ECOTIN AND HOMOLOGS THE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,501
; FILING DATE: 4-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 004
; FILING DATE: (null)
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Daryl B.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: 859C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1249
; TELEFAX: 415/952-9881
; TELEX: 910371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-319-501-10

Query Match 100 0%; Score 21; DB 3; Length 4;
; Best Local Similarity 100.0%; Pred. No. 2e+05; Length 4;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 AAPF 4
; Db 1 AAPF 4
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukkila, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; TITLE OF INVENTION: Delivery Using Same
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal succinyl group
; US-09-168-010-18

Query Match 100 0%; Score 21; DB 4; Length 4;
; Best Local Similarity 100.0%; Pred. No. 2e+05; Length 4;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 AAPF 4
; Db 1 AAPF 4
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukkila, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; TITLE OF INVENTION: Delivery Using Same
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal succinyl group
; US-09-168-010-18

```

```

RESULT 36
US-09-168-010-3
; Sequence 3, Application US/09168010A
; Patent No. 6143716

```

RESULT 38
US-09-168-010-31 ;
Sequence 31; Application US/09168010A
Patent No. 6143716

GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shakut
APPLICANT: Janoff, Andrew S
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
Title of Invention: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010A
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: US 60/027,544
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 31
LENGTH: 4

TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)..(1)

OTHER INFORMATION: N-terminal carboxy sugar group

US-09-168-010-31

RESULT 39
US 08-905-359A-25
Sequence 25, Application US/08905359A

GENERAL INFORMATION:
APPLICANT: Frances H. Arnold
APPLICANT: Zhixin Shao
APPLICANT: Joseph A. Affholter
APPLICANT: Ruimin Zhao
TITLE OF INVENTION: Recombination of Polynucleotide
TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,556
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/905,359
FILING DATE: August 4, 1997
APPLICATION NUMBER: 60/041,666
FILING DATE: March 25, 1997
APPLICATION NUMBER: 60/045,211
FILING DATE: April 30, 1997
APPLICATION NUMBER: 60/046,256
FILING DATE: May 12, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 330187-84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5300
TELEFAX: (310) 277-1237

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-905-359A-25

RESULT 40
US-09-353-556-25
Sequence 25, Application US/09353556

PATENT NO. 6177263

GENERAL INFORMATION:
APPLICANT: Frances H. Arnold
APPLICANT: Zhixin Shao
APPLICANT: Joseph A. Affholter
APPLICANT: Ruimin Zhao
APPLICANT: Lori Giver
TITLE OF INVENTION: Recombination of Polynucleotide
TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,556
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/905,359
FILING DATE: August 4, 1997
APPLICATION NUMBER: 60/041,666
FILING DATE: March 25, 1997
APPLICATION NUMBER: 60/045,211
FILING DATE: April 30, 1997
APPLICATION NUMBER: 60/046,256
FILING DATE: May 12, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 330187-84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5300

; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-353-556-25

Query Match Similarity Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPF 4
| || |
Db 1 AAPF 4

Search completed: December 6, 2002, 13:31:50
Job time : 10.3333 secs

PRIOR APPLICATION NUMBER: US 09/326,039
 PRIOR FILING DATE: 1999-06-04
 PRIOR APPLICATION NUMBER: US 60/088,136
 PRIOR FILING DATE: 1998-06-04
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 15 LENGTH: 4 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-757-908A-15

Query Match 100.0%; Score 21; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4 Db 1 AAPF 4

RESULT 3
 US-09-117-380B-2
 Sequence 2, Application US/09117380B
 ; Patent No. US20020119917A1
 GENERAL INFORMATION:
 ; APPLICANT: FRIDKIN, Matityahu
 ; APPLICANT: YAVIN, Eran J.
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE PROTEIN
 FILE REFERENCE: FRIDKIN-1
 CURRENT APPLICATION NUMBER: US/09/117,380B
 PRIOR APPLICATION NUMBER: PCT/IL97/00032
 PRIOR FILING DATE: 1997-01-27
 PRIOR APPLICATION NUMBER: IL 116976
 PRIOR FILING DATE: 1996-01-31
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: The N-terminal Ala residue is modified with a succinyl group; the C-terminal Phe residue is modified with a nitroanilide group.
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-117-380B-2

Query Match 100.0%; Score 21; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4 Db 1 AAPF 4

RESULT 4
 US-09-935-744-1
 Sequence 1, Application US/09935744
 ; Patent No. US20020137118A1
 GENERAL INFORMATION:
 ; APPLICANT: Inouye, Masayori
 ; APPLICANT: Shunde, Ujwal
 ; APPLICANT: Fu, Xuan
 ; TITLE OF INVENTION: Biologically Active Protein Folding Intermediates
 FILE REFERENCE: 266723
 CURRENT APPLICATION NUMBER: US/09/935,744
 CURRENT FILING DATE: 2001-08-24
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn version 3.1

RESULT 5
 US-10-090-624-33
 Sequence 33, Application US/10090624
 ; Patent No. US20020132335A1
 GENERAL INFORMATION:
 ; APPLICANT: TAKAKURA, Hikaru
 ; APPLICANT: MORISHITA, Mio
 ; APPLICANT: SHIMOJO, Tomoko
 ; APPLICANT: ASADA, Kiyoko
 ; APPLICANT: KATO, Ikunoshin
 ; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE FILE REFERENCE: TAKAKURA-6
 CURRENT APPLICATION NUMBER: US/10/090,624
 CURRENT FILING DATE: 2002-03-06
 PRIOR APPLICATION NUMBER: 09/445,472
 PRIOR FILING DATE: 1999-12-06
 PRIOR APPLICATION NUMBER: 151969/1997
 PRIOR FILING DATE: 1997-06-10
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 33 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 FEATURE:
 NAME/KEY: misc-feature
 OTHER INFORMATION: Residue 1 is modified by a succinyl group.
 FEATURE:
 NAME/KEY: misc-feature
 OTHER INFORMATION: Residue 4 is modified by a p-nitroaniline group.
 US-10-090-624-33

Query Match 100.0%; Score 21; DB 12; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4 Db 1 AAPF 4

RESULT 6
 US-10-056-371-7
 Sequence 7, Application US/10036371
 ; Patent No. US20020141987A1
 GENERAL INFORMATION:
 ; APPLICANT: BJARNARSON, Jon B.
 ; TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND
 ; TITLE OF INVENTION: COSMETIC USE

CURRENT APPLICATION NUMBER: US/10/033,526
 CURRENT FILING DATE: 2001-11-02
 PRIOR APPLICATION NUMBER: 60/245,737
 PRIOR FILING DATE: 2000-11-03
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic peptide
 US-10-033-526-4

Query Match	Similarity	Score	DB	Length	Best Local	Similarity	Score	DB	Length	Best Local	Similarity	Score	DB	Length
Matches	4	100.0%	12	6	Matches	4	100.0%	12	12	Matches	4	100.0%	14	12
Qy	1 AAPF 4				Qy	1 AAPF 4				Qy	1 AAPF 4			
Db	3 AAPF 6				Db	5 AAPF 8				Db	5 AAPF 8			

RESULT 11
 US-10-068-965-4
 Sequence 4, Application US/10068965
 Patent No. US2002015612A1
 GENERAL INFORMATION:
 APPLICANT: BALLIGNAD, JEAN-LUC
 TITLE OF INVENTION: NOVEL PHARMACEUTICAL COMPOSITIONS FOR MODULATING FILE REFERENCE: DCLERC-2_P1
 CURRENT APPLICATION NUMBER: US/10/068,965
 PRIOR APPLICATION NUMBER: PCT/EP00/07731
 PRIOR FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: 9980171
 PRIOR FILING DATE: 1999-08-09
 NUMBER OF SEQ ID NOS: 86
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 4
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Caveolin
 US-10-068-965-4

Query Match Similarity 100.0%; Score 21; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 US-09-864-761-38169
 Sequence 38169, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Weiseng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-07-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-01-04
 PRIOR APPLICATION NUMBER: US 60/235,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203

RESULT 12
 US-09-985-157-11
 Sequence 11, Application US/09985157
 Patent No. US20020145797A1
 GENERAL INFORMATION:
 APPLICANT: SHOKAT, Kevin M.
 TITLE OF INVENTION: Engineered Protein Kinases Which Can Utilize Modified Nucleotide FILE REFERENCE: 5158-5002-05
 CURRENT APPLICATION NUMBER: US/09/985,157
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: US 09/367,065
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: PCT/US98/02522

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; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 38169
; LENGTH: 25
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050342_36
; OTHER INFORMATION: EXPRESSED IN BP474, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
; US-09-864-761-38169

Query Match          100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 29; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;
QY      1 AAPF 4
Db      2 AAPF 5

RESULT 14
US-09-864-761-48747
; Sequence 48747, Application US/09864761
; GENERAL INFORMATION:
; Patent No. US20020048763A1
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheung
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Neomica-X_1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

RESULT 15
US-09-929-566
; Sequence 566, Application US/09925297
; Patent No. US2002008159A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 923
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 566
; LENGTH: 51
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; US-09-929-566

Query Match          100.0%; Score 21; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 61; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;
QY      1 AAPF 4
Db      21 AAPF 24

RESULT 16
US-09-864-761-42500
; Sequence 42500, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheung
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Neomica-X_1

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CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIORITY APPLICATION NUMBER: US 60/180,312
 PRIORITY FILING DATE: 2000-02-04
 PRIORITY APPLICATION NUMBER: US 60/207,456
 PRIORITY FILING DATE: 2000-05-26
 PRIORITY APPLICATION NUMBER: US 09/632,366
 PRIORITY FILING DATE: 2000-08-03
 PRIORITY APPLICATION NUMBER: GB 24263,6
 PRIORITY FILING DATE: 2000-10-04
 PRIORITY APPLICATION NUMBER: US 60/236,359
 PRIORITY FILING DATE: 2000-09-27
 PRIORITY APPLICATION NUMBER: PCT/US01/00666
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00667
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00664
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00669
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00662
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00661
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00670
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: US 60/234,687
 PRIORITY FILING DATE: 2000-09-21
 PRIORITY APPLICATION NUMBER: US 09/608,408
 PRIORITY FILING DATE: 2000-05-30
 PRIORITY APPLICATION NUMBER: US 09/774,203
 PRIORITY FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO 42500
 LENGTH: 62
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC05323.1
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
 OTHER INFORMATION: EXPRESSED IN HEIA, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
 OTHER INFORMATION: EST_HUMAN HIT: AA77043.1, EVALUATE 6.00e-21
 ; OTHER INFORMATION: SWISSPROT HIT: P13535, EVALUATE 2.00e-25
 US-09-864-761-42500
 Query Match 100.0%; Score 21; DB 10; Length 62;
 Best Local Similarity 100.0%; Pred. No. 74; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 13 AAPF 16
 RESULT 17
 US-09-864-761-38957
 ; Sequence 38957, Application US/09864761
 ; Patent No US2002008763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Neomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIORITY APPLICATION NUMBER: US 60/180,312
 PRIORITY FILING DATE: 2000-02-04
 PRIORITY APPLICATION NUMBER: US 60/207,456
 PRIORITY FILING DATE: 2000-05-26
 PRIORITY APPLICATION NUMBER: PCT/US01/00666
 PRIORITY FILING DATE: 2000-08-03
 PRIORITY APPLICATION NUMBER: GB 24263,6
 PRIORITY FILING DATE: 2000-10-04
 PRIORITY APPLICATION NUMBER: US 60/236,359
 PRIORITY FILING DATE: 2000-09-27
 PRIORITY APPLICATION NUMBER: PCT/US01/00667
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00668
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00669
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00665
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00664
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00663
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00662
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00661
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: PCT/US01/00670
 PRIORITY FILING DATE: 2001-01-30
 PRIORITY APPLICATION NUMBER: US 60/234,687
 PRIORITY FILING DATE: 2000-05-21
 PRIORITY APPLICATION NUMBER: US 09/608,408
 PRIORITY FILING DATE: 2000-06-30
 PRIORITY APPLICATION NUMBER: US 09/774,203
 PRIORITY FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO 38957
 LENGTH: 75
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC004636.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.3
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN HEIA, SIGNAL = 4.3
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.0
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.3
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
 OTHER INFORMATION: EST_HUMAN HIT: AA469992.1, EVALUATE 5.20e+00
 ; OTHER INFORMATION: SWISSPROT HIT: P07744, EVALUATE 5.20e+00
 US-09-864-761-38957
 Query Match 100.0%; Score 21; DB 10; Length 75;
 Best Local Similarity 100.0%; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;

```

; RESULT 18
; US-09-925-300-1841
; Sequence 1841, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P10101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60/124,270
; PRIORITY FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1841
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; RESULT 19
; US-09-925-301-1206
; Sequence 1206, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P105
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1206
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; RESULT 20
; US-09-893-737-4
; Sequence 737, Application US/09893737
; Query Match 100.0%; Score 21; DB 10; Length 89;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 AAPF 4
; Db 78 AAPF 81
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; RESULT 21
; US-09-764-668-986
; Sequence 986, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P7232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-03-17
; PRIORITY APPLICATION DATA REMOVED - REFER TO PALM OR FILE WRAPPER
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 986
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (62)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (77)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; LOCATION: (90)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; RESULT 22
; US-09-738-973-59
; Sequence 973, Application US/097389737
; Query Match 100.0%; Score 21; DB 9; Length 113;
; Best Local Similarity 100.0%; Pred. No. 1.4e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 AAPF 4
; Db 8 AAPF 11

```

; Sequence 59, Application US/09738973
; Patent No. US2002110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Filing, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 2110121475C9
; CURRENT APPLICATION NUMBER: US/097738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapien
; US 09-738-973-59

RESULT 23
US 09-739-907-99
; Sequence 99, Application US/09739907
; Patent No. US200100122889A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/097739,907
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/3348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: (132)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-739-907-99

Query Match 100.0%; Score 21; DB 10; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Length 132;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: Allen, Stephen
; APPLICANT: Kinney, Anthony
; APPLICANT: Mao, Guo-Hua
; APPLICANT: Orozco, Emil

RESULT 24
US-09-908-322-51
; Sequence 51, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique-Domingos, Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Penne & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
; US-09-908-322-51

Query Match 100.0%; Score 21; DB 10; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Length 135;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: Allen, Stephen
; APPLICANT: Kinney, Anthony
; APPLICANT: Mao, Guo-Hua
; APPLICANT: Orozco, Emil

RESULT 25
US-09-140-289A-2
; Sequence 2, Application US/09740288A
; Patent No. US20010039042A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen
; APPLICANT: Kinney, Anthony
; APPLICANT: Mao, Guo-Hua
; APPLICANT: Orozco, Emil

RESULT 27
US-09-902-941-1822
; Sequence 1822, Application US/09902941
; Patent No. US20030166637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carrer, Darrick
; APPLICANT: Reitter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Ligun
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121-478C17
; CURRENT APPLICATION NUMBER: US/09/902, 457
; CURRENT FILING DATE: 2000-02-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1822
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 21; DB 10; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 4; Conservative 0; Indels 0; Gaps 0;
Matches 4; Other Information: Xaa = any amino acid

Qy 1 AAPF 4
Db 23 AAPF 26

RESULT 26
US-09-736-457-1822
; Sequence 1822, Application US/09736457
; Patent No. US20030166637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carrer, Darrick
; APPLICANT: Reitter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Ligun
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: DIAGNOSTICS OF LUNG CANCER
; FILE REFERENCE: 210121-478C15
; CURRENT APPLICATION NUMBER: US/09/736, 457
; CURRENT FILING DATE: 2000-02-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1822
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 21; DB 10; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 4; Conservative 0; Indels 0; Gaps 0;
Matches 4; Other Information: Xaa = any amino acid

Qy 1 AAPF 4
Db 25 AAPF 28

RESULT 28
US-09-916-790-30
; Sequence 30, Application US/09916790
; Patent No. US2002061573A1
; GENERAL INFORMATION:
; APPLICANT: Meyls, Rachael
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 18431 AND 32374, NOVEL HUMAN PROTEIN
; FILE REFERENCE: 381552002700
; CURRENT APPLICATION NUMBER: US/09/916, 790
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221, 543
; PRIORITY DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence

Query Match 100.0%; Score 21; DB 9; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 4; Conservative 0; Indels 0; Gaps 0;
Matches 4; Other Information: Consensus amino acid sequence

Qy 1 AAPF 4
Db 25 AAPF 28

RESULT 29
US-09-916-790-30
; Sequence 30, Application US/09916790
; Patent No. US2002061573A1
; GENERAL INFORMATION:
; APPLICANT: Craig, Rosen
; APPLICANT: Steve, Rubin
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS AND ANTIBODIES
; FILE REFERENCE: PA10
; CURRENT APPLICATION NUMBER: US/09/925, 300

CURRENT FILING DATE: 2001-08-10
 PRIORITY APPLICATION NUMBER: PCT/US00/05988
 PRIORITY FILING DATE: 2000-03-08
 PRIORITY APPLICATION NUMBER: 60/124,270
 PRIORITY FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1890
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1092
 LENGTH: 158
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-925-30-1092

Query Match 100.0%; Score 21; DB 10; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 Db 50 AAPF 53

RESULT 30
 US-09-925-30-1170
 Sequence 1170, Application US/09925301
 PRIORITY APPLICATION NUMBER: PCV/US00/05882
 PRIORITY FILING DATE: 2000-03-08
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA106
 CURRENT APPLICATION NUMBER: US/09/925,301
 CURRENT FILING DATE: 2001-08-10
 PRIORITY APPLICATION NUMBER: PCV/US00/05882
 PRIORITY FILING DATE: 2000-03-08
 SEQ ID NO: 1170
 LENGTH: 166
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (170)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-739-907-87

Query Match 100.0%; Score 21; DB 10; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 Db 28 AAPF 31

RESULT 32
 US-10-052-586-512
 Sequence 512, Application US/10052586
 Patent No. US2002127584A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gutierrez, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Zhang, Zemin
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: 3430R1
 CURRENT APPLICATION NUMBER: US/10/052,586
 CURRENT FILING DATE: 2002-01-15
 PRIORITY APPLICATION NUMBER: 60/059263
 PRIORITY FILING DATE: 1997-09-18
 PRIORITY APPLICATION NUMBER: 60/059266
 PRIORITY FILING DATE: 1997-09-18
 PRIORITY APPLICATION NUMBER: 60/062250
 PRIORITY FILING DATE: 1997-10-17
 PRIORITY APPLICATION NUMBER: 60/063120
 PRIORITY FILING DATE: 1997-10-24
 PRIORITY APPLICATION NUMBER: 60/063121
 PRIORITY FILING DATE: 1997-10-24
 PRIORITY APPLICATION NUMBER: 60/063486
 PRIORITY FILING DATE: 1997-10-21
 PRIORITY APPLICATION NUMBER: 60/063540
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063541
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063544
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063564
 PRIORITY FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: 60/063734

RESULT 31
 US-09-739-907-87
 Sequence 87, Application US/09739907
 PRIORITY APPLICATION NUMBER: 60/02889A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 36 Human Secreted Proteins
 FILE REFERENCE: P2022P1
 CURRENT APPLICATION NUMBER: US/09/739,907
 CURRENT FILING DATE: 2000-12-20

PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089105
 CURRENT APPLICATION NUMBER: US/09/764,864
 CURRENT FILING DATE: 2001-01-17
 PRIOR application data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 1792
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1280
 LENGTH: 184
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (35)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-764-864-1280
 Query Match, 100.0%; Score 21; DB 12; Length 178;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089908
 Query Match, 100.0%; Score 21; DB 12; Length 178;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 85 AAPF 88
 Query Match, 100.0%; Score 21; DB 10; Length 184;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 21 AAPF 24
 RESULT 33
 US-09-739-907-191
 Sequence 191, Application US/09739907
 ; Sequence 191, Application US/09739907
 ; Patent No. US20010012089A1
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 36 Human Secreted Proteins
 ; FILE REFERENCE: P20281
 ; CURRENT APPLICATION NUMBER: US/09/739, 907
 ; CURRENT FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: 09/348, 457
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: 60/070, 567
 ; PRIOR FILING DATE: 1998-01-07
 ; PRIOR APPLICATION NUMBER: 60/070, 692
 ; PRIOR FILING DATE: 1998-01-07
 ; PRIOR APPLICATION NUMBER: 60/070, 704
 ; PRIOR FILING DATE: 1998-01-07
 ; PRIOR APPLICATION NUMBER: 60/070, 658
 ; PRIOR FILING DATE: 1998-01-07
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 191
 ; LENGTH: 182
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (180)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-739-907-191
 Query Match, 100.0%; Score 21; DB 10; Length 182;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 38 AAPF 41
 RESULT 34
 US-09-764-864-1280
 Sequence 1280, Application US/09764864
 Patent No. US20020133753A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PT223
 Query Match, 100.0%; Score 21; DB 10; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 42 AAPF 45
 Query Match, 100.0%; Score 21; DB 10; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 42 AAPF 45

RESULT 36
US-09-811-284-225
; Sequence 225, Application US/09811284
; Patent No. US20020058306A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. 0520020058306A1 G Protein-Coupled Receptors
; FILE REFERENCE: 00167US1
; CURRENT APPLICATION NUMBER: US/09/811,284
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/189,783
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,907
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,918
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,960
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,917
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/192,945
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,916
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,923
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,933
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,830
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,234
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/192,155
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,935
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 225
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-811-284-225

Query Match 100.0%; Score 21; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.6e-02; Mismatches 0; Indels 0; Gaps 0;

QY	1 AAPF 4	Db	16 AAPF 19

RESULT 37
US-09-925-302-652
; Sequence 652, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 652
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 21; DB 10; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;

QY	1 AAPF 4	Db	194 AAPF 197

RESULT 38
US-09-820-893-67
; Sequence 67, Application US/09820893
; Patent No. US20020076705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: PZ033P1
; CURRENT APPLICATION NUMBER: US/09/820,893
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/531,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 67
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-820-893-67

Query Match 100.0%; Score 21; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;

QY	1 AAPF 4	Db	45 AAPF 48

RESULT 39
US-09-815-242-5294
; Sequence 5294, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.031A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-22
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5294
 LENGTH: 216
 TYPE: PRT
 ; ORGANISM: *Staphylococcus aureus*
 US-09-815-242-5294

Query Match 100.0%; Score 21; DB 10; Length 216;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 99 AAPF 102

RESULT 40
 US-09-815-242-10051
 ; Sequence 10051, Application US/09815242
 ; PATENT NO. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Travick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: XU, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; PROKARYOTES
 ; FILE REFERENCE: ELTRRA.01A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 10051
 ; LENGTH: 217
 ; TYPE: PRT
 ; ORGANISM: *Escherichia coli*
 US-09-815-242-10051

Query Match 100.0%; Score 21; DB 10; Length 217;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 100 AAPF 103

Search completed: December 6, 2002, 13:42:05
 Job time : 5.88889 secs

cytochrome-c oxidase (EC 1.9.3.1) chain VIIC - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C;Accession: PN0607
 R;Sillard, R.; Joeval, H.; Mutz, V.
 A;Title: Characterization of porcine intestinal cytochrome c oxidase subunit VIIC, purified
 A;Accession: PN0607; MUID:93384597; PMID:8396926
 A;Molecule type: protein
 A;Residues: 1-47 <SIL>
 A;Experimental source: intestine
 C;Keywords: mitochondrial; oxidoreductase; respiratory chain
 C;Superfamily: cytochrome-c oxidase chain VIIC
 C;Keywords: mitochondrial; oxidoreductase; respiratory chain
 Query Match 100.0% Score 21; DB 2; Length 47;
 Best Local Similarity 100.0% Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 34 AAPF 37

RESULT 4
 AD3575
 hypothetical protein BMRII0525 [imported] - Brucella melitensis (strain 16M)
 C;Species: Brucella melitensis
 C;Accession: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C;Accession: AD3575
 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A;Reference number: AD3252; PMID:11756688
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-50 <KUR>
 A;Cross-references: GB:AE009918; PIDN:AAL53767.1; PID:917984695; GSPDB:GN00191
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BMRII0525
 A;Map position: II

Query Match 100.0% Score 21; DB 2; Length 50;
 Best Local Similarity 100.0% Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 Db 44 AAPF 47

RESULT 5
 OSB08A
 cytochrome-c oxidase (EC 1.9.3.1) chain VIIC precursor [validated] - bovine
 N;Alternate names: Cytochrome-c oxidase chain VIIa
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-May-1979 #sequence_revision 31-Dec-1992 #text_change 15-Sep-2000
 C;Accession: JH0473; S00597; A00498; H29968; S18834
 R;Aqua, M.S.; Bachman, N.J.; Lomax, M.I.; Grossman, L.I.
 Gene 104, 211-217, 1991.
 A;Title: Characterization and expression of a cDNA specifying subunit VIIc of bovine cyt
 A;Reference number: JH0473; MUID:92009215; PMID:1655579
 A;Accession: JH0473
 A;Molecule type: DNA
 A;Residues: 1-63 <AQUT>
 A;Cross-references: GB:X58823
 R;Aqua, M.S.; Lomax, M.I.; Schon, E.A.; Grossman, L.I.
 Nucleic Acids Res. 17, 8376, 1989
 A;Title: Nucleotide sequence of a cDNA for bovine cytochrome c oxidase subunit VIIc.
 A;Reference number: S06597; MUID:90045968; PMID:2554257

Query Match 100.0% Score 21; DB 1; Length 63;
 Best Local Similarity 100.0% Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 Db 50 AAPF 53

RESULT 6
 S10303
 cytochrome-c oxidase (EC 1.9.3.1) chain VIIC - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: S10303
 C;Accession: S10303
 R;Akamatsu, M.; Grossman, L.I.
 Nucleic Acids Res. 18, 3645, 1990
 A;Title: Nucleotide sequence of a cDNA for mouse cytochrome c oxidase subunit VIIc.
 A;Reference number: S10303; MUID:9031494; PMID:2163523
 A;Accession: S10303
 A;Molecule type: mRNA
 A;Residues: 1-63 <AKA>
 A;Cross-references: EMBL:X52940; NID:950524; PIDN:CAA37115.1; PID:950525
 A;Genetics:
 C;Superfamily: cytochrome-c oxidase chain VIIC

C;Keywords: mitochondrion; oxidoreductase

Query Match 100.0%; Score 21; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPF 4
|||
Db 50 AAPF 53

RESULT 7

AB2778 hypothetical protein Atu1639 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AB2778
R;Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Zhang, S.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, M.; Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-80 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK78418.1; PID:915023293; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

A;Gene: CAC0438

A;Map position: circular chromosome

A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPF 4
|||
Db 50 AAPF 53

RESULT 8

C69125 hypothetical protein MTH206 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C;Accession: C69125

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadacora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Olu, D.; Spadacora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: C69125

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-79 <MIN>

A;Cross-references: GB:AB000807; GB:AB000666; PIDN:92621239; PIDN:AA84712.1; PID:g262125

A;Experimental source: strain Delta H

A;Gene: MTH206

A;Start codon: TTG

Query Match 100.0%; Score 21; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPF 4
|||
Db 36 AAPF 39

RESULT 9

G66953 probable metal-binding protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: G66953

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.; J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: G66953

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-80 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK78418.1; PID:915023293; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

A;Gene: CAC0438

Query Match 100.0%; Score 21; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPF 4
|||
Db 63 AAPF 66

RESULT 10

E90905 hypothetical protein ECs2213 [imported] - Escherichia coli (strain 0157:H7, substrate

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C;Accession: E90905

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C; gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: E90905

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-86 <HY>

A;Cross-references: GB:AB000007; PIDN:BA35636.1; PID:913361679; GSPDB:GN00154

A;Experimental source: strain 0157:H7, substrate RIMD 0509952

C;Genetics:

A;Gene: ECS2213

Query Match 100.0%; Score 21; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPF 4
|||
Db 26 AAPF 29

RESULT 11

F97429 f110 protein (AF300968) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C;Accession: F97429

R;Goodier, B.; Hinkley, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm; Best, Local Similarity 100.0%; Pred. No. 2e+02; C.; Allinger, M.; Dougherty, D.; Scott, C.; Iappas, C.; Markelz, Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A;Reference number: A97359; PMID:11743194

A;Accession: F97429

A;Status: preliminary

A; Molecule type: DNA
A; Residues: 1-88 <KUR>
A; Cross-references: GB:AE007869; PIDN:AAK86391.1; PID:91515521; GSPDB:GN00169
C; Genetics:
A; Map position: circular chromosome

Query Match 100 %; Score 21; DB 2; Length 88;
Best Local Similarity 100 %; Pred. No. 2.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 65 AAPF 68

RESULT 12

AG2647 flagellar biosynthetic protein [imported] - Agrobacterium tumefaciens (strain C58, Dupon C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002
C; Accession: AG2647
R; Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S. ; Science 294, 217-233, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; PMID:11743193
A; Accession: AG2647
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-88 <KUR> GB:AB008688; PIDN:AAI41597.1; PID:917738933; GSPDB:GN00186
A; Cross-references: 1-88 <KUR>
A; Experimental source: strain C58 (Dupont)
C; Genetics:
A; Gene: flfQ
A; Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 65 AAPF 68

RESULT 13

S02854 male accessory gland secretory protein 26Ab precursor - fruit fly (*Drosophila melanogaster*)
N; Alternative names: male accessory gland secretory protein msP35b; male paragonial prote C; Species: *Drosophila melanogaster*
C; Accession: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jul-2000
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jul-2000
C; Accession: S02854; S30408; S30416; S30420; S30426; S30410; S30424
R; Monsma, S.A.; Wolfner, M.F.
Genes Dev., 2, 1063-1073, 1988
A; Title: Structure and expression of a *Drosophila* male accessory gland gene whose product A; Reference number: S02853; MUID:8905045; PMID:3142402
A; Accession: S02854
A; Molecule type: DNA
A; Residues: 1-90 <MOND>
A; Cross-references: EMBL:Y00219; NID:98264; PIDN:CAA68367.1; PID:98266
A; Experimental source: strain Canton-S
R; Aquade, M.; Miyashita, N.; Langley, C.H.
Genes Dev., 7, 755-770, 1992
A; Title: Polymorphism and divergence in the Mst26A male accessory gland gene region in A; Reference number: S30407; MUID:93106377; PMID:1361475
A; Accession: S30409
A; Molecule type: DNA
A; Residues: 1-90 <ANGU>
A; Cross-references: EMBL:X70888; NID:93402845; PIDN:CAA50233.1; PID:98234

A; Experimental source: allele NC5
A; Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1993
A; Accession: S30420
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-90 <AGP>
A; Experimental source: allele NC7
A; Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1993
A; Accession: S30425
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-90 <AGA>
A; Cross-references: EMBL:X70897; NID:98259; PID:98260
A; Experimental source: allele NC10
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
A; Accession: S30410
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-79, 'V', 81-90 <AG3>
A; Cross-references: EMBL:X70899; NID:93402846; PIDN:CAA50235.1; PID:98237
A; Experimental source: allele NC2
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
A; Accession: S30424
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-63, 'H', 65-90 <AG4>
A; Cross-references: EMBL:X70896; NID:93406838; PIDN:CAA50249.1; PID:98258
A; Experimental source: allele NC9
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C; Genetics:
C; Gene: FlyBase:AC26Ab
A; Cross-references: FlyBase:FBgn0002856
A; Map position: 2
A; Introns: 11/1
C; Superfamily: male accessory gland secretory protein 26Ab F;1-18/Domain: signal sequence #status predicted <SIG> F;19-90/Product: male accessory gland secretory protein 26Ab
Query Match 100.0%; Score 21; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 21 AAPF 24

RESULT 14

S30428 Mst26Ab protein - fruit fly (*Drosophila mauritiana*)
C; Species: *Drosophila mauritiana*
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C; Accession: S30428
R; Aquade, M.; Miyashita, N.; Langley, C.H.
Genetics, 132, 755-770, 1992
A; Title: Polymorphism and divergence in the Mst26A male accessory gland gene region 1 A; Reference number: S30407; MUID:93106377; PMID:1361475
A; Accession: S30428
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-90 <ANGU>
A; Cross-references: EMBL:X70898; NID:98261; PIDN:CAA50253.1; PID:98263
C; Genetics:
A; Gene: FlyBase:Dnaa/AP26Ab
A; Cross-references: FlyBase:FBgn0012495
A; Introns: 11/1

C;Superfamily: male accessory gland secretory protein 26ab
 Query Match 100.0%; Score 21; DB 2; Length 90;
 Best Local Similarity 100.0%; No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 21 AAPF 24

RESULT 15

S30412
 male accessory gland secretory protein 26ab precursor (variant 1) - fruit fly (Drosophila
 N;Alternate names: male accessory gland secretory protein 355b; Mst26Ab protein
 C;Species: Drosophila melanogaster
 C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
 C;Accession: S30412; S30114; S30118; S30622
 R;Aquade, M.; Miyashita, N.; Langley, C.H.
 Genetics 132, 755-770, 1992
 A;Title: Polymorphism and divergence in the Mst26A male accessory gland gene region in Drosophila
 A;Reference number: S30407; MUID:93106377; PMID:1361475
 A;Accession: S30412
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-90 <AGU>
 A;Cross-references: EMBL:X70890; NID:93402847; PIDN:CA50237.1; PID:98240
 A;Experimental source: allele NC3
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 A;Accession: S30414
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-90 <AGU>
 A;Cross-references: EMBL:X70891; NID:98241; PID:98243
 A;Experimental source: allele NC4
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 A;Accession: S30418
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-90 <AGP>
 A;Cross-references: EMBL:X70893; NID:98247; PID:98249
 A;Experimental source: allele NC6
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 A;Accession: S30422
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-90 <AGN>
 A;Cross-references: EMBL:X70895; NID:98253; PID:98255
 A;Experimental source: allele NC8
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 C;Genetics:
 A;Gene: FLBase:Acp26Aa
 A;Cross-references: FlyBase:FBgn0002835
 A;Map position: 2
 A;Introns: 11/1
 C;Superfamily: male accessory gland secretory protein 26ab
 F;1-18/Domain: signal sequence status predicted <SIG>
 F;19-90/Product: male accessory gland secretory protein 26Ab #status predicted <MAT>>

Query Match 100.0%; Score 21; DB 2; Length 90;
 Best Local Similarity 100.0%; No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 21 AAPF 24

RESULT 16

S30430
 Mst26Ab protein - fruit fly (Drosophila simulans)
 C;Species: Drosophila simulans
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000

RESULT 17

C;Accession: S30430
 R;Aquade, M.; Miyashita, N.; Langley, C.H.
 Genetics 132, 755-770, 1992
 A;Title: Polymorphism and divergence in the Mst26A male accessory gland gene region in Drosophila
 A;Reference number: S30407; MUID:93106377; PMID:1361475
 A;Accession: S30430
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-90 <AGU>
 A;Cross-references: EMBL:X70899; NID:9134; PID:99136
 C;Genetics:
 A;Gene: FlyBase:Dsim:Acc26Ab
 A;Cross-references: FlyBase:FBgn0012821
 A;Introns: 11/1
 C;Superfamily: male accessory gland secretory protein 26ab
 Query Match 100.0%; Score 21; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 21 AAPF 24

RESULT 18

AB1502
 probable cell surface protein (LPXTG motif) [imported] - Listeria innocua (strain Cli
 C;Species: Listeria innocua
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C;Accession: AB1502
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloch, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.; Science 294, 847-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A;Title: Comparative genomics of Listeria species
 A;Reference number: AB1077; MUID:21537279; PMID:1679669
 A;Accession: AB1502
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-97 <GLA>
 A;Cross-references: GB:AL592022; PIDN:CA95786.1; PID:916412994; GSPPDB:GN00178

A; Experimental source: strain Clip11262
 C; Genetics:
 A; Gene: lin0554

RESULT 19

G86174 hypothetical protein [imported] - *Arabidopsis thaliana* (mouse-ear cress)
 C; Species: *Arabidopsis thaliana* (mouse-ear cress)
 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C; Accession: G86174
 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Soutzick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A; Title: Sequence and analysis of chromosome 1 of the Plant *Arabidopsis*.
 A; Reference number: A86141; MUID:21016719; PMID:11130712
 A; Accession: G86174
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-100 <STO>
 A; Cross-references: GB:AB005172; NID:92341040; PIDN:AAB70444.1; GSPDB:GN00141
 C; Genetics:
 A; Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 Db 16 AAPF 19

RESULT 20

D90761 hypothetical protein Ers1060 [imported] - *Escherichia coli* (strain 0157:H7, substrain RI) DNA Res. 8, 11-22, 2001
 C; Species: *Escherichia coli*
 C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C; Accession: D90761
 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gassawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A; Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7 and genetic features of the phage lambda-K15. A; Reference number: A95629; MUID:21156231; PMID:11250796
 A; Accession: D90761
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-101 <HAY>
 A; Cross-references: GB:BA000007; PIDN:BAB34483.1; PIDN:g13360520; GSPDB:GN00154
 C; Genetics:
 A; Gene: ECS1060

Query Match 100.0%; Score 21; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 Db 16 AAPF 19

RESULT 21

B86976 probable PE protein - *Mycobacterium leprae*
 C; Species: *Mycobacterium leprae*
 C; PE-family protein [imported] - *Mycobacterium leprae*
 C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C; Accession: B86976
 R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A; Authors: Rutte, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A; Title: Massive gene decay in the leprosy bacillus.
 A; Reference number: A86909; MUID:21128732; PMID:11234002
 A; Accession: B86976
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-102 <STO>
 A; Cross-references: GB:AL450380; NID:913092742; PIDN:CAC30046.1; GSPDB:GN00147
 C; Genetics:
 A; Gene: PE

Query Match 100.0%; Score 21; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 Db 31 AAPF 34

RESULT 22

H70898 probable PE protein - *Mycobacterium tuberculosis* (strain H37RV)
 C; Species: *Mycobacterium tuberculosis*
 C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C; Accession: H70898
 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 333, 537-544, 1998
 A; Authors: Sagres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A; Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A; Reference number: A70500; MUID:98295987; PMID:9634230
 A; Accession: H70898
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-102 <COL>
 A; Cross-references: GB:Z80108; GB:AL123456; NID:93256012; PIDN:CAB02191.1; PID:e26555
 A; Experimental source: strain H37RV
 C; Genetics:
 A; Gene: PE

Query Match 100.0%; Score 21; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 Db 31 AAPF 34

RESULT 23

H75397 hypothetical protein - *Deinococcus radiodurans* (strain RI)
 C; Species: *Deinococcus radiodurans*
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C; Accession: H75397
 R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Smith, M.; Yamada, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Qy 1 AAPF 4
Db 106 AAPF 109

RESULT 28

PC4280 anti-ss-A/RO 60k peptide heavy chain E-60 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: PC4280
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Setine, Y.; Kashiwagi, H.
A;Title: Molecular cloning of anti-ss-A/RO 60-kDa peptide fab fragments from infiltrating
A;Reference number: PC4279; MUID:97236289; PMID:9125110
A;Accession: PC4280
A;Molecule type: protein
A;Residues: 1-122 <SUTZ>
C;Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren's syndrome.
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMH>

Query Match 100.0%; Score 21; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 106 AAPF 109

RESULT 29

C83501 hypothetical protein PA1149 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83501
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: C83501
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-122 <STOZ>
A;Cross-references: GB:AE004545; GB:AE004091; NID:99947070; PIDN:AG04538.1; GSPDB:GN001
A;Experimental source: strain PA01
A;Residues: 1-122 <STOZ>
A;Experimental source: strain PA01
C;Genetics:
C;Gene: PA1149

Query Match 100.0%; Score 21; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 106 AAPF 109

RESULT 30

AD0605 Query Match 100.0%; Score 21; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 106 AAPF 109

Query Match 100.0%; Score 21; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 106 AAPF 109

RESULT 31

A83048 hypothetical protein PA4795 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83048
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: A83048
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <STO>
A;Cross-references: GB:AE004892; GB:AE004091; NID:99951049; PIDN:AG08181.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
C;Gene: PA4795

Query Match 100.0%; Score 21; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 106 AAPF 109

RESULT 32

T05908 probable ribosomal protein S8 - barley (fragment)
C;Species: Hordeum vulgare (barley)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 20-Jun-2000
C;Accession: T05908
R;Hess, W.R.; Goetz, R.R.; Boerner, T.
Plant Sci. 133, 191-201, 1998
A;Title: Analysis of randomly selected cDNAs reveals the expression of stress- and developmental genes in barley roots
A;Reference number: Z15411
A;Accession: T05908
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-126 <HES>
A;Cross-references: EMBL:AU00228; PIDN:CAA03954.1
A;Experimental source: cv. Haifa
C;Superfamily: rat ribosomal protein S8
C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 21; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 106 AAPF 109

RESULT 33

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulé, S.; O'Gara, P.; Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

QY	1 AAPF 4	A; Accession: A71334
Db	1111	A; Status: preliminary; nucleic acid sequence not shown; translation not shown
Db	107 AAPF 110	A; Molecule type: DNA
RESULT	33	A; Residues: 1-127 <COL>
A25864		A; Cross-references: GB:AE001215; GB:AE000520; NTID:93322631; PID:9332
N; Alternative names: calcitonin gene-related peptide II		C; Genomics:
C; Species: Homo sapiens (man)		A; Gene: Tpp355
C; Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997		C; Superfamily: syphilis spirochete hypothetical protein TP0355
C; accession: A25864; JH0620; B26142; A34665		A; Experimental source: Strain Nichols
R; Steenbergh, P.H.; Hoepener, J.W.M.; Zandberg, J.; Visser, A.; Lips, C.J.M.; Jansz, H.		A; Gene:
FEBS Lett. 209, 97-103, 1986		A; Residues: 1-127 <TE>
A; Title: Structure and expression of the human calcitonin/CGRP genes.		A; Molecule type: DNA
A; accession: A25864; MUID:87105923; PMID:3492393		A; Residues: 1-17 <TE>
R; Itaiwara, K.; Kanawa, K.; Kawamoto, M.; Ichiki, Y.; Matsuo, H.; Eto, T.		A; Residues: 1-17 <WIM>
Biochem. Biophys. Res. Commun. 185, 134-141, 1992		A; Title: Isolation and characterization of peptides which act on rat platelets, from a R
A; Reference number: JH0618; MUID:92287083; PMID:1318039		A; Residues: 1-17 <TE>
A; Accession: JH0620		A; Molecule type: protein
A; Experimental source: pheochromocytoma		A; Residues: 82, 'X', 84-87, 'X', 89-104 <KIT>
R; Petermann, J.B.; Born, W.; Chang, J.Y.; Fischer, J.A.		A; Residues: 82, 'X', 84-87, 'X', 89-104 <KIT>
J. Biol. Chem. 262, 5425-545, 1987		A; Title: Identification in the human central nervous system, pituitary, and thyroid of a
A; Title: Identification in the human central nervous system, pituitary, and thyroid of a		A; Residues: 82, 'X', 84-87, 'X', 89-104 <KIT>
A; Reference number: A92637; MUID:87109142; PMID:3492492		A; Molecule type: protein
A; Accession: B26142		A; Residues: 82, 'X', 84-87, 'X', 89-104 <WIM>
A; Molecule type: protein		A; Title: Isolation, purification and characterization of beta-hcGRP from human spinal co
A; Residues: 82, 'X', 84-87, 'X', 89-91, 'X', 93-98, 'X' 100-105, 'X' 107-109 <PET>		A; Residues: 82, 'X', 84-87, 'X', 89-104 <WIM>
R; Imaiawansa, S.J.; Morris, H.R.; Etienne, A.; Blenck, I.; Panico, M.; MacIntyre, I.		A; Title: Isolation, purification and characterization of beta-hcGRP from human spinal co
Biochem. Biophys. Res. Commun. 167, 993-1000, 1990		A; Residues: 82, 'X', 84-87, 'X', 89-104 <WIM>
A; Title: Isolation, purification and characterization of beta-hcGRP from human spinal co		A; Molecule type: protein
A; Reference number: A34665; MUID:90211348; PMID:3322288		A; Residues: 82, 'X', 84-87, 'X', 89-104 <WIM>
A; Accession: A34665		A; Title: Calcitonin gene-related peptide II peptide is a potent vasorelaxant.
A; Molecule type: protein		C; Comment: Calcitonin gene-related peptide II peptide is a potent vasorelaxant.
A; Residues: 82-86; 104-117 <WIM>		C; Genetics:
C; Comment: Calcitonin gene-related peptide II peptide is a potent vasorelaxant.		A; Gene: GDB:CALCB; CALC2
C; Superfamily: calcitonin		A; Cross-references: GDB:120572; OMIM:114160
C; Keywords: amidated carboxyl end; neuropeptide F; 82-118/product: calcitonin gene related peptide		A; Map position: 1p15.2-11p15.1
F; 82-118/modified site: amidated carboxyl end (Phe) (amide in mature form from following 91		A; Map position: 1p15.2-11p15.1
Query Match	100.0%	Best Local Similarity
Best Local Similarity	100.0%	Score
Matches	4	21
Conservative	0	DB
Mismatches	0	2
Indels	0	Length
Gaps	0	127
OY	1 AAPF 4	A; Status: experimental <MAT>
Db	25 AAPF 28	A; Residues: 1-128 <JON>
RESULT	34	A; Cross-references: EMBL:X15943; NTID:929613; PIDN:CAA34070.1; PID:9296638
A71334		A; Note: the authors translated the codon CAG for residue 19 as Glu
hypothetical protein tp0355 - syphilis spirochete		R; Jones, V.; Lin, C.R.; Kawashima, E.; Semon, D.; Swanson, L.W.; Mermoud, J.J.; Evans,
C; Species: Treponema pallidum subsp. Pallidum (<i>syphilis spirochete</i>)		Proc. Natl. Acad. Sci. U.S.A. 82, 1994-1998, 1995
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999		A; Title: Alternative RNA processing events in human calcitonin/calcitonin gene-related
C; Accession: A71334		A; Reference number: A91034; MUID:85166239; PMID:33872459
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin		A; Accession: A22949
r; Carlson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo		A; Molecule type: mRNA
lly, L.; Weidman, J.; Smith, H.O.; Venter, J.C.		A; Residues: 1-128 <JON>
Science 281, 375-388, 1998		A; Cross-references: GB:ML2667; NTID:9179825; PIDN:AA51914.1; PID:9179828
A; Title: Complete genome sequence of <i>Treponema pallidum</i> , the syphilis spirochete.		A; Reference number: B22716
A; Reference number: A71250; MUID:98332770; PMID:665876		A; Molecule type: mRNA
A; Molecule type: protein		A; Residues: 1-128 <JON>
A; Residues: 77-122 <RES>		A; Cross-references: EMBL:X15943; NTID:929613; PIDN:CAA34070.1; PID:9296638
A; Cross-references: GB:M28637; NTID:9180467; PIDN:AA52012.1; PID:9457134		A; Reference number: B22716
R; Morris, H.R.; Panico, M.; Etienne, T.; Tippins, J.; Gigris, S.I.; MacIntyre, I.		A; Molecule type: protein
Nature 308, 746-748, 1984		A; Residues: 1-127 <COL>
A; Title: Isolation and characterization of human calcitonin gene-related peptide.		A; Residues: 83-119 <MOR>
A; Reference number: A93329; MUID:84191466; PMID:6609312		A; Note: this peptide was detected in medullary thyroid carcinoma tissue and in plasma
A; Accession: JU0005		R; Zaidi, M.; Brain, S.D.; Tippins, J.R.; di Marzo, V.; Moonga, B.S.; Chambers, T.J.;
A; Molecule type: protein		Biochem. J. 265, 775-780, 1990
A; Residues: 83-119 <MOR>		A; Title: Structure-activity relationship of human calcitonin-gene-related peptide.
A; Title: Isolation and characterization of human calcitonin gene-related peptide.		A; Reference number: S10813; MUID:9035880; PMID:2390067
A; Reference number: A71250; MUID:98332770; PMID:665876		A; Accession: S10813
A; Molecule type: protein		A; Molecule type: protein

A; Residues: 83-99, 'A', 101-119 <ZAI>
 R; Petermann, J.B.; Born, W.; Chang, J.Y.; Fischer, J.A.
 J. Biol. Chem. 262, 542-545, 1987
 A; Title: Identification in the human central nervous system, pituitary, and thyroid of a
 A; Reference number: A26142; MUID:87109142; PMID:3492492

A; Accession: JH0619
 A; Molecule type: protein
 A; Residues: 83, 'X', 85-88, 'X', 90-108 <KIT>
 A; Experimental source: Pheochromocytoma
 R; Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
 Biochem. Biophys. Res. Commun. 185, 136-141, 1992

A; Title: Isolation and characterization of peptides which act on rat platelets, from a P
 A; Accession: JH0618; MUID:92287083; PMID:1318039

A; Residues: 83-88, 'X', 90-101, 'X', 103-111, 'X', 113-115, 'X', 117 <PER>
 R; Neikin, B.D.; Rosenfeld, de Bustros, A.; Leong, S.S.; Roos, B.A.; Baylin, S.B.
 Biochem. Biophys. Res. Commun. 123, 648-655, 1984

A; Reference number: 152204; MUID:8502253; PMID:6148938

A; Status: translated from GB/EMBL/DDJB

A; Residues: 48-119 <RE2>
 A; Cross-references: GB:Q03512; NID:9180465; PIDN:AAA2011.1; PID:9180466
 R; Craig, R.K.; Riley, J.H.; Edbrooke, M.R.; Broad, P.M.; Foord, S.M.; Al-Kazwini, S.J.;
 Biochem. Soc. Symp. 52, 91-105, 1986

A; Title: Expression and function of the human calcitonin/alpha-CGRP gene in health and disease
 A; Reference number: 139387; MUID:87213363; PMID:3034287

A; Accession: I84508
 A; Status: translated from GB/EMBL/DDJB

A; Molecule type: DNA
 A; Residues: 77-128 <RE3>
 A; Cross-references: GDB:120571; OMIM:114130

A; Map position: 1p15.2-11p15.1
 A; Intron: 29/2; 76/2

C; Superfamily: calcitonin
 C; Keywords: alternative splicing; amidated carboxyl end; neuropeptide; vasodilator
 F; 83-119/Protein: calcitonin gene-related peptide alpha #status experimental <CTN>
 F; 119/Modified site: amidated carboxyl end (Phe) (amide in mature form from following 91

Query Match 100.0% Score 21; DB 1; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 25 AAPF 28

RESULT 36
 I3779
 Ig variable region (VDJ) (clone T20-24) - human (fragment)
 C; Species: Homo sapiens (man)

C; Accession: 15-Feb-1996 #sequence_revision 15-Feb-1996 #text_change 21-Jan-2000
 R; Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A; Title: Somatic diversification in the heavy chain variable region genes expressed by B
 A; Reference number: A36876; MUID:94119917; PMID:8290556

A; Accession: I3779
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-129 <RES>

A; Cross-references: EMBL:X67910; NID:933576; PIDN:CAA48108.1; PID:933577

C; Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 F; 23-105/Domain: immunoglobulin homology <IMM>

RESULT 37
 T29498
 hypothetical protein K00B9.3 - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
 C; Accession: T29498
 R; Miller, N.; Bradshaw, H.
 submitted to the EMBL Data Library, February 1996
 A; Description: The sequence of *C. elegans* cosmid K00B9.
 A; Reference number: Z20628

A; Accession: T29498
 A; Status: preliminary; translated from GB/EMBL/DDJB

A; Molecule type: DNA
 A; Residues: 1-130 <ML>
 A; Cross-references: EMBL:U50072; PIDN:AAA93448.1; CESP:K00B9.3
 C; Genetics:
 A; Gene: CESP:K00B9.3
 A; Intron: 32/3; 64/1

Query Match 100.0% Score 21; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 4 AAPF 7

RESULT 38
 S36196
 hypothetical protein 122.1 - *Haloferax mediterranei*
 C; Species: *Haloferax mediterranei*

C; Accession: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 R; Mojica, F.J.M.; Juez, G.; Rodriguez-Valera, F.
 Mol. Microbiol. 9, 613-621, 1993

A; Title: Transcription at different salinities of *Haloferax mediterranei* sequences and
 A; Reference number: S36196; MUID:94018655; PMID:8412707

A; Accession: S36196
 A; Molecule type: DNA
 A; Residues: 1-132 <MOJ>
 A; Cross-references: EMBL:X73453; NID:9437778; PIDN:CAA51831.1; PID:9437779

Mol. Microbiol. 17, 85-93, 1995
 A; Title: Long stretches of short tandem repeats are present in the largest replicons
 A; Reference number: S69772; MUID:96020664; PMID:7476211

A; Contents: annotation
 C; Superfamily: *Haloferax mediterranei* hypothetical protein 122.1

Query Match 100.0% Score 21; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 125 AAPF 128

RESULT 39
 S76285
 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
 C; Species: *Synechocystis* sp.
 A; Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C:Accession: S76285
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O., K.; Okumura, S.; Shimpoo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 s.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76285
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-133 <RAN>
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Superfamily: Escherichia coli protein P15B

Query Match 100.0%; Score 21; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; caps 0;
 QY 1 AAPF 4
 |||||
 Db 73 AAPF 76

RESULT 40

F75297 hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: F75297

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

, M.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75297

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-133 <WHI>

A:Cross-references: GB:AE002057; GB:AE000513; NID:96460050; PID:AAFI1800.1; PID:9646005

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2252

A:Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; caps 0;

QY 1 AAPF 4
 |||||
 Db 7 AAPF 10

Search completed: December 6, 2002, 13:31:01

Job time : 10.2222 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.				
GenCore version 5.1.3				
Run on:	December 6, 2002, 13:20:29 ; Search time 5.5556 Seconds (without alignments)			
Title:	US-10-033-526-1			
Sequence:	Perfect score: 21 AAFF 4			
Scoring table:	BLOSUM62			
Gapcp	10.0 , Gapext 0.5			
Searched:	112892 seqs, 41476328 residues			
Total number of hits satisfying chosen parameters:	112892			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0%			
Maximum Match 100%				
Listing first 45 summaries				
Database:	SwissProt_40; *			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Length	DB ID	Description
1	21	100.0	5	SUGA_ACHDO
2	21	100.0	63	COKO_BOVIN
3	21	100.0	63	COXO_MOUSE
4	21	100.0	90	MS2B_DRDRA
5	21	100.0	90	MS2B_DROME
6	21	100.0	90	MS2B_DROS1
7	21	100.0	90	MS2B_DROS1
8	21	100.0	102	YD86_MYCTU
9	21	100.0	102	CAL2_HUMAN
10	21	100.0	127	Y355_TREPA
11	21	100.0	128	CALI_HUMAN
12	21	100.0	130	CAL2_MOUSE
13	21	100.0	130	SZ05_RAT
14	21	100.0	133	P2Y2_BOVIN
15	21	100.0	133	RBF4_SKN13
16	21	100.0	134	CAL2_RAT
17	21	100.0	134	CU3A_TENMO
18	21	100.0	136	NU2M_ARTSA
19	21	100.0	136	NU2M_ARTSA
20	21	100.0	141	CALO_HUMAN
21	21	100.0	141	YEF5_YEAST
22	21	100.0	142	PSAH_MAZIE
23	21	100.0	143	PSAH_HORVU
24	21	100.0	144	PSAH_SPITOL
25	21	100.0	145	PSAH_BRARA
26	21	100.0	145	PSH1_ARATH
27	21	100.0	145	PSH2_ARATH
28	21	100.0	165	VNS3_CVPPU
29	21	100.0	168	RBS_SACCHY
30	21	100.0	181	RBS_LACSA
31	21	100.0	182	PAAD_ARCFU
32	21	100.0	186	PI152_METHP
33	21	100.0	190	AFT_TREPA
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
ALIGNMENTS				
RESULT 1	ID: SUGA_ACHDO	STANDARD:	PRT:	5 AA.
AC	P1991;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-FEB-1996 (Rel. 34, Last annotation update)			
DE	Suboesophageal ganglion pentapeptide.			
OS	Acheta domesticus (House cricket).			
OC	Euarayota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;			
OX	NCBI_TaxID:6997;			
RN	[1]			
RP	SEQUENCE..			
RA	Wicker C., Wicker C.;			
RT	"Isolation and structure of a peptide isolated from the suboesophageal ganglion of Acheta domesticus (orthoptera).";			
RL	Comp. Biochem. Physiol. B8C:185-187(1987).			
CC	-!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL Gанглия.			
DR	PIR_J50319; J50319;			
SQ	SEQUENCE 5 AA: 476 MM: 69D76DDDBB00000 CRC64;			
Query Match	100.0%; Score 21; DB 1; Length 5;			
Best Local Similarity	100.0%; Pred. No. 1.1e+05;			
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 AAFF 4			
Db	2 AAFF 5			
RESULT 2	ID: COXO_BOVIN	STANDARD:	PRT:	63 AA.
AC	P00430;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Cytochrome c oxidase polypeptide VIIC, mitochondrial precursor (EC 1.9.3.1). (VIIC).			
DE	COTC OR COX7C1.			
GN	Cox1			
OS	Bos taurus (Bovine).			
OC				
RA	Euarayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RA	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
RA	Bovidae; Bovines; Bos.			
OC	NCBI_TaxID:9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:90045968; PubMed:2554257;			
RA	Aqua M.S., Lomax M.I., Schon E.A., Grossman L.I.;			
RA	"Nucleotide sequence of a cDNA for bovine cytochrome c oxidase subunit VIIC.";			
RT	Subunit VIIC.;			
RT	Nucleic Acids Res. 17:8376-8376(1989).			
RN	[2]			

RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92009215; PubMed=1655579;
 RA Aqua M.S., Bichman N.J., Lomax M.I., Grossman L.I.;
 RT "Characterization and expression of a cDNA specifying subunit VIIC of bovine cytochrome c oxidase.";
 RL Gene 104:211-217(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97248578; PubMed=9092564;
 RA Seelam R.S., Grossman L.I.;
 RT "Structural organization and promoter analysis of the bovine cytochrome c oxidase subunit VIIC gene. A functional role for Y11.";
 J. Biol. Chem. 272:10175-10181(1997).
 RN [4]
 RP SEQUENCE OF 17-63.
 RC TISSUE=Heart;
 RX MEDLINE=9046803; PubMed=213363;
 RA Buse G., Steffens G.J.;
 RT "Studies on cytochrome c oxidase, II. The chemical constitution of a short polypeptide from the beef heart enzyme";
 RL Hoppe-Seyler's Z. Physiol. Chem. 359:1005-1009(1978).
 RN [5]
 RP SEQUENCE OF 17-42.
 RC TISSUE=Liver.
 RX MEDLINE=8900697; PubMed=2844245;
 RA Yamamura W., Zhang Y.-Z., Takamiya S., Capaldi R.A.;
 RT "Tissue-specific differences between heart and liver cytochrome c oxidase.;"
 RL Biochemistry 27:4909-4914(1988).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=96216288; PubMed=8638158;
 RA Tsukihara T., Aoyama H., Yamashita E., Tomizaki T., Yamaguchi H., Shinzawa-Itoh K., Nakashima R., Yaono R., Yoshikawa S.;
 RT "The whole structure of the 13-subunit oxidized cytochrome c oxidase at 2.8 Å";
 RL Science 272:1136-1144(1996).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RC TISSUE=Heart;
 RX MEDLINE=99190827; PubMed=10089392;
 RA Tomizaki T., Yamashita E., Yamaguchi H., Aoyama H., Tsukihara T., Shinzawa-Itoh K., Nakashima R., Yaono R., Yoshikawa S.;
 RT "Structure analysis of bovine heart cytochrome c oxidase at 2.8 Å resolution.;"
 RL Acta Crystallogr. D 55:31-45(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RC TISSUE=Heart;
 RX MEDLINE=20235645; PubMed=10771420;
 RA Fei M.-J., Yamashita E., Inoue N., Yao M., Yamaguchi H., Tsukihara T., Shinzawa-Itoh K., Nakashima R., Yoshikawa S.;
 RT "X-ray structure of azide-bound fully oxidized cytochrome c oxidase from bovine heart at 2.9 Å resolution.;"
 RL Acta Crystallogr. D 56:529-535(2000).
 CC -I- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -I- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O₂ = 4 ferricyanochrome c + 2 H₂O.
 CC -I- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -I- TISSUE SPECIFICITY: LIVER, HEART, MUSCLE AND BRAIN. CONTAIN THE SAME ISOFORM OF COX VIIC, BUT AT DIFFERENT CONCENTRATIONS.
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
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 CC ---
 CC CC ---
 CC DR EMBL; X15725; CAB57793; 1;
 CC DR EMBL; X58823; CAA41627; 1;
 CC DR EMBL; U58655; AAC48719; 1;
 CC DR PIR; JH0473; OS08A.
 CC DR PDB; I0CC; 07-DEC-96.
 CC DR PDB; 20CC; 13-JAN-99.
 CC DR PDB; I0CR; 21-JUL-99.
 CC DR PDB; I0CO; 22-JUL-99.
 CC DR InterPro; IPR04202; COX7C.
 CC DR Pfam; PF02935; COX7C; 1.
 CC KW Oxidoreductase; Mitochondrion; Transit peptide; 3D-structure; Inner membrane; Transmembrane.
 CC FT TRANSIT DOMAIN TRANSMEM
 CC FT CHAIN 17 33
 CC FT DOMAIN 17 33
 CC FT COX7C
 CC FT DOMAIN 34 60
 CC FT DOMAIN 61 63
 CC SQ SEQUENCE 63 AA: MITOCHONDRIAL INTERMEMBRANE.
 CC Qy 1 AAPF 4 7331 MW: C6A2ADSC4E63C0B CRC64;
 CC Db 50 AAPF 53
 CC Query Match Best Local Similarity 100.0%; Score 21; DB 1; Length 63;
 CC Matches 4; Conservative 100.0%; Pred. No. 82; Mismatches 0; Indels 0; Gaps 0;
 CC RN
 CC RESULT 3
 CC COXO_MOUSE STANDARD: PRT: 63 AA.
 CC ID COXO_MOUSE P17665;
 CC AC 01-AUG-1990 (Rel. 15, Created)
 CC DT 01-AUG-1990 (Rel. 15, last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, last annotation update)
 CC DE Cytochrome c oxidase polypeptide VIIC, mitochondrial precursor (EC 1.9.3.1).
 CC DE COX7C OR COX7C.
 CC OS Mus musculus (Mouse).
 CC OC Butarayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC RN NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=BALB/C/ TISSUE=Heart;
 CC RX MEDLINE=90301494; PubMed=2163523;
 CC RA Akamatsu M., Grossman L.I.;
 CC RT "Nucleotide sequence of a cDNA for mouse cytochrome c oxidase subunit VIIC.";
 CC RL Nucleic Acids Res. 18:3645-3645(1990).
 CC -I- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -I- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O₂ = 4 ferricyanochrome c + 2 H₂O.
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
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 CC ---
 CC DR EMBL; X52940; CAA37115; 1;
 CC DR PIR; S10303; S10303.
 CC DR MGI; MGI:103226; Cox7c.
 CC DR InterPro; IPR04202; cox7c.
 CC DR Pfam; PF02935; Cox7c; 1.
 CC KW Oxidoreductase; Mitochondrion; Transmembrane.

FT TRANSIT 1 16 MITOCHONDRION
FT CHAIN 17 63 CYTOCHROME C OXIDASE POLYPEPTIDE VIIC.
SEQUENCE 63 AA: 7333 MW: C6A2AD4ABFEB2C7B CRC64;

Query Match Similarity 100.0%; Score 21; DB 1; length 63;
Best local similarity 100.0%; Pred. No. 82; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; N mismatches 0; N indels 0; N gaps 0;

OY 1 AAPF 4
Db 50 AAPF 53

RESULT 4
MS2B_DROMA STANDARD; PR#: 90 AA.

ID MS2B_DROMA STANDARD; PR#: 90 AA.

AC P3738; (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)
DT DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Accessory gland-specific peptide 26Ab precursor (Male accessory gland secretion protein 35B).

DE Accessory gland-specific peptide 26Ab precursor (Male accessory gland secretion protein 35B).

GN ACP26AB OR MST26AB OR MST35B.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Mandibulata; Pancrustacea; Hexapoda; Insecta; Piergota; Neoptera; Endopterygota; Diptera; Brachycera; Drosophilidae; Drosophila.

OC Miscomorpha; Ephydriidae; Drosophilidae; Drosophila.

OC NCBI_TaxID=7226; [1]

RN SEQUENCE FROM N.A.

RC STRAIN=Robertson C140; Arguado M., Miyashita N., Langley C.H.; RT polymorphism and divergence in the *Mst26A* gene region in *Drosophila*. ";

RL Genetics 112:755-770(1992).

CC -!!- FUNCTION: THIS PROTEIN IS TRANSFERRED FROM MALE TO FEMALE DURING MATING AND MAY AFFECT ESLAYING AND BEHAVIOR AFTER MATING.

CC -!!- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -!!- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES.

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CC SEQUENCE FROM N.A.

CC DR EMBL; X70899; CRA050253.1; PIR; S30428; S30428; FlyBase; FBgn012495; Dmna\Acp26Ab.

CC KW Behavior; Signal; FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 90 ACCESSORY GLAND-SPECIFIC PEPTIDE 26AB.

SEQUENCE 90 AA: 10255 MW: 1BCFC4BE69BA0BF CRC64;

Query Match Similarity 100.0%; Score 21; DB 1; length 90;
Best local similarity 100.0%; Pred. No. 1, 2e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAPF 4
Db 21 AAPF 24

RESULT 5
MS2B_DROMA STANDARD; PR#: 90 AA.

ID MS2B_DROMA STANDARD; PR#: 90 AA.

AC P10334; 076300; 076302; 077456; 09w432; DT 01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)

DE Accessory gland-specific peptide 26Ab precursor (Male accessory gland secretory protein 35B).

DE whose product resembles a peptide pheromone precursor.";

DE Genes Dev. 2:1063-1073(1988).

DE [2]

RN SEQUENCE FROM N.A.

RC STRAIN=NCI; NC2, NC3, NC4, NC5, NC6, NC7, NC8, NC9, and NC10; RX MEDLINE=9316327; PubMed=1361475;

RC Arguado M., Miyashita N., Langley C.H.; RT "Polymorphism and divergence in the *Mst26A* male accessory gland gene region in *Drosophila*."; RT Genetics 112:755-770(1992).

RN [3]

RP SEQUENCE FROM N.A.

RC Monsma S.A., Wolfner M.F.; RT "Structure and expression of a *Drosophila* male accessory gland gene whose product resembles a peptide pheromone precursor.";

RC Genes Dev. 2:1063-1073(1988).

RN [4]

RP SEQUENCE FROM N.A.

RC Teaur S.-C., Ting C.-T., Wu C.-I.; RT "Positive selection driving the evolution of a gene of male reproduction, *Acp26Ab*, of *Drosophila*: II. Divergence versus RT polymorphism.";

RC Mol. Biol. Evol. 15:1040-1046(1998).

RN [5]

RP SEQUENCE FROM N.A.

RC MEDLINE=9838483; PubMed=9718731;

RC Arguado M., Miyashita N., Langley C.H.; RT different forces drive the evolution of the *Acp26Ab* and *Acp26Ab* accessory gland genes in the *Drosophila melanogaster* species complex.";

RC MEDLINE=9316006; PubMed=10731132;

RC Genetics 150:1079-1089(1998).

CC SEQUENCE FROM N.A.

CC DR Sutton G.G., Wortsman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blaize R.G., Champe M., Pfleiffer B.D., Wan K.H., Doyle C., Batter E.G., Helt G., Nelson C.R., Miklos G.I.G., Abril J.-F., Agbayani A., An H.-J., Andrews-Tammoch C., Baldwin D., Bailew R.M., Basu A., Boxendale J., Bayraktaroglu L., Beasley E.M., Beezon K.Y., Benos P.V., Belman B.P., Bhandari D., Bolshakov S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlke C., Davernport L.E., Center A., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dobson K., Doup L.E., Downes M., Duran-Rocha S., Dunikov B.C., Dunn P., Durbin K.J., Evangelista C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabriellian A.E., Garg N.S., Gilbert W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M.M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svärksas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000)
 CC -!- FUNCTION: THIS PROTEIN IS TRANSFERRED FROM MALE TO FEMALE DURING
 CC MATING AND MAY AFFECT EGGLAYING AND BEHAVIOR AFTER MATING.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF053276; AAC28843.1;
 DR EMBL: AJ231353; CAB37201.1;
 DR EMBL: AJ231353; CAB37203.1;
 DR EMBL: AJ231356; CAB37207.1;
 DR EMBL: AJ231358; CAB37211.1;
 DR EMBL: AJ231359; CAB37213.1;
 DR EMBL: AJ231365; CAB37225.1;
 DR EMBL: AJ231372; CAB37239.1;
 DR EMBL: AJ231379; CAB37251.1;
 DR EMBL: AE003611; AAF22297.1;
 DR PIR: S02854; S02854.
 DR PIR: S30408; S30408.
 DR PIR: S30410; S30410.
 DR PIR: S30424; S30424.
 DR FlyBase; FBgn0002856; Acp26Ab.

KW Behavior; Signal; Polymorphism.

FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 90 ACCESSORY GLAND-SPECIFIC PEPTIDE 26Ab.

FT VARIANT 64 64 O -> H (IN STRAINS AFL, AF2, AF3, AF5,
 FT VARIANT 89 89 AF6, AF7, AF9, AF10, AU4, AU7, AUB,
 FT VARIANT 90 90 NC3, NC4, NC5, NC8, NC9, NY2, NY3, NY4,
 FT VARIANT 90 90 NY5, TW1, TW2, TW5, TW6, TW7, TW8, TW10
 AND TW11).
 P -> R (IN STRAIN TW9).
 I -> V (IN STRAINS NC2, NC3, NC4, NC6,
 AND TW11).
 M -> I (IN STRAIN AU4).
 A -> E (IN STRAINS TW1, TW6, AFL, AF1, AF2,
 AF3, AF5, AF6, AF7, AF8, AF9 AND AF10).

SQ SEQUENCE 90 AA; 10162 MW; 1FDPDC7951F9BDDF CRC64;

Query Match 100.0%; Score 21; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AAPF 4
Db	21 AAPF 24

RESULT 5

MS2B_DROSE	STANDARD:	PRT:	90 AA.
AC P33739;			
DT 01-FEB-1994 (Rel. 28, Created)			
DT 01-FEB-1994 (Rel. 28, last sequence update)			
DT 16-OCT-2001 (Rel. 40, last annotation update)			
DE Accessory gland-specific peptide 26Ab precursor (Male accessory gland secretory protein 35B).			
GN ACP26Ab OR MS26Ab OR MST35B.			
OS <i>Drosophila sechellia</i> (fruit fly).			
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; OC Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila.			
OX NCBI_TaxID=7238;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE:93105377; PubMed:1361475;			
RA Aguado M., Miyashita N., Langley C.H.,			
RT "Polymorphism and divergence in the Mst26A male accessory gland gene region in <i>Drosophila</i> "; Genetics 132:755-770(1992).			
CC -!- FUNCTION: THIS PROTEIN IS TRANSFERRED FROM MALE TO FEMALE DURING CC MATING AND MAY AFFECT EGGLAYING AND BEHAVIOR AFTER MATING. CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR. CC -!- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES.			
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CC EMBL; X72630; CNA51207_1;

DR FT FlyBase; FBgn0012778; bsec\AcP2Ab.

KW Behavior; Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 90 ACCESSORY GLAND-SPECIFIC PEPTIDE 26AB.

SQ SEQUENCE 90 AA; 10270 MW; 99CFC4EE6B7782E CRC64;

Query Match Best Local Similarity 100.0%; Score 21; DB 1; Length 90; Matches 4; Conservative 0; Mismatches 0; Pred. No. 1.2e+02; Indels 0; Gaps 0; RT [1]

QY 1 AAPF 4 RP SEQUENCE FROM N.A.

DB 21 AAPF 24 RC STRAIN=PC;

RESULT 7 ID MS2B_DROS1 STANDARD; PRT; 90 AA.

AC P33740; PRINTER; 28, Created)

DT 01-FEB-1994 (Rel. 28, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Accessory gland-specific peptide 26AB precursor (Male accessory gland secretory protein 35kB).

GN ACP26AB OR MST26AB OR MST35B.

OS Drosophila simulans (Fruit fly)

OC Eukaryota; Metazoa; Arthropoda; Pancrustacea; Hexapoda; Insecta; Piergota; Neoptera; Endopterygota; Diptera; Brachycera; Oligochaeta; Ephydriidae; Drosophilidae; Drosophila.

OC Miscomorpha; Ephydriidae; Drosophilidae; Drosophila.

OX NCBI_TaxID=7240;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PC;

RA MEDLINE=93106377; PubMed=1361475;

RT "Polyorphism and divergence in the Mst26A male accessory gland gene in Drosophila".

RL Genetics 132:755-770(1992).

CC -4- FUNCTION: THIS PROTEIN IS TRANSFERRED FROM MALE TO FEMALE DURING MATING AND MAY AFFECT GAMBLING AND BEHAVIOR AFTER MATING.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES.

CC

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CC

DR EMBL; X70899; CAA50255_1;

DR PIR; S30430; S30430.

DR FlyBase; FBgn0012821; Dsim\AcP2Ab.

KW Behavior; Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 90 ACCESSORY GLAND-SPECIFIC PEPTIDE 26AB.

SQ SEQUENCE 90 AA; 10189 MW; F7FB8D6B6D04F02B5 CRC64;

Query Match Best Local Similarity 100.0%; Score 21; DB 1; Length 90; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT [1]

QY 1 AAPF 4 RP SEQUENCE FROM N.A.

DB 21 AAPF 24 RC STRAIN=H37Rv;

RESULT 9 ID YP06_MCTU STANDARD; PRT; 102 AA.

AC P71656; PRINTER; 39, Created)

DT 30-MAY-2000 (Rel. 39, last sequence update)

DT 15-JUN-2002 (Rel. 41, last annotation update)

DE Hypothetical protein Rv1386 precursor.

GN Rv1386 OR Mtb130 OR MTB2194.03.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinomycetaceae; Actinomycetales; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37Rv;

RA MEDLINE=99295987; PubMed=9634230;

RA Cole S., T.B. Brosch, R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S., Ellington K., Gas S., Barry C.P., III, Tekala F., Braddock S., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jangels K., Kroth A., McLean J., Moulle S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; RT Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

RT Nature 393:537-544(1998).

RN [2]

RESULT 8

RP SEQUENCE FROM N.A.
 RN STRAIN=CDC 1551 / Oshkosh;
 RC Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.R., DeBoy R., Dodson R., Gwyn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Unayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.

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CC -----

CC DR EMBL: ZB0108; CAB02191; 1; -.
 CC DR EMBL: AE007014; ARK45695; 1; -.
 CC DR TIGR: MT430; -.
 CC DR TubercuList: Rv1386; -.
 CC DR InterPro: IPR00084; PE_region.
 DR Pfam: PF00934; PE: 1.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 102 MW: HYPOTHETICAL PROTEIN Rv1386.

SQ SEQUENCE 102 AA: 9862 MW: 8165F09BBDB9D752 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0;
 Matches 4; Conservative 0; Signal 1; Potential 31.

QY 1 AAPF 4
 Db 31 AAPF 34

RESULT 10

CC CA12_HUMAN STANDARD: PRT: 127 AA.
 TD CA12_HUMAN STANDARD: PRT: 127 AA.
 AC P0092; Q9UCV9; 1; JOINED.
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type
 DE CGRP).
 GN CALCB OR CALC2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 OC NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=87105923; Published=3492393;
 RA Sreenanbh P.H., Hoepener J.W.M., Zandberg J., Visser A.,
 RA Lips C.J.M., Jansz H.S.;
 RT "Structure and expression of the human calcitonin/CGRP genes.";
 RL FEBS Lett. 209:97-103(1986);
 RN [2] SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RA Strausberg R.;
 RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [3] SEQUENCE OF 56-127 FROM N.A.
 RP MEDLINE=85180007; Published=2885435;
 RA Steenbergh P.H., Hoepener J.W.M., Zandberg J., Lips C.J.M.,
 RA Jansz H.S.;
 RT "A second human calcitonin/CGRP gene.";
 RL FEBS Lett. 183:403-407(1985).

DR EMBL: X04855; CAC05295; 1; JOINED.
 DR EMBL: X04861; CAC05295; 1; JOINED.
 DR EMBL: BC008438; AAB08428; 1; -.
 DR EMBL: X0204; CAZ26249; 1; -.
 DR PIR: A23864; A25864.
 DR PIR: A34565; A34565.
 DR PIR: B26142; B26142.
 DR Genew; HGNC:438; CALC2B.
 DR InterPro: IPR01693; Calcitonin-like.
 DR InterPro: IPR02163; Calcitonin_B.
 DR Pfam: PF00214; Calc_CGPR_IAPP; 1.
 DR PRINTS: PRO0817; CALCITONIN_B.
 DR SMART: SM00113; CALCITONIN; 1.
 DR PROSITE: PS00258; CALCITONIN; 1.
 DR Cleaveage on pair of basic residues; Amidation; Hormone; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 79
 FT PEPTIDE 82 118
 FT PROPEP 124 127
 FT DISULFID 88 88
 FT MOD_RES 118 118
 FT CONFLICT 73 73
 SQ SEQUENCE 127 AA: 13706 MW: B071A063CD5ACE7 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0;
 Matches 4; Conservative 0; Signal 1; Potential 25.

QY 1 AAPF 4
 Db 25 AAPF 28

RESULT 11
 Y55_TREPA STANDARD; PRT; 127 AA.
 AC 083374;
 DT 16-OCT-2001 (rel. 40, created)
 DT 16-OCT-2001 (rel. 40, last sequence update)
 DT 16-OCT-2001 (rel. 40, last annotation update)
 DE Hypothetical protein TIP0355.
 GN TIP0355.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TAXID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9333270; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwyn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khaliq H., Richardson D., Howell J.K., Chisholm M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C., "Complete genome sequence of *Treponema pallidum*, the syphilis
 RT spirochete.",
 RL Science 261:375-380 (1998).
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 CC -----
 DR EMBL: AE001215; AAC65353.1; -.
 DR TIGR: TP0355; -.
 KW Hypothetical Protein; Complete Proteome.
 SQ SEQUENCE 127 AA; 14526 MW; 1BA8EF0DAC4ADC4 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 AAPF 4
 Db 85 AAPF 88

RESULT 12
 ID_CRL_HUMAN STANDARD; PRT; 128 AA.
 AC PG6881; Q9UCP0;
 DT 01-JAN-1988 (rel. 06, last created)
 DT 01-MAR-1989 (rel. 10, last sequence update)
 DT 16-OCT-2001 (rel. 40, last annotation update)
 DE Calcitonin gene-related peptide I precursor (CGRP-I) (Alpha-type
 CGRP).
 GN CALCA OR CALCL.
 OS Homo sapiens ('Human').
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=69386053; PubMed=2571128;
 RA Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;
 RT "Structure and methylation of the human calcitonin/alpha-CGRP gene.",
 RL Nucleic Acids Res. 17:6999-7011(1989).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=85166259; PubMed=3872459;
 RA Jonas V., Lin C.R., Kawashima M., Simon D., Swanson L.W.,
 RA Mermod J.-J., Evans R.M., Rosenfeld M.G.;
 RT "Alternative RNA processing events in human calcitonin/calcitonin
 gene-related peptide gene expression.";
 RT proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).
 RL [3]
 RP SEQUENCE OF 49-119 FROM N.A.
 RX MEDLINE=8502253; PubMed=6148938;
 RA Neikin B.D., Rosenfeld K.I., de Bustros A., Leong S.S., Roos B.A.,
 RA Baylin S.B.;
 RT "Structure and expression of a gene encoding human calcitonin and
 calcitonin gene related peptide";
 RL Biochem. Biophys. Res. Commun. 123:648-655(1984).
 RN [4]
 RP SEQUENCE OF 49-128 FROM N.A.
 RX MEDLINE=8523041; PubMed=2408883;
 RA Ebdrøke M.R., Parker D., McVey J.H., Riley J.H., Sorenson G.D.,
 RA Petengill O.S., Craig R.K.,
 RT Expression of the human calcitonin/CGRP gene in lung and thyroid
 carcinoma.";
 RL EMBL: J. 4:715-724(1985).
 RN [5]
 RP SEQUENCE OF 77-128 FROM N.A.
 RC TISSUE_Thyroid_Carcinoma;
 RX MEDLINE=84240116; PubMed=6610687;
 RA Steenbergh P.H., Hoppenier J.W., Zandberg J., de Ven W.J., Jansz H.S.,
 RA Lips C.J.;
 RT "Calcitonin gene related peptide coding sequence is conserved in the
 human genome and is expressed in medullary thyroid carcinoma.";
 RL J. Clin. Endocrinol. Metab. 59:358-360(1984).
 RN [6]
 RP SEQUENCE OF 77-128 FROM N.A.
 RX MEDLINE=87213363; PubMed=3034287;
 RA Craig R.K., Rilly J.H., Ebdrøke M.R., Broad P.M., Foord S.M.,
 RA Al-Kawwari S.J., Holman J.J., Marshall I.;
 RT Expression and function of the human calcitonin/alpha-CGRP gene in
 RT health and disease";
 RL Biochem. Soc. Symp. 52:91-105(1986).
 RN [7]
 RP SEQUENCE OF 83-119.
 RX MEDLINE=84191466; PubMed=6609312;
 RA Morris H.R., Panico M., Etienne T., Tippins J., Grgis S.I.,
 RA McIntyre I.;
 RT "Isolation and characterization of human calcitonin gene-related
 RT peptide";
 RL Nature 308:746-748(1984).
 RN [8]
 RP PARTIAL SEQUENCE OF 83-117.
 RX MEDLINE=87109142; PubMed=492492;
 RA Petermann J.B., Born W., Chang J.Y., Fischer J.A.;
 RT Identification in the human central nervous system, pituitary, and partial amino
 acid sequence in the spinal cord.";
 RL J. Biol. Chem. 262:542-545(1987).
 RP SEQUENCE OF 83-108, AND FUNCTION.
 RC TISSUE_Pheochromocytoma;
 RX MEDLINE=87228703; PubMed=1318039;
 RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Matsuo H., Eto T.,
 RT "Isolation and characterization of peptides which act on rat
 platelets, from a pheochromocytoma";
 RL Biochem. Biophys. Res. Commun. 185:134-141(1992).
 RN [10]
 RP STRUCTURE BY NMR OF CGRP.
 RX MEDLINE=9115142; PubMed=1988044;
 RA Breeze A.L., Harvey T.S., Bazzo R., Campbell I.D.;
 RT "Solution structure of human calcitonin gene-related peptide by 1H
 NMR and distance geometry with restrained molecular dynamics.";
 RL Biochemistry 30:575-582(1991).
 RN [11]
 RP STRUCTURE BY NMR OF CGRP.
 RX MEDLINE=91246117; PubMed=2039456;

RA Hubbard J.A.M., Martin S.R., Chaplin L.C., Bose C., Kelly S.M.,
 RA Price N.C.;
 RT "Solution structures of calcitonin-gene-related-peptide analogues of
 calcitonin-gene-related peptide and amylin.";
 RL Biochem. J. 275:785-788(1991).
 CC -!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of
 vessels including the coronary, cerebral and systemic vasculature.
 CC Its abundance in the CNS also points toward a neurotransmitter or
 neuromodulator role. It also elevates platelet cAMP.
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (AC P0158), 2 (AC P01258) AND
 CC 3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPlicing.
 CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 CC
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 CC
 CC -----
 DR EMBL: X15943; CAA34070_1; -.
 DR EMBL: X22330; CAA26190_1; -.
 DR EMBL: M2667; AAA1914_1; -.
 DR EMBL: M2664; AAA1914_1; JOINED.
 DR EMBL: M2665; AAA1914_1; JOINED.
 DR EMBL: K03512; AA552011_1; -.
 DR EMBL: M8857; AAA52012_1; -.
 DR EMBL: M26094; AAA1912_1; -.
 DR PIR: B22716; TCHUR.
 DR PIR: A22949; A22949.
 DR PIR: A22142; A22642.
 DR PIR: S07644; S07644.
 DR Genew; HGNC:1437; CALCA.
 DR MIM: 114130; -.
 DR InterPro: IPR001633; Calcitonin-like.
 DR InterPro: IPR002153; Calcitonin_B.
 DR Pfam: PF00214; Calc_CGRP_IAPP; I.
 DR PRINTS: PR00517; CALCITONINB.
 DR SMART: SM00113; CALCTONIN; I.
 DR PROSITE: PS00258; CALCITONIN; I.
 KW Cleavage on pair of basic residues; Amidation; Alternative splicing;
 Hormone; Signal.
 FT SIGNAL; 1 25 POTENTIAL.
 FT PROPEP; 26 80
 FT PEPTIDE; 83 119
 FT PROPEP; 125 128
 FT DISULFID; 84 89
 FT MOD_RES; 119 119 AMIDATION (G-120 PROVIDE AMIDE GROUP).
 FT CONFLICT; 48 48 R -> V (IN REF. 4).
 FT CONFLICT; 76 76 R -> V (IN REF. 3).
 SQ SEQUENCE 128 AA; 13899 MW; A003A1069260D9B8; CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 128;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4;
 保守性 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 1111
 Db 25 AAPF 28
 RESULT 13
 CALL_MOUSE STANDARD; PRNT; 130 AA.
 ID CALL_MOUSE
 AC Q99MP3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type
 DE CGRP).
 GN CALCB.
 OS MUS musculus (Mouse).
 RA Hubbard J.A.M., Martin S.R., Chaplin L.C., Bose C., Kelly S.M.,
 RA Price N.C.;
 RT "Solution structures of calcitonin-gene-related-peptide analogues of
 calcitonin-gene-related peptide and amylin.";
 RL Biochem. J. 275:785-788(1991).
 CC -!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of
 vessels including the coronary, cerebral and systemic vasculature.
 CC Its abundance in the CNS also points toward a neurotransmitter or
 neuromodulator role. It also elevates platelet cAMP.
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (AC P0158), 2 (AC P01258) AND
 CC 3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPlicing.
 CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL: AF325526; AAK16431_1; -.
 DR EMBL: AR325524; AAK16431_1; JOINED.
 DR MGD; MGI:2151254; Calcb.
 DR InterPro: IPR000443; Amylin.
 DR InterPro: IPR001633; Calcitonin_B.
 DR InterPro: IPR00214; Calc_CGRP_IAPP; I.
 DR Pfam: PF00214; Calc_CGRP_IAPP; I.
 DR PRINTS: PR00517; CALCITONINB.
 DR SMART; SM00113; CALCTONIN; I.
 DR PROSITE: PS00258; CALCITONIN; I.
 DR KW Cleavage on pair of basic residues; Amidation; Hormone; Signal.
 FT SIGNAL; 1 26 POTENTIAL.
 FT PROPEP; 27 82 BY SIMILARITY.
 FT PEPTIDE; 84 120 CALCITONIN GENE-RELATED PEPTIDE II.
 FT PROPEP; 127 130 BY SIMILARITY.
 FT DISULFID; 85 90 BY SIMILARITY.
 FT MOD_RES; 120 120 BY SIMILARITY.
 FT SEQUENCE 130 AA; 14623 MW; 97299244E8F6C536 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 4;
 保守性 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 1111
 Db 26 AAPF 29
 RESULT 14
 SZ05_RAT STANDARD; PRNT; 130 AA.
 ID SZ05_RAT
 AC P07885;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX).
 GN SCYB5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE:21604266; PubMed=1761712;
 RA Thomas P.M., Nasonkin I., Zhang H., Gagel R.F., Cote G.J.;
 RT "Structure of the mouse calcitonin/calcitonin gene-related peptide
 alpha and beta genes.";
 RL DNA Seg. 12:131-135 (2001).
 CC -!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of
 vessels including the coronary, cerebral and systemic vasculature.
 CC Its abundance in the CNS also points toward a neurotransmitter or
 neuromodulator role (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL: AF325526; AAK16431_1; -.
 DR EMBL: AR325524; AAK16431_1; JOINED.
 DR MGD; MGI:2151254; Calcb.
 DR InterPro: IPR000443; Amylin.
 DR InterPro: IPR001633; Calcitonin_B.
 DR InterPro: IPR00214; Calc_CGRP_IAPP; I.
 DR Pfam: PF00214; Calc_CGRP_IAPP; I.
 DR PRINTS: PR00517; CALCITONINB.
 DR SMART; SM00113; CALCTONIN; I.
 DR PROSITE: PS00258; CALCITONIN; I.
 DR KW Cleavage on pair of basic residues; Amidation; Hormone; Signal.
 FT SIGNAL; 1 26 POTENTIAL.
 FT PROPEP; 27 82 BY SIMILARITY.
 FT PEPTIDE; 84 120 CALCITONIN GENE-RELATED PEPTIDE II.
 FT PROPEP; 127 130 BY SIMILARITY.
 FT DISULFID; 85 90 BY SIMILARITY.
 FT MOD_RES; 120 120 BY SIMILARITY.
 FT SEQUENCE 130 AA; 14623 MW; 97299244E8F6C536 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 4;
 保守性 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 1111
 Db 26 AAPF 29
 RESULT 14
 SZ05_RAT STANDARD; PRNT; 130 AA.
 ID SZ05_RAT
 AC P07885;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX).
 GN SCYB5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Kelner G.S., Maciejewski-Lenoir D., Lee E.D., Maki R.A.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY PARTICIPATE IN THE RECRUITMENT OF INFLAMMATORY CELLS
 CC BY INJURED OR INFECTED TISSUE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
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 CC -----
 DR EMBL; U90448; AAB61460; 1; .
 DR HSSP; P10889; IM2.
 DR InterrPro; IPR001089; CXC_chunkine_sm1.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR00037; SMALLCYTOKX.
 DR SMART; SM0139; SCY; 1.
 DR PROSITE; PS00411; SMALL_CYTOKINES_CXC; 1.
 KW CYTOKINE; Signal.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 130 SMALL INDUCIBLE CYTOKINE B5.
 FT DISULFID 50 93 BY SIMILARITY.
 FT DISULFID 52 93 BY SIMILARITY.
 SQ SEQUENCE 130 AA; 14263 MW; C00f6B360524F4E CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 37 AAPF 40
 RESULT 15
 P2Y2_BOVIN STANDARD; PRT; 133 AA.
 AC 018951;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE P2Y purinoreceptor 2 (P2Y2) (Fragment).
 GN P2Y2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TAXID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kameko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N,
 RA Sugura M., Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RL region from map positions 64% to 92% of the genome";
 DNA Res. 2:133-166(1995).
 CC -!- FUNCTION: ASSOCIATES WITH FREE 30S RIBOSOMAL SUBUNITS (BUT NOT
 CC WITH 30S SUBUNITS THAT ARE PART OF 70S RIBOSOMES OR POLYSOMES).
 CC ESSENTIAL FOR EFFICIENT PROCESSING OF 16S RNA. MAY INTERACT WITH
 CC THE 5' TERMINAL HELIX REGION OF 16S RNA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE RBF FAMILY.
 CC -----
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 CC or send an email to license@isp-sib.ch).
 CC -----
 DR EMBL; D64000; BAA10137; 1; .
 DR InterPro; IPR000238; Rib_bind_factA.
 DR Pfam; PF02035; RBFa; 1.
 DR Prodom; P0001327; Rib_bind_factA; 1.
 DR TIGRFAMs; TIGR00082; rbfA; 1.
 DR PROSITE; PS01319; RBFa; 1.
 KW rRNA processing; Complete proteome
 SQ SEQUENCE 133 AA; 14749 MW; LAYC07689F/B9829 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 17			OY
CAL2_RAT	STANDARD;	PRT;	134 AA.
ID P10093;			DT 01-OCT-1996 (Rel. 34, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)			DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)			DE Larval cuticle protein A3A (TM-LCP A3A).
CALCitonin gene-related peptide II precursor (CGRP-II) (Beta-type CGRP).			OS Tenebrio molitor (Yellow mealworm).
CALCB.			OC Insecta; Pterygota; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Cucujiformia; Tenebrionidae; Tenebrio.
Rattus norvegicus (Rat).			OC NCBI_TAXID=7067;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			OX RN [1]
[1]			RP TISSUE=Cuticle;
SEQUENCE FROM N.A.			RX MEDLINE=97218698; PubMed=9056122;
RX MEDLINE=85300490; PubMed=2994212;			RA Andersen S.O., Rafn K., Reepstorff P.;
RA Amara S.G., Arriiza J.L., Leff S.E., Swanson L.W., Evans R.M., Rosenfeld M.G.			RT Sequence studies of proteins from larval and pupal cuticle of the yellow meal worm, <i>Tenebrio molitor</i> .";
"Expression in brain of a messenger RNA encoding a novel neuropeptide homologous to calcitonin gene-related peptide.";			RL Insect Biochem. Mol. Biol. 27:121-131(1997).
-1- FUNCTION: CGRP induces vasodilatation. It dilates a variety of vessels including the coronary, cerebral and systemic vasculature.			CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF TENEBRIOTOLITOR.
CC its abundance in the CNS also points toward a neurotransmitter or neuromodulator role.			CC -1- DOMAIN: THE TETRAPEPTIDE (A-A-P-[AV]) REPEATS FOUND THROUGHOUT THE PROTEIN ARE ALSO PRESENT IN MANY PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES.
CC -1- SIMILARITY: CONTAINS 1 CUTICLE CONSENSUS DOMAIN.			CC -1- MASS SPECTROMETRY: MW=1374.3; METHOD=Electrospray.
CC DR InterPro: IPR00618; Insect cuticle.			DR InterPro: IPR00379; Chitin_bind_4; 1.
CC DR Pfam: PF00379; Chitin_bind_4; 1.			DR PRINTS: PR00947; CUTICLE.
CC DR PROSITE: PS00233; CUTICLE; 1.			DR REPEAT: PS00233; CUTICLE; 1.
CC KW Structural protein; Cuticle; Repeat.			KW REPEAT: 23 26 1.
CC FT REPEAT: 111 114 2.			FT REPEAT: 111 114 2.
CC SQ SEQUENCE 134 AA; 13976 MW; F6AAAF0644FE93E CRC64;			SQ SEQUENCE 134 AA; 13976 MW; F6AAAF0644FE93E CRC64;
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RESULT 19			
NU2M_ARTSA	STANDARD;	PRT;	136 AA.
ID NU2M_ARTSA			AC P19042;
AC P19042;			DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)			DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3) (Fragments).			DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3) (Fragments).
DE NAD2.			GN NAD2.
GN NAD2.			OS Artemia salina (Brine shrimp).
OS Artemia salina (Brine shrimp).			OG Mitochondrion.
OG Mitochondrion.			OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Branchiopoda; Anostraca; Artemiidae; Artemia.
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Branchiopoda; Anostraca; Artemiidae; Artemia.			OX NCBI_TaxID=85549;
OX NCBI_TaxID=85549;			RN [1]
RN SEQUENCE FROM N.A.			RP SEQUENCE FROM N.A.
RP MEDLINE=88289417; PubMed=3135541;			RX MEDLINE=88289417; PubMed=3135541;
RA Batuecas B., Garesse R., Calleja M., Valverde J.R., Marco R., Genomic organization of Artemia mitochrondrial DNA.,";			RA Batuecas B., Garesse R., Calleja M., Valverde J.R., Marco R., Genomic organization of Artemia mitochrondrial DNA.,";
RA Nucleic Acids Res. 16:6515-6529(1988).			RT Nucleic Acids Res. 16:6515-6529(1988).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.			RL Nucleic Acids Res. 16:6515-6529(1988).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.			CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.			CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
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RX MEDLINE=9210517; PubMed=1761559;

RX MEDLINE=X07670; CA30517.1; -;

RX EMBL: X07671; CA30518.1; -;

RX PIR: S01220; S01220

RX oxdoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.

FT NON_TER 1 1

FT NON_CONS 83 84

FT NON_TER 136 136

FT NON_CONS 136 AA; 15330 MW; FFD3D8FB4DE9BA17 CRC64;

SEQUENCE 136 AA; 15330 MW; FFD3D8FB4DE9BA17 CRC64;

Best Local Similarity 100.0%; Score 21; DB 1; Length 136;

Matches 4; Consistency 100.0%; preNo. 1; 7e+02; Mismatches 0; Indels 0; Gaps 0;

RESULT 20

CALO_HUMAN ID=CALO_HUMAN STANDARD; PRT: 141 AA.

AC P01258; 013937; 01_CREATED

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-APR-1988 (Rel. 07, Last annotation update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Calcitonin precursor [Contains: Calcitonin; Kattacalcin (Calcitonin carboxyl-terminal peptide) (CCP) (PDN-21)].

GN CALCA OR CALC1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TAXID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=89386053; PUBMED=2571128;

RX Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;

RX RT "Structure and methylation of the human calcitonin/alpha-CGRP gene.";

RX Nucleic Acids Res. 17:6999-7011(1989).

[2]

RX SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=8412556; PUBMED=6545550;

RX Le Moulllec J.M., Juillenne A., Chenais J., Lasnoles F.,

RX Guillau J.-M., Milhaud G., Monkhett M.S.;

RX "The complete sequence of human procalcitonin.";

RX FEBS Lett. 167:93-97(1984).

[3]

RX SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=85166259; PUBMED=3872459;

RX Jonas V., Lin C.R., Kawashima E., Semon D., Swanson L.W.,

RX Mermod J.-J., Evans R.M., Rosenfeld M.G.;

RX "Alternative RNA processing events in human calcitonin gene-related peptide gene expression.";

RX Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).

RX SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=86134952; PUBMED=3483540;

RX Riley J.H., Edbrooke M.R., Craig R.K.;

RX "Ectopic synthesis of high-Mr calcitonin by the BEN lung carcinoma cell line reflects aberrant proteolytic processing.";

RX FEBS Lett. 198:71-79(1986).

RX [5]

SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=87213363; PUBMED=303287;

RX Craig R.K., Riley J.H., Edbrooke M.R., Foord S.M.,

RX Al-Kalawi S.J., Holman J.J., Marshall I.;

RX "Expression and function of the human calcitonin/alpha-CGRP gene in health and disease.";

RX Biomed. Soc. Symp. 52:91-105(1986).

RX SEQUENCE FROM N.A. (ISOFORM 2).

RX TISSUE=Thyroid carcinoma;

RX MEDLINE=9210517; PubMed=1761559;

RX Minville S., Giscard-Dartemelle S., Cohen R., Taboulet J., Labey F.,

RX Juilletne A., Rivaille P., Milhaud G., Moukhtar M.S., Lamotte F.;

RX "A novel calcitonin carboxyl-terminal peptide produced in medullary thyroid carcinoma by alternative RNA processing of the calcitonin/calcitonin gene-related peptide gene.";

RX J. Biol. Chem. 266:24627-24631(1991).

RX [7]

RP SEQUENCE OF 49-141 FROM N.A. (ISOFORM 1).

RX MEDLINE=5230541; PUBMED=2408833;

RX Edbrooke M.R., Parker D., McVey J.H., Riley J.H., Sorenson G.D., Pettengill O.S., Craig R.K.;

RX "Expression of the human calcitonin/CGRP gene in lung and thyroid carcinoma";

RX EMBO J. 4:715-724(1985).

RN [8]

RP SEQUENCE OF 48-83 FROM N.A. (ISOFORM 1).

RX MEDLINE=85022523; PUBMED=6148938;

RX Neilin B.D., Rosenthal K.T., de Bustros A., Leong S.S., Roos B.A., Baylin S.B.;

RX "Structure and expression of a gene encoding human calcitonin and calcitonin gene related peptide.";

RX Biochem. Biophys. Res. Commun. 123:648-655(1984).

RN [9]

RP SEQUENCE OF 85-116. MEDLINE=7216220; PUBMED=5760861;

RX Neher R., Riniker B., Ritter W., Zuber H.;

RX "Human calcitonin structure of calcitonin M and D.";

RX Hely. Chim. Acta 51:1900-1905(1968).

RN [10]

RP STRUCTURE BY NMR OF CALCITONIN. MEDLINE=91159141; PUBMED=2001366;

RX RA Motta A., Temussi P.A., Wunsch E., Bovermann G.;

RX RT "A 1H NMR study of human calcitonin in solution.";

RX RL Biochemistry 30:2364-2371(1991).

RN [11]

RP CHARACTERIZATION OF KATACALCIN. MEDLINE=83166029; PUBMED=6132180;

RX RA Hillyard C.J., Myers C., Abeysekera G., Stevensen J.C., Craig R.K., MacIntyre I.;

RX RT "Kattacalcin: a new plasma calcium-lowering hormone.";

RX Lancet 1:846-848(1983).

RN [12]

RP FUNCTION: CALCITONIN CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION OF THOSE IONS IN THE BONES.

RN [13]

CC CC -!- FUNCTION: Kattacalcin is a potent plasma calcium-lowering peptide.

CC CC -!- SUBCELLULAR LOCATION: Secreted.

CC CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3 (AC P0681); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.

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CC DR EMBL X15943; CA334070.1; ALT_SEQ.

CC DR EMBL X03556; CA35103.1; -.

CC DR EMBL K03513; AA2124.1; -.

CC DR EMBL M12666; AA51913.1; -.

CC DR EMBL M12664; AA51913.1; JOINED.

CC DR EMBL M12665; AA51913.1; JOINED.

CC DR EMBL X03652; CA32799.1; -.

CC DR EMBL M64486; AA538403.1; -.

CC DR EMBL M22095; AA55501.1; -.

CC DR EMBL K03513; AA2124.1; -.

CC DR EMBL M12666; AA51913.1; -.

CC DR EMBL M12664; AA51913.1; JOINED.

CC DR EMBL M12665; AA51913.1; JOINED.

CC DR EMBL X03652; CA32799.1; -.

CC DR EMBL M64486; AA538403.1; -.

CC DR EMBL M22095; AA55501.1; -.

DR PIR: A2216; TCHU.

DR PIR: C22949; C22949.

DR PIR: S0738; S07238.

DR PIR: S0742; S07742.

DR PIR: S07643; S07643.

DR HSSP; P01262; 1BKU.
 DR Genew; HGNC:1437; CALCA.
 DR MM: 114130; -.
 DR InterPro; IPR01693; Calcitonin-like.
 DR Pfam; PF00214; Calc_CGRD_IAPP; 1.
 DR PRINTS; PR00210; Calcitonin_A.
 DR SMART; SM00113; CALCITONIN; 1.
 DR PROSITE; PS00258; CALCTONIN; 1.
 KW Cleavage on pair of basic residues; Amidation; Alternative splicing;
 KW Hormone; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 82
 PEPTIDE 85 116 CAICTONIN.
 FT PEPTIDE 121 141 KATACALCIN.
 FT DISULFID 85 91
 MOD_RES 116 116 AMIDATION (G-117 PROVIDE AMIDE GROUP).
 FT VARSPIC 134 141 VSMQAN->NHCPEESL (IN ISOFORM 2).
 FT CONFLICT 92 92 M->I (IN REF. 3).
 SQ SEQUENCE 141 AA; 15467 MW; 99622305DD88286F CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 Db 25 AAPF 28

RESULT 21

YEF5_YEAST STANDARD; PRT; 141 AA.

AC P32616; 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE HYPOTHETICAL 16.5 kDa protein in GLYI-GDA1 intergenic region.

GN YE045C OR SYGP-ORF33.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

RN [1]

RN NCBI_TaxID=4932;

RN [2]

RN SEQUENCE FROM N.A.

RA Mulligan J.T., Hennessey K.M., Sehl P., Komp C.,
 Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
 submitted (FEB-1993) to the EMBL/Genbank/pDBJ databases.

RN [2]

RN SEQUENCE FROM N.A.

RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
 Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M.,
 Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
 Hyman R., Kaiser A., Komp C., Lashkari D., Lew H., Lin D.,
 Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
 Petel F.X., Roberts D., Sehl P., Schramm S., Shogen T., Smith V.,
 Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
 submitted (DEC-1994) to the EMBL/Genbank/pDBJ databases.

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 or send an email to license@isb-sib.ch).

CC DR InterPro; IPR04938; PSI_PSAH.

CC DR Pfam; PF03244; PSI_PSAH; 1.

CC KW Photosynthesis; Photosystem I; Chloroplast; transit peptide;

CC KW Transmembrane.

FT TRANSIT 1 48 CHLOROPLAST (BY SIMILARITY)
 FT CHAIN 49 142 PHOTOSYSTEM I REACTION CENTER SUBUNIT VI.

FT TRANSMEM 99 119 POTENTIAL.

SQ SEQUENCE 142 AA; 14929 MW; C8E9540210026B96 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC or send an email to license@isb-sib.ch).

CC DR EMBL; U18779; AAC64997; 1; -.

CC DR PIR; S2032; S3032.

CC DR SGD; S000071; YEL045C.

CC KW Hypothetical protein; ATP-binding; Transmembrane.

CC NP_BIND 15 22 ATP (POTENTIAL).

RESULT 22

PSAH_MAIZE STANDARD; PRT; 142 AA.

AC ID PSAH_MAIZE 065101; 15-JUN-2002 (Rel. 41, Last annotation update)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein).

DE PSAN.

OS Zea mays (Maize).

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=CV_B73;

RA Heck D.A., Chitnis P.R.;

RT "Nucleotide sequence of cDNAs encoding the psah and psan subunits of the maize photosystem I complex." (In) Plant Gene Register PG98-107.

RL -1- FUNCTION: POSSIBLE ROLE COULD BE THE DOCKING OF THE LHC I ANTENNA COMPLEX TO THE CORE COMPLEX.

CC -1- SIMILARITY: BELONGS TO THE PSAH FAMILY

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 or send an email to license@isb-sib.ch).

CC DR EMBL; AR052076; AAC26196; 1.

CC DR InterPro; IPR04938; PSI_PSAH.

CC DR Pfam; PF03244; PSI_PSAH; 1.

CC KW Photosynthesis; Photosystem I; Chloroplast; transit peptide;

CC KW Transmembrane.

FT TRANSIT 1 48 CHLOROPLAST (BY SIMILARITY)
 FT CHAIN 49 142 PHOTOSYSTEM I REACTION CENTER SUBUNIT VI.

FT TRANSMEM 99 119 POTENTIAL.

SQ SEQUENCE 142 AA; 14929 MW; C8E9540210026B96 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC or send an email to license@isb-sib.ch).

CC DR EMBL; U18779; AAC64997; 1; -.

CC DR PIR; S2032; S3032.

CC DR SGD; S000071; YEL045C.

CC KW Hypothetical protein; ATP-binding; Transmembrane.

CC NP_BIND 15 22 ATP (POTENTIAL).

RESULT 23

PSAH_HORVU STANDARD; PRT; 143 AA.

AC ID PSAH_HORVU P20143;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Photosystem I reaction center subunit VI, chloroplast precursor
 DE (PSI-H) (light-harvesting complex I 11 kDa protein).
 GN PSB-H.
 OS *Hordeum vulgare* (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NEBI_TAXID=4513;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=8932536; PUBMED=2666162;
 RA Okteles J.S., Scheller H.V., Jeppen L.B., Moeller B.L.;
 RT "A cDNA clone encoding the precursor for a 10.2 kDa photosystem I
 polypeptide of barley";
 RL PDB; Iett, 250:575-579;1989.
 CC -!- FUNCTION: POSSIBLE ROLE COULD BE THE DOCKING OF THE LHC I ANTENNA
 CC COMPLEX TO THE CORE COMPLEX.
 CC -!- SIMILARITY: BELONGS TO THE PSB-H FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X16092; CAA34218_1; -.
 DR PIR; S05012.
 DR InterPro; IPR004928; PSI_PsbH.
 DR PRO; PR0124; PSI_PsbH_1.
 KW Photosynthesis; Photosystem I; Chloroplast; transit peptide;
 KW Transmembrane.
 FT CHLOROPLAST. PHOTOSYSTEM I REACTION CENTER SUBUNIT VI.
 FT CHAIN 49 143 POTENTIAL.
 FT TRANSMEM 100 120 MW; 16D72FF36C9D46C2 CRC64;
 SQ 143 AA;
 Query Match 100.0%; Score 21; DB 1; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 |||||
 Db 93 AAPF 96
 |||||
 RESULT 24
 PSB-H_SP10L STANDARD; PRM; 144 AA.
 ID PSB-H_SP10L
 AC P22179;
 DT 01-AUG-1991 (Rel. 19, created)
 DT 01-AUG-1991 (Rel. 19, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Photosystem I reaction center subunit VI, chloroplast precursor
 DE (PSB-H) (light-harvesting complex I 11 kDa protein).
 GN
 OS Brassica rapa (Turnip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spelmatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Brassica.
 OX NEBI_TAXID=51350;
 RN [1]
 RP
 RA SON D.; JO J.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DDJB databases.
 CC -!- FUNCTION: POSSIBLE ROLE COULD BE THE DOCKING OF THE LHC I ANTENNA
 CC COMPLEX TO THE CORE COMPLEX.
 CC -!- SIMILARITY: BELONGS TO THE PSB-H FAMILY.
 CC
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 CC
 DR EMBL; U92204; AAB51159_1; -.
 DR InterPro; IPR004928; PSI_PsbH.
 DR PRO; PR0124; PSI_PsbH_1.
 KW Photosynthesis; Photosystem I; Chloroplast; transit peptide;
 KW Transmembrane.
 FT CHAIN 51 145 PHOTOSYSTEM I REACTION CENTER SUBUNIT VI.
 FT TRANSMEM 102 122 POTENTIAL.
 SQ SEQUENCE 145 AA;
 Query Match 100.0%; Score 21; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AAPE 4	Db	1111
Qy	1 AAPE 4	Db	94 AAPE 97
RESULT 26		RESULT 27	
PSHL_ARATH	STANDARD;	PSH2_ARATH	STANDARD;
ID PSHL_ARATH	PRT; 145 AA.	ID PSH2_ARATH	PRT; 145 AA.
AC Q9SUT7; Q42295;		AC Q9SUT6;	
DT 15-JUN-2002 (Rel. 41, created)		DT 15-JUN-2002 (Rel. 41, created)	
DT 15-JUN-2002 (Rel. 41, Last sequence update)		DT 15-JUN-2002 (Rel. 41, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)		DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE Photosystem I reaction center subunit VI-1, chloroplast precursor (PST-H1).		DE Photosystem I reaction center subunit VI-2, chloroplast precursor (PST-H1).	
DE PSAH1 OR AT3G1614 OR MSU.1.18.		DE PSAH2 OR AT1G52230 OR F9T5.11.	
GN Arabidopsis thaliana (Mouse-ear cress).		GN Arabidopsis thaliana (Mouse-ear cress).	
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
OC OC		OC OC	
OX OX		OX OX	
RA NCBI_TAXID=3702;		RA NCBI_TAXID=3702;	
RN [1]		RN [1]	
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Columbia;		RC STRAIN=cv. Columbia;	
RA Legen J., Misra S., Hermann R.G., Altschmied L.;		RA Legen J., Misra S., Hermann R.G., Altschmied L.;	
RT "Sequences and map position of 31 Arabidopsis thaliana cDNAs encoding organellar polypeptides";		RT "Sequences and map position of 31 Arabidopsis thaliana cDNAs encoding organellar polypeptides";	
RT Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.		RT Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	
RL [2]		RL [2]	
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Columbia;		RC STRAIN=cv. Columbia;	
RA MEDLINE=21016719; PubMed=11130712;		RA Theologis A., Ecker J.R., Palm C.J., Feddersiel N.A., Kaul S., White O., Alonso J., Aliafi H., Araujo R., Bowman C.L., Brooks S.Y., Buelher E., Chan Q., Chen R.F., Chin C.W., Chung M.K., Conn L., Conway T.H., Creasy T.H., Dewar K., Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Ropson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenskaya T., Kurtz D.B., Kwon A., Lam B., Landin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Mazzali A., Miltscaler J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.-K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Sinn P., Southwick A.M., Sun H., Tallon L.J., Tambung G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana";	
CC Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.		CC Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.	
CC -!- FUNCTION: POSSIBLE ROLE COULD BE THE DOCKING OF THE LHC 1 ANTENNA COMPLEX TO THE CORE COMPLEX.		CC -!- FUNCTION: POSSIBLE ROLE COULD BE THE DOCKING OF THE LHC 1 ANTENNA COMPLEX TO THE CORE COMPLEX.	
CC -!- SIMILARITY: BELONGS TO THE PEAH FAMILY.		CC -!- SIMILARITY: BELONGS TO THE PEAH FAMILY.	
CC STRAIN=cv. Columbia;		CC STRAIN=cv. Columbia;	
RA Bardet C., Dabos P., Tremousaygue D., Lescure B.;		RA Bardet C., Dabos P., Tremousaygue D., Lescure B.;	
RA Submitter (JUL-1994) to the EMBL/GenBank/DDBJ databases.		RA Submitter (JUL-1994) to the EMBL/GenBank/DDBJ databases.	
CC -!- FUNCTION: POSSIBLE ROLE COULD BE THE DOCKING OF THE LHC 1 ANTENNA COMPLEX TO THE CORE COMPLEX.		CC -!- FUNCTION: POSSIBLE ROLE COULD BE THE DOCKING OF THE LHC 1 ANTENNA COMPLEX TO THE CORE COMPLEX.	
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CC -----		CC -----	
DR EMBL; ARB1247; BAB2600.1; -.		DR EMBL; ARB1247; BAB2600.1; -.	
DR 25381; CAAB4571.1; -.		DR 25381; CAAB4571.1; -.	
DR InterPro; IPR004928; PSI_Peah.		DR InterPro; IPR004928; PSI_Peah.	
DR Pfam; PF03244; PSI_Peah; 2.		DR Pfam; PF03244; PSI_Peah; 2.	
KW Photosynthesis; Photosystem I; Chloroplast; Transit peptide; Transmembrane.		KW Photosynthesis; Photosystem I; Chloroplast; Transit peptide; Transmembrane.	
FT TRANSIT 1 50 CHLOROPLAST (BY SIMILARITY).		FT TRANSIT 1 50 CHLOROPLAST (POTENTIAL).	
FT CHAIN 51 145 PHOTOSYSTEM I REACTION CENTER SUBUNIT VI-1.		FT CHAIN 51 145 PHOTOSYSTEM I REACTION CENTER SUBUNIT VI-1.	
FT CONFLICT 112 127 GSLLIVYVATSTGVVL -> RLFGYLORYYRRSS (IN REF. 3).		FT CONFLICT 112 127 GSLLIVYVATSTGVVL -> RLFGYLORYYRRSS (IN REF. 3).	
SQ SEQUENCE 145 AA; 15216 MW; 4BF2A5JDC17072E CRC64;		SQ SEQUENCE 145 AA; 15273 MW; E2884F419908CD30 CRC64;	
Query Match 100.0%; Score 21; DB 1; Length 145;		Query Match 100.0%; Score 21; DB 1; Length 145;	
Best Local Similarity 100.0%; Pred. No. 1 9e+02;		Best Local Similarity 100.0%; Pred. No. 1 9e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 AAPE 4		Qy 1 AAPE 4	

CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-phospho-D-glycerate + 2-phosphoglycolate.
 CC !- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC !- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC !- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.

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DR EMBL; D14001; BAA03103.1;
 DR InterPro; IPR00894; RUBISCO_small.
 DR Pfam; PF00101; RUBISCO_small; 1.
 DR PRINTS; PR00132; RUBISCO_SMALL.
 DR PRODOM; PD000290; RUBISCO_small; 1.
 DR KW Photosynthesis; Carbon dioxide fixation; Photorespiration;
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide.
 FT TRANSIT 1 57 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 58 181 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL.
 FT CHAIN 181 AA; 20359 MW; CEBF3A4E81F6075 CRC64;

SEQUENCE 181 AA; 20359 MW; CEBF3A4E81F6075 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 181;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 |||||
 Db 23 AAPF 26

RESULT 31

PAD_ARCFU STANDARD; PRT; 182 AA.

ID O29054; DT 16-OCT-2001 (Rel. 40, created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DE Probable aromatic acid decarboxylase (EC 4.1.1.-).
 GN AF2124.
 OS Archaeoglobus fulgidus.
 OC Archaeobacteraeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=NC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=939475;
 RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirchner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weilman J.F., McDonald L., Utterback T.,
 RA Sodt M.D., Spriggs T., Arriach P., Kaine B.P., Sykes S.M.,
 RA Sodt P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.",
 RL Nature 390:364-370(1997).
 CC !- SIMILARITY: BELONGS TO THE POLYPHENYL-P-HYDROXYBENZOATE / PHENYLACRYLIC ACID DECARBOXYLASES FAMILY.

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DR EMBL; AE001020; AAB90031.1;
 DR TIGR; AF1214;
 DR InterPro; IPR003382; Flavoprotein.
 DR InterPro; IPR004507; UbIIX.
 DR Pfam; PF02441; Flavoprotein; 1.
 DR TIGRFAMS; TIGR00421; ubIx; 1.
 KW Hypothetical protein; Lyase; Decarboxylase; Complete proteome.
 SQ SEQUENCE 182 AA; 19968 MW; 65f015f8d130768 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 182;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 |||||
 Db 67 AAPF 70

RESULT 32

P152_METTH STANDARD; PRT; 186 AA.

ID P152_METTH DT 02655; DE 16-OCT-2001 (Rel. 40, created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DE Protein MHI152.
 GN MHI152.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchabota; Methanobacteria; Methanobacteriales;
 OC Metianobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cock R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu R.,
 RA Spadafora R., Vicere R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwanji N., Caruso A., Bush D., Saffer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum delta: functional analysis and comparative genomics.",
 RT J. Bacteriol. 179:7135-7155(1997).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=20472232; PubMed=11017201;
 RA Christendat D., Yee A., Dharamsi A., Kluger Y., Savchenko A.,
 RA Cort J.R., Booth V., Mackereth C.D., Saridakis V., Ekiel I.,
 RA Kozlov G., Maxwell K.L., Wu N., McIntosh L.P., Gehring K.,
 RA Kennedy M.A., Davidson A.R., Pai E.F., Gerstein M., Edwards A.M.,
 RA Arrowsmith C.H.,
 RT "Structural proteomics of an archaeon.",
 RL Natl. Struct. Biol. 7:903-909(2000).
 CC !- COFACTOR: FMN
 CC !- SUBUNIT: HOMODIMER
 CC !- SIMILARITY: BELONGS TO THE FLAVOREDOXIN FAMILY.

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DR EMBL; AE000803; AAB84658.1; - .
 DR PDB; 1EJE; 11-OCT-00.

DR InterPro; IPR02563; Flavin_Reduct.

DR Pfam; PF01613; Flavin_Reduct; 1.

KW Flavoprotein; FMN; 3D-structure; Complete proteome.

SQ 186 AA; 2023 MW; 69978C6b923A89 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 186;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAPF 4

Db 37 AAPF 40

RESULT 33

APR_TREPA

ID APR_TREPA

STANDARD; PRT; 190 AA.

AC 084 001;

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).

GN APR OR TP1039.

OS Treponema pallidum.

OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI_TaxID=150;

RN [1]

RP Sequence FROM N.A.

RC STRAIN=NICHOLS;

RX MEDLINE=98332770; PubMed=9665876;

RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwynn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Utterback T., McDonald L., Howell J.K., Chidambaram M., Fujii C., Garland S., R.A. Khaliak H., Richardson D., Utterback T., R.A. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C., "Complete genome sequence of Treponema pallidum, the syphilis spirochete,"; Science 281:375-388(1998).

CC -I- FUNCTION: CATALYZES A SALVAGE REACTION RESULTING IN THE FORMATION OF AMP THAT IS ENERGETICALLY LESS COSTLY THAN DE NOVO SYNTHESIS.

CC -I- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5'-phospho-alpha-D-ribose 1-diphosphate.

CC -I- PATHWAY: Purine salvage.

CC -I- SUBUNIT: HOMODIMER (By SIMILARITY).

CC -I- SUBCELLULAR LOCATION: Cytosolic.

CC -I- SIMILARITY BELONGS TO THE FURANPYRIMIDINE PHOSPHORYBOSYLTRANSFERASE FAMILY.

CC -----

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CC -----

CC DR EMBL; MI2021; AAA23359_1; -.

CC DR YHBP68; YHBP68; YHBP68; YHBP68;

CC SQ SEQUENCE 195 AA; 20293 MW; 460727BD81BF60B CRC64;

Query Match 100.0%; Score 21; DB 1; Length 195;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAPF 4

Db 153 AAPF 156

RESULT 35

ACD2_CLOAB

ID ACD2_CLOAB

STANDARD; PRT; 200 AA.

AC 097DOI;

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE putative acyl carrier protein phosphodiesterase 2 (EC 3.1.4.14) (ACP phosphodiesterase 2).

GN CAC3421

OS Clostridium acetobutylicum

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OX Clostridium

RN NCBI_TaxID=1498;

RN [1]

RP Sequence FROM N.A.

RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

RX MEDLINE=21359325; PubMed=11466386;

RA Neeliling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J.J., Oiu D., Hitti J., Wolf Y.I., Daly M.J., Taturov R.L., Sabaté F., Doucette-Stamm L., Soucaille P., Bennett G.N., Koonin E.V., Smith D.R.;

RA "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum."

RT J. Bacteriol. 183:4823-4838(2001).

RL -----

CC -I- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity).

CC -----

CC -I- CATALYTIC ACTIVITY: Holo-fatty-carrier protein] + H₂O = 4-

QY 1 AAPF 4

|||

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CC EMBL; 299259; CAB16376_1; -.

DR InterPro; IPR01047; Ribosomal_S8B.

DR Pfam; PF01201; Ribosomal_S8e; 1.

DR PRODOM; PD005658; Ribosomal_S8E; 1..

DR TIGRFAMS; TIGR00307; S8e; 1.

DR PROSITE; PS01193; RIBOSOMAL_S8E; 1..

KW Ribosomal protein; Multigene family.

SEQUENCE 200 AA; 22593 MW; F03C815C75E35E3B CRC64;

		Score 21;	DB 1;	Length 200;
OY	1 AAPF 4	Best Local Similarity 100.0%	Pred. No. 2 Set02;	Mismatches 0;
CC		Conservative	Indels 0;	Gaps 0;
Db	106 AAPF 109			
RESULT	37			
RSB8_SCOPO				
ID	RSB8_SCOPO	STANDARD;	PRT;	200 AA.
AC	Q9P7B2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	40S ribosomal protein S8-B.			
GN	RPS8B OR SPAC521.05.			
OS	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomyces pombe (Fission yeast).			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.			
OX	NCBI_TAXID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=21848401; PubMed=11859360;			
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourouss J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks M., Brown D., Brown C., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Oddil C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutledge K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Tayor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodford J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieder M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrbach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedder H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaike V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bentito J., Dominguez A., Revuelta J., Moreno S., Armstrong J., Forbush S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussey R., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).			
RL	Nature 415:871-880(2002).			
CC	- - MISCELLANEOUS: THERE ARE TWO GENES FOR S8 IN S.POMBE.			
CC	- - SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.			
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CC

DR EMBL; ALI63481; CAB8649.1; -.

DR InterPro; IPR001047; Ribosomal_S8E.

DR Pfam; PF0201; Ribosomal_S8E; 1.

DR Prodom; PDO005658; Ribosomal_S8E; 1.

DR TIGRFAMS; TIGR0307; S8E; 1.

DR PROSITE; PS01193; RIBOSOMAL_S8E; 1.

KW Ribosomal protein; Ribosomal_S8E; 1.

SQ Sequence 200 AA; 2264 MP; 282A4D930033B6 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;

Db 16 AAPF 4
 Db 106 AAPF 109

RESULT 38

YD9_HAEIN STANDARD: PRT; 202 AA.

ID YD9_HAEIN STANDARD: PRT; 202 AA.

AC P44175; (Rel. 32, created)

DT 01-NOV-1995 (Rel. 32, last sequence update)

DT 01-NOV-1995 (Rel. 32, last annotation update)

DT 15-JUN-2002 (Rel. 41, last annotation update)

DE Hypothetical protein H11399.

GN H11399.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

OC Hemophilus.

OX NCBI_Taxid=727;

[1]

RP SEQUENCE FROM N.A.

RC MDDLINE=9535030 / ATCC 51907;

RX MDDLINE=9535030; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Walzschmidt J.P., Phillips C.A., Spriggs T., Heidelberg E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Sudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geesey G.E., Nierman W.C.,
 RA Graham C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RT "whole-genome random sequencing and assembly of *Haemophilus influenzae*
 RT Rd", Science 269:496-512(1995).
 RL Science 269:496-512(1995).

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CC

DR EMBL; U32820; AAC23051.1; -.

DR TIGR; H11399; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 202 AA; 23238 MW; D55017DAB9D191C4 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;

Db 1 AAPF 4

Db 106 AAPF 109

RESULT 39

YWRF_BACSU STANDARD: PRT; 205 AA.

ID YWRF_BACSU STANDARD: PRT; 205 AA.

AC 005220; (Rel. 40, created)

DT 16-OCT-2001 (Rel. 40, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DT 15-JUN-2002 (Rel. 41, last annotation update)

DE Hypothetical protein ywrF.

GN YWRF.

OS *Bacillus subtilis*.

OC bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_Taxid=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC MDDLINE=9501517; PubMed=9353933;

RA Presecan B., Moszer I., Boursier L., Cruz Ramos H.C., De La Fuente V.,
 RA Hullio M.-F., Lelong C., Schleicher S., Sekowska A., Song B.H.,
 RA Villani G., Kunst F., Danchin A., Glaser P.;
 RT "The *Bacillus subtilis* genome from gerBC (311 degrees) to licR (334
 RT degrees)", Microbiology 143:3313-3328(1997).

RL Microbiology 143:3313-3328(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RX MDDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bartero M.G., Bessieres P., Boilotin A., Borchart S.,
 RA Borriiss R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA BroUILLET S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Cocani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Delizot F., Devine R.M., Dusterhoff A., Ehrlich S.D., Eunmeson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferraci E., Fouger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Gilim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Herault A.,
 RA Hilbert H., Hollsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamoto D., Kasahara S., Klaer Blanchard M., Klein C.,
 RA Kobayashi Y., Koettner P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidoth A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maeli C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parlo V., Pohl T.M., Porteille D., Powalki S., Prescott A.M.,
 RA Presecan B., PuJic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanian E., Schleicht S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Tagagi T., Takahashi H., Takeuchi K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandemboul M., Vannier F., Vassarotti A.,
 RA Vilar A., Wambutt R., Wedler H., Weitzengruber T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yonetani H.F., Zunstra E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT subtilis", Nature 390:249-256(1997).

CC -1-- COFACTOR: FMN (BY SIMILARITY)

CC -1-- SIMILARITY: BELONGS TO THE FLAVOREDOXIN FAMILY

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DR EMBL; Z99122; CAB15625.1; -.

DR HSSP; 026255; 1EJE.
 DR Subtilist; BG12525; ywrf.
 KW Hypothetical protein; Flavoprotein; FMN; Complete proteome.
 SEQUENCE 205 AA; 22584 MW; 28A3A8F5CCC4529F CRC64;

Query Match	Best Local Similarity	Score	DB	Length	Matches
Qy 1 AAPF 4	100.0%	21	1	205	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 41 AAPF 44					

RESULT 40
 YM80_YEAST STANDARD; PRT; 206 AA.
 AC 004019;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Hypothetical 23. kDa protein in ZRC1_FAA4 intergenic region.
 GN YM845W OR YM8408_07.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomyctaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB372;
 RA Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (MAR 1995) to the EMBL/GenBank/DDBJ databases.
 CC -----
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 CC -----
 DR EMBL; ZA8756; CAA8655; 1; -.
 DR SGD; S004859; YM845W.
 KW Hypothetical protein.
 SEQUENCE 206 AA; 23194 MN; 8794E591DAB49C6E CRC64;

Query Match 100.0% Score 21; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 138 AAPF 141

Search completed: December 6, 2002, 13:28:33
 Job time : 6.55556 secs

Om protein - protein search, using sw model

Run on: December 6, 2002, 13:25:09 ; Search time 19.5556 Seconds
 (without alignments)
 42.146 Million cell updates/sec

title:	US-10-033-526-1
Perfect score:	21
Sequence:	1 AAPF 4
Scoring table:	BioSUM62
Gapop:	10.0 , Gapext: 0.5
Searched:	671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters:	671580
Minimum DB seq length: 0	
Maximum DB seq length: 200000000	
Post-processing:	Minimum Match 0%
Maximum Match 100%	
Listing first 45 summaries	
Database :	
SP TREMBL 21; *	
1: sp_archaea;*	
2: sp_bacteria;*	
3: sp_fungi;*	
4: sp_human;*	
5: sp_invertebrate;*	
6: sp_mammal;*	
7: sp_mhc;*	
8: sp_organelle;*	
9: sp_pragae;*	
10: sp_plant;*	
11: sp_rabbit;*	
12: sp_virus;*	
13: sp_vertebrate;*	
14: sp_uniclassified;*	
15: sp_rvirus;*	
16: sp_bacteriav;*	
17: sp_archeap;*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	21	10.0 .0	41	10 Q9SF1	Q9SF1 brassica napus
2	21	10.0 .0	45	2 P7057	P7057 bacillus st
3	21	10.0 .0	47	6 Q9TRE9	Q9TRE9 sus scrofa
4	21	10.0 .0	47	6 Q9TX9	Q9TX9 bos taurus
5	21	10.0 .0	50	16 Q9CCK3	Q9CCK3 brucella me
6	21	10.0 .0	51	4 Q9Y5N3	Q9Y5N3 homo sapien
7	21	10.0 .0	57	10 Q9MNL1	Q9MNL1 triticum ae
8	21	10.0 .0	59	16 Q9ADG2	Q9ADG2 streptomyce
9	21	10.0 .0	69	10 Q84B7	Q84B7 ambystegiu
10	21	10.0 .0	70	12 Q9PWS4	Q9PWS4 hepatitis c
11	21	10.0 .0	72	7 Q9MWJ2	Q9MWJ2 certithidea o
12	21	10.0 .0	73	5 Q26512	Q26512 schistosoma
13	21	10.0 .0	75	16 Q8PBW5	Q8PBW5 agrobacteri
14	21	10.0 .0	76	13 Q9DPN1	Q9DPN1 gillitchtys
15	21	10.0 .0	77	16 Q8167	Q8167 rhizobium l
16	21	10.0 .0	78	10 Q85493	Q85493 amblystegiu

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	41 AA.
09SF1	09SF1			
AC	09SF1;			
DT	01-MAY-2000 (TREMBLrel. 13. Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13. Last annotation update)			
DE	Napin short chain S4-CALMODULIN antagonist/calmodulin-dependent protein kinase substrate.			
OS	Brassica napus (rape)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyt; Magnoliophyt; eudicotyledons; core eudicots; Rosidae; euclads II; Brassicales; Brassicaceae; Brassica.			
OX	NCBI_TAXID=3708;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE:96283790; PubMed=8679670;			
RA	Neuman G.M., Condon R., Thomas T., Polya G.M.;			
RT	"Purification and sequencing of multiple forms of Brassica napus seed napin small chains that are calmodulin antagonists and substrates for plant calcium-dependent protein kinase";			
RT	Biochim Biophys Acta 1205:23-31(1996).			
RL	SEQUENCE 41 AA; 462 MW; BBC6738503380553 CRC64;			
Query	Match	100.0 %;	Score 21;	DB 10;
Best	Local Similarity	100.0 %;	Length 41;	Matches 4;
Matches	Conservative	0;	Mismatches 0;	Indels 0;
QY	1 AAPF 4			Gaps 0;
Db	2 AAPF 5			

RESULT 2

ID	PRELIMINARY;	PRT;	45 AA.
P7057			
AC	P7057;		
DT	01-FEB-1997 (TREMBLrel. 02. Created)		
DT	01-FEB-1997 (TREMBLrel. 02. Last sequence update)		

DT 01-NOV-1998 (TREMBREL. 08, Last annotation update)
DE Alpha-amylase precursor (Fragment).
GN AMYS.
OS Bacillus stearothermophilus group; Bacillales;
OC Geobacillus.
NCBI_TAXID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91024999; PubMed=2265757;
RA Jorgensen P.L., Hansen C.K., Poulsen G.B., Diderichsen B.;
RT "In vivo genetic engineering: homologous recombination as a tool for
plasmid construction.", Gene 96:37-41(1990).
RL EMBL: M62638; AAA2242.1; -.
DR
KW SIGNAL.
FT CHAIN 1 34 POTENTIAL.
FT NON_TER 35 >45 POTENTIAL.
FT SEQUENCE 45 AA; 5119 MW; 192F623EA13E6DA6 CRC64;
SQ Best Local Similarity 100.0%; Score 21; DB 2; Length 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
Db 35 AAPF 38

RESULT 3
Q9TRB9 PRELIMINARY; PRT; 47 AA.
ID Q9TRB9
AC 08YCK3
DT 01-MAY-2000 (TREMBREL. 13, Created)
DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)
DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)
DE Cytochrome c oxidase subunit VIIC (Fragment).
OS Sus scrofa (Pig).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TAXID=9823;
SEQUENCE, MEDLINE=93384597; PubMed=8396926;
RA Sillard R., Jornvall H., Mutt V.;
RT "Characterization of porcine intestinal cytochrome c oxidase subunit VIIC, purified by affinity chromatography";
RL Biochem. Biophys. Res. Commun. 195:746-750(1993).
DR InterPro; IPR04242; COX7C.
DR Pfam; PF02935; COX7C; 1.
SQ SEQUENCE 47 AA; 5457 MW; E11E89CFBC18B5D7 CRC64;

Query Match 100.0%; Score 21; DB 6; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
Db 34 AAPF 37

RESULT 4
Q9TQX9 PRELIMINARY; PRT; 47 AA.
ID Q9TQX9
AC 08YCK3
DT 01-MAY-2000 (TREMBREL. 13, Created)
DT 01-JUN-2002 (TREMBREL. 21, Last annotation update)
DE Desoxyribonuclease F (Fragment).
OS Bos taurus (Bovine).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Query Match 100.0%; Score 21; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
Db 44 AAPF 47

RESULT 5
Q8YCK3 PRELIMINARY; PRT; 50 AA.
ID Q8YCK3
AC 08YCK3
DT 01-MAR-2002 (TREMBREL. 20, Last sequence update)
DT 01-MAR-2002 (TREMBREL. 20, Last annotation update)
DE Hypothetical protein BMPII025.
GN BMPII025.
OS
OC Brueellaceae; Bruecella.
NCBI_TAXID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DeVecchio V.G., Kapatral V., Rekar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidas A., Mujer C., Los T.,
RA Jablonski L., Larsen N., D'Souza M., Bernal M., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
Bruecella melitensis. ";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
DR EMBL; AR00968; AAL53167.1; -.
KW Hypothetical Protein; Complete Proteome.
SQ SEQUENCE 50 AA; 5208 MW; 8DE59A82243ERC17 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
Db 44 AAPF 47

RESULT 6
Q9Y5N3 PRELIMINARY; PRT; 51 AA.
ID Q9Y5N3
AC 08Y5N3
DT 01-Nov-1999 (TREMBREL. 12, Created)
DT 01-Nov-1999 (TREMBREL. 12, Last sequence update)
DT 01-Mar-2002 (TREMBREL. 20, Last annotation update)
DE Lecithin-cholesterol acyltransferase (EC 2.3.1.43) (Fragment).
GN LCAT.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA OI J.-P., Saku K., Liao Y.-L., Jinji S., Jin W.-J., Arakawa K.;
 RA "A novel missense variant Thr137 in the lecithin cholesterol
 RT acyltransferase (LCAT) gene associated with fish eye disease.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF10503; AAD28434; 1; -.
 KW Acyltransferase; transferase.
 FT VARIANT 37
 FT NON_TER 51
 SQ SEQUENCE 51 AA; 566 MW; EB511439A5129965 CRC64;
 Query Match 100.0%; Score 21; DB 4; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 |||||
 Db 22 AAPF 25

RESULT 7

Q9M7N1 ID OM87N1 PRELIMINARY; PRT; 57 AA.
 AC Q9M7N1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MAP1 attachment factor 1 (Fragment).
 GN OS triticum aestivum (Wheat).
 OC Embryophyta; Viridiplanteae; Streptophyta; Tracheophyta;
 OC Sporophytophyta; Magnoliophyta; Liliopsida; Poales; Pooidae;
 OC Triaceae; Triticeae;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99A1888; PubMed=10882011;
 RA Gindullis F., Peffer N.J., Meier I.;
 RT "MAP1, a novel plant protein interacting with matrix attachment region
 binding protein MAP1 is located at the nuclear envelope.";
 RL Plant Cell 11:1755-1768(1999).
 DR EMBL; AF118118; AAF03662.1; -.
 FT NON_TER 57
 SQ SEQUENCE 57 AA; 6085 MW; E35FF7AC99E250F78 CRC64;
 Query Match 100.0%; Score 21; DB 10; Length 57;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 |||||
 Db 17 AAPF 20

RESULT 8

Q9ADG2 ID Q9ADG2 PRELIMINARY; PRT; 59 AA.
 AC Q9ADG2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein SC06101.
 GN SC06101 or SCBAC1A6_25C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2); / M145;

RESULT 9

Q834B7 ID Q8S4B7 PRELIMINARY; PRT; 69 AA.
 AC Q8S4B7;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Adenosine kinase (Fragment).
 OS Ambystegium humile.
 OC Embryophyta; Viridiplanteae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Ambystegium.
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AH2C;
 RA Vanderpoorten A., Shaw A.J., Cox C.J.;
 RT "reconciled gene trees, molecular evolution, and species relationships
 in Ambystegium",
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF465020; AAL96411.1; -.
 KW Kinase.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 69 AA; 7793 MW; 81C1C22B4EAC30AC CRC64;
 Query Match 100.0%; Score 21; DB 10; Length 69;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 |||||
 Db 40 AAPF 43

RESULT 10

Q9WMS4 ID Q9WMS4 PRELIMINARY; PRT; 70 AA.
 AC Q9WMS4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 19, Last annotation update)
 DE Genome polyprotein [Contains: envelope glycoprotein E1 (GP32), (GP35)]
 DE (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Herpesvirus.
 OX NCBI_TaxID=1103;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=VE3216;
 RX MEDLINE=20394384; PubMed=10935993;
 RA Argentino C., Dettori S., Villano U., Guadagnino V., Infantolino D.,
 RA Dentico P., Coppola R.C., Ricicetta M.;
 RT "Molecular characterisation of HCV genotype 4 isolates circulating in
 RT Italy.";
 RL J. Med. Virol. 62:84-90(2000);
 CC -1 SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: AJ250216; CAC16883; 1; -.
 DR InterPro: IPR002519; HCV_env.
 Pfam: PF01539, HCV_env; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 NON_TER 1 1
 NON_TER 70 70
 FT SEQUENCE 70 AA; 7698 MW; BD360B781C3BF80F CRC64;
 Query Match 100.0%; Score 21; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPF 4
 Db 54 AAPF 57

RESULT 11
 09MWJ2 PRELIMINARY; PRT; 72 AA.
 ID 09MWJ2; AC 09MWJ2;
 DT 01-OCT-2000 (TREMBUREL. 15, Created)
 DT 01-OCT-2000 (TREMBUREL. 15, Last sequence update)
 DE MHC class II B antigen (Fragment).
 OS Certhidea olivacea
 OC Bukiyotter; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauia; Aves; Neognathae; Passeriformes; Passeroidea;
 OC Fringillidae; Emberizinae; Certhidea;
 OX NCBI_TAXID=48880;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=D104RF.
 RA Sato A., Figuerola F., Mayer W.E., Grant P.R., Klein J.;
 RT "MHC class II genes of Darwin's finches: divergence by point mutations
 and reciprocal recombination.";
 RT (In) Kaschera M. (eds.);
 RL Major histocompatibility complex:
 RL evolution, structure, and function, pp.518-541, Springer-Verlag,
 RL Tokyo (2000).
 DR EMBL: AEI64163; AAPF36228; 1; -.
 DR InterPro: IPR00353; MHC_II_beta.
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR ProDom: PD000328; MHC_II_beta; 1.
 FT NON_TER 1 1
 FT NON_TER 72 72
 SQ SEQUENCE 72 AA; 8760 MW; F62FF27A7B4A672B CRC64;

Query Match 100.0%; Score 21; DB 7; Length 72;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 Db 63 AAPF 66

RESULT 12
 Q26512 PRELIMINARY; PRT; 73 AA.
 ID Q26512; AC 026512;
 DT 01-NOV-1996 (TREMBUREL. 01, Created)
 DT 01-NOV-1996 (TREMBUREL. 01, Last sequence update)

RP 01-TUN-2002 (TREMBUREL. 21, Last annotation update)
 DE Triosephosphate isomerase (Fragment).
 DE Schistosoma japonicum (Blood fluke).
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OC NCBI_TAXID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHINESE AND PHILIPPINE STRAINS;
 RX MEDLINE=97101875; PubMed=8946393;
 RA Hooper C.W., Brindley P.J.;
 RT "Cloning and characterisation of strain-specific transcripts encoding
 triosephosphate isomerase, a candidate vaccine antigen from
 Schistosoma japonicum.",
 RL Mol. Biochem. Parasitol. 82:265-269(1996).
 DR EMBL: U57557; AAC47394; 1; -.
 DR HSSP; P00940; 1TM.
 DR InterPro: IPR00652; Triophos_ismase.
 DR Pfam: PF00121; TIM; 1.
 DR ProDom: PD001005; Triophos_ismase; 1.
 DR KW Isomerase.
 FT NON_TER 1 1
 FT SEQUENCE 73 AA; 7982 MW; 6B10DB35955F5A33 CRC64;

RESULT 13
 Q8UEW5 PRELIMINARY; PRT; 75 AA.
 ID Q8UEW5; AC 08UEW5;
 DT 01-JUN-2002 (TREMBUREL. 21, Created)
 DT 01-JUN-2002 (TREMBUREL. 21, Last sequence update)
 DE Hypothetical protein AtU1639.
 GN ATU1639.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TAXID=176299;
 RN [1]
 SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21605550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendening J., Deatherage G., Gillet W., Grant C.,
 RA Kuykavim T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kraspen W., Perry M.,
 RA Gordon-Kamm T., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58";
 RL Science 294:2317-2323(2001).
 DR EMBL: AE009121; AA14260; 1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 75 AA; 8397 MW; B3B9DD20CE8EE82DD CRC64;

Query Match 100.0%; Score 21; DB 16; Length 75;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 Db 1111

Db	50 AAPF 53	QY	1 AAPF 4
RESULT 14		PRELIMINARY;	PRT; 76 AA.
ID Q9DFN9			
AC Q9DFN9;			
DT 01-MAR-2001	(TREMBLrel. 16, Created)		
DT 01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT 01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE Formyl-tetrahydrofolate dehydrogenase (Fragment).			
OS Gillichthys mirabilis (long-jawed mudsucker).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Neoteleostei; Actinopterygii; Neopterygii; Teleostei; Butteleosteal; Neoteleosteal; Gobiidae; Gillichthys.			
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidae; OX NCBI_TaxID:8222;			
RN [1]			
RN RSEQUENCE FROM N.A.			
RC TISSUE=LIVER;			
RX MEDLINE:21117151; PUBMED=11172064;			
RA Graczyk A.Y., Troll J.V., Somero G.N.;			
RT "Hypoxia-induced gene expression profiling in the euryoxic fish Gillichthys mirabilis".			
RL Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).			
DR EMBL: AP266196; AAG133161.1; -.			
DR HSSP: P05031; ICM3.			
DR InterPro: IPR002086; Aldehyde_dehydr.			
DR Pfam: PF00171; aldedh; 1.			
FT NON_TER 1			
SQ SEQUENCE 76 AA; 8189 MW; 787505071A1ACFA3 CRC64;			
Query Match 100.0%; Score 21; DB 13; Length 76; Best Local Similarity 100.0%; Pred. No. 5.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 AAPF 4	QY 1 AAPF 4	QY 1 AAPF 4
Db 43 AAPF 46			
RESULT 15			
ID Q9B167	PRELIMINARY;	PRT; 77 AA.	
AC Q9B167;			
DT 01-OCT-2001	(TREMBLrel. 18, Created)		
DT 01-OCT-2001	(TREMBLrel. 18, Last sequence update)		
DE Hypothetical protein msrl158.			
GN MSRL158.			
OS Rhizobium loti (Mesorhizobium loti).			
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; OC Phyllobacteriaceae; Mesorhizobium.			
OC OX NCBI_TaxID:381;			
RN [1]			
RN RSEQUENCE FROM N.A.			
RC STRAIN=MAFF03039;			
RX MEDLINE:21082930; PubMed=11214968;			
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S., Matsuno M., Matsunaga A., Idezawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Matsunaga S., Nakazaki N., Shimpo S., Sugimoto M., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Sasamoto S., Nakao S., RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti".			
DR DNA Res. 7:331-338(2000); DR EMBL: AP002396; BAB80596.1; -.			
KW Hypothetical protein; Complete proteome.			
SQ SEQUENCE 77 AA; 8189 MW; 8A2BF074E4C16806 CRC64;			
Query Match 100.0%; Score 21; DB 15; Length 77; Best Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 AAPF 4	QY 1 AAPF 4	QY 1 AAPF 4
Db 54 AAPF 57			
RESULT 16			
ID Q8S493	PRELIMINARY;	PRT; 78 AA.	
AC Q8S493;			
DT 01-JUN-2002	(TREMBLrel. 21, Created)		
DT 01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DE Adenosine kinase (Fragment).			
OS Amblystegium fluvatile.			
DR Adenosine kinase (Fragment).			
DR EMBL: AF46154; AAL96478.1; -.			
DR SEQUENCE 78 AA; 8863 MW; 10D283D076391CBC CRC64;			
Query Match 100.0%; Score 21; DB 10; Length 78; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 AAPF 4	QY 1 AAPF 4	QY 1 AAPF 4
Db 40 AAPF 43			
RESULT 17			
ID Q8S4B6	PRELIMINARY;	PRT; 79 AA.	
AC Q8S4B6;			
DT 01-JUN-2002	(TREMBLrel. 21, Created)		
DT 01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DE Adenosine kinase (Fragment).			
OS Amblystegium humile.			
OC Bryopsida; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; OC NCBI_TaxID=11433;			
OX NCBI_TaxID=11433;			
RN [1]			
RN RSEQUENCE FROM N.A.			
RC STRAIN=AH2;			
RT Vanderpoorten A., Shaw A.J., Cox C.J.;			
RT "Reconciled gene trees, molecular evolution, and species relationships in Amblystegium",			
RL Submitted (JAN 2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL: AF465022; AAL96443.1; -.			
DR Kinase.			
FT NON_TER 1			
SQ SEQUENCE 79 AA; 9026 MW; 9520D283C42A091C CRC64;			
Query Match 100.0%; Score 21; DB 10; Length 79; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 AAPF 4	QY 1 AAPF 4	QY 1 AAPF 4
Db 40 AAPF 43			

RESULT 18
 Q8S4B4 PRELIMINARY; PRT; 79 AA.
 ID 08S4B4; PRELIMINARY; PRT; 79 AA.
 AC 08S4B4;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE Adenosine kinase (Fragment).
 DE Amblystegium varium.
 OS Amblystegium serpens.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
 OC NCBI-Taxid=99400;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=AHPRIMD;
 RC "Reconciled gene trees, molecular evolution, and species relationships
 in Amblystegium.";
 RA Vanderpoorten A., Shaw A.J., Cox C.J.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBBJ databases.
 RL EMBL; AF465024; AAL96445.1; -.
 DR EMBL; AF465032; AAL96453.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9010 MW; 9520D283D07A091C CRC64;
 Query Match 100.0%; Score 21; DB 10; Length 79;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 DB 40 AAPF 43

RESULT 19
 Q8S4B2 PRELIMINARY; PRT; 79 AA.
 ID 08S4B2; PRELIMINARY; PRT; 79 AA.
 AC 08S4B2;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Adenosine kinase (Fragment).
 OS Amblystegium humile.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
 OC NCBI-Taxid=111433;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=ANSBCB;
 RA Vanderpoorten A., Shaw A.J., Cox C.J.;
 RT "Reconciled gene trees, molecular evolution, and species relationships
 in Amblystegium.";
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBBJ databases.
 RL EMBL; AF465026; AAL96447.1; -.
 DR EMBL; AF465026; AAL96447.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9010 MW; 9520D283D07A091C CRC64;
 Query Match 100.0%; Score 21; DB 10; Length 79;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 21
 Q8S499 PRELIMINARY; PRT; 79 AA.
 ID 08S499; PRELIMINARY; PRT; 79 AA.
 AC 08S499;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE Adenosine kinase (Fragment).
 OS Amblystegium varium.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
 OC NCBI-Taxid=111436;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=AVERCB;
 RA Vanderpoorten A., Shaw A.J., Cox C.J.;
 RT "Reconciled gene trees, molecular evolution, and species relationships
 in Amblystegium (Bryopsis).";
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBBJ databases.
 RL EMBL; AF465146; AAL96470.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9010 MW; 9520D283D07A091C CRC64;
 Query Match 100.0%; Score 21; DB 10; Length 79;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPF 4
 DB 40 AAPF 43

RESULT 22
 Q26308 PRELIMINARY; PRT; 79 AA.
 ID 026308; PRELIMINARY; PRT; 79 AA.
 AC 026308;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein MTH206.

OS	Methanobacterium thermoautotrophicum.	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
OC	Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;		DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OC	Methanobacteriaceae; Methanothermobacter.		DE	Hypothetical 8.5 kDa protein.
OX	NCBI_TaxID=187420;		OS	Pseudomonas aeruginosa.
RN	[1]		OG	Plasmid R033.
RP	SEQUENCE FROM N.A.		OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
RC	STRAIN=DELTA H;		OC	Pseudomonas;
RX	MEDLINE=98037514; PubMed=9371463;		OX	NCBI TaxID=287;
RA	Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,		RA	(1)
RA	Alfredson T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,		RA	SEQUENCE FROM N.A.
RA	Harrison D., Huang L., Keagle P., Lum W., Pothier B., Qiu D.,		RC	TRANSPONSON-1S6100DELTA;
RA	Spedatora R., Vicare R., Wang Y., Wierzbski J., Gibson R.,		RX	MEDLINE=89364659; PubMed=2549372;
RA	Jiwani N., Caruso A., Bush D., Safer H., Pavell D., Prabhakar S.,		RA	Whibley W., Arnold W., Bissonette L., Pelletier A., Tanguay A.,
RA	McBougill S., Shimer G., Goyal A., Pietrovski S., Church G.M.,		RA	Roy P.H., Gamboa G.C., Barry G.F., Aubert E., Davies J., Kagan S.A.;
RA	Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.,		RT	"On the evolution of <i>Tn21</i> -like multiresistance transposons: sequence analysis of the gene (<i>acc1</i>) for gentamicin acetyltransferase 3."
RT	"complete genome sequence of <i>Methanobacterium thermoautotrophicum</i> RT IAAC(3)-1, another member of the <i>Tn21</i> -based expression cassette.";		RL	deletah: functional analysis and comparative genomics.,"
RL	deletah: 179;135-715(1997).		DR	ML. Genet. 217:202-205(1989).
DR	EML; AE000807; AAB87412.1; -		DR	EMBL; U12338; AAB6001.1; -
KW	Hypothetical protein; Complete proteome.		KW	Hypothetical protein; Plasmid
SQ	SEQUENCE 79 AA; 9126 MW; F55F5E4B36C31635 CRC64;		SQ	SEQUENCE 81 AA; 8524 MW; 61c21Cf47F15Ec50 CRC64;
Query Match	Score 100.0%; Score 21; DB 17; Length 79;		Query Match	Score 100.0%; Score 21; DB 2; Length 81;
Best Local Similarity	100.0%; Pred. No. 6e+02; Mismatches 0;		Best Local Similarity	100.0%; Pred. No. 6.1e+02; Mismatches 0;
Matches	4; Conservative 0; Indels 0; Gaps 0;		Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAPF 4		QY	1 AAPF 4
Db	36 AAPF 39		Db	49 AAPF 52
RESULT	23		RESULT	25
ID	971LW6	PRELIMINARY; PRM; 80 AA.	ID	P77449
AC	971LW6;		AC	PP9449
DT	01-OCT-2001 (TREMBLrel. 18, Created)		DT	P77449;
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)		DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)		DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE	Predicted metal-binding protein.		DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN	CAC0438		DE	Major histocompatibility complex class II (fragment).
OS	Clostridium acetobutylicum.		GN	DBI.
OC	Bacteria; Firmicutes; Clostridia; Clostridiaceae; Clostridium;		OS	Bos taurus (Bovine)
OC	Clostridiales; Clostridiaceae; Clostridium.		OC	Rukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	NBCL_TAXID=1488;		OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
RN	[1]		OC	Bovidae; Bovidae; Bos.
RP	SEQUENCE FROM N.A.		RN	NCBI_TAXID=9913;
RC	STRAIN=ATCC 824 / DSM 792 / VKM B-1787;		RP	SEQUENCE FROM N.A.
RX	MEDLINE=2139325; PubMed=11466286;		RX	MEDLINE=92165319; PubMed=1537611;
RA	Noelling J., Breton G., Omechenko M.V., Makarova K.S., Zeng Q.,		RA	Sigurdardottir S., Borsch C., Gustafsson K., Andersson L.;
RA	Gibson R., Lee H.M., Dubois J., Qiu D., Hitti Y.I., Wolf Y.I.,		RT	"Gene duplications and sequence polymorphism of bovine class II DQB genes"; Immunogenetics 35:205-213(1992).
RA	Tatusov R.L., Sabatelle-Stamm L., Soucaille P., Daly M.J.,		RT	Immunogenetics 35:205-213(1992).
RA	Bennett G.N., Koonin E.V., Smith D.R.,		RL	[2]
RT	"Genome sequencing and comparative analysis of the solvent producing bacterium Clostridium acetobutylicum";		RL	SEQUENCE FROM N.A.
RL	J. Bacteriol. 183:4823-4838(2001).		RA	Mikko S.;
DR	DR		RL	Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
KW	Complete proteome.		DR	EMBL; U7793; AAB33395.1; -; InterPro; IPR000357; MHC_II_beta.
SQ	SEQUENCE 80 AA; 9080 MW; 9C900BD213AC22BB CRC64;		DR	PFam; PF00499; MHC_II_beta; 1; ProDom; PD000348; MHC_II_beta; 1.
Query Match	Score 100.0%; Score 21; DB 16; Length 80;		FT	Non_TER; Glycoprotein; MHC_II_beta; 1; Transmembrane.
Best Local Similarity	100.0%; Pred. No. 6e+02; Mismatches 0;		FT	SEQUENCE 81 AA; 9727 MW; D8F1F1663F4187DD CRC64;
Matches	4; Conservative 0; Indels 0; Gaps 0;		FT	Query Match
QY	1 AAPF 4		FT	Best Local Similarity 100.0%; Pred. No. 6.1e+02; Mismatches 0; Indels 0; Gaps 0;
			QY	1 AAPF 4
Db	63 AAPF 66		Db	78 AAPF 81.
RESULT	24			
Q51347	PRELIMINARY; PRM; 81 AA.			
ID	051347			
AC	051347;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			

RESULT 26
P79450 PRELIMINARY; PRT; 81 AA.
ID P79450
AC DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Major histocompatibility complex class II (Fragment).
GN QBLI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buteraria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OCC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN {1}
RP SEQUENCE FROM N.A.
RX MEDLINE=92165349; PubMed=1537611;
RA Sigurdardottir S., Borsig C., Gustafsson K., Andersson L.;
RT "Gene duplications and sequence polymorphism of bovine class II DQB
genes"; RQ
RL Immunogenetics 35:205-213(1992).
RN {2}
RP SEQUENCE FROM N.A.
RA Mikko S.; Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U77794; AAB33951; -.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR Prodom: P000028; MHC_II_beta; 1.
KW Glycoprotein; MHC_II; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 81 AA; 9808 MW; 7BDFA930A6FEA1B6 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPF 4
Db 7B AAPF 81

RESULT 27
P9DKP9 PRELIMINARY; PRT; 83 AA.
ID P9DKP9
AC DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Mutant polymerase (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN {1}
RP SEQUENCE FROM N.A.
RA DONG J., Cheng J., Wang Q., Shi S., Zhang J., Xia X., Si C.;
RT "HBV quasi-species: RT region and S gene mutant";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF329860; AF448741; 1.
InterPro: IPR01462; DNAPOL viral_C.
DR Pfam: PF00336; DNA_pol_viral_C; 1.
DR Prodom: PD000814; DNAPOL_viral_C; 1.
FT NON_TER 1
SQ SEQUENCE 83 AA; 9409 MW; 48C125F9A0657A13 CRC64;

Query Match 100.0%; Score 21; DB 12; Length 83;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPF 4

RESULT 28
P9FSP9 PRELIMINARY; PRT; 86 AA.
ID P9FSP9
AC DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein ECS2213.
GN EC2213.
OS Escherichia coli 0157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN {1}
RP SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11288796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Onitsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001);
DR EMBL: AP002557; BAB35636.1; -.
KW Hypothetical protein.
SQ SEQUENCE 86 AA; 9659 MW; B034A45AFCCF137F CRC64;

Query Match 100.0%; Score 21; DB 16; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPF 4
Db 26 AAPF 29

RESULT 29
P9FSP9 PRELIMINARY; PRT; 87 AA.
ID P9FSP9
AC DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Hypothetical 9.8 kDa protein.
GN H0711G06.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN {1}
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Mu J., Zhou B., Chen Z.H., Li Y., Zhu J.J.,
Tang Y.S., Zhao Q., Liu Y.L., Huang Y.C., Yu Z., Fan D.L., Chen L.,
Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,
Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.,
RT "Oryza sativa indica (Guangluai4) genomic DNA, chromosome 4, BAC
clone: H0711G06 (+0011c06)." ;
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL442115; CAG09495.1; -.
KW Hypothetical protein.
SQ SEQUENCE 87 AA; 9791 MW; BE347F35755D6A06 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPF	4
Db	43	AAPF	46
RESULT	30		
QBUH9		PRELIMINARY;	PRT;
OBUH9			88 AA.
OBHU9;			
01-JUN-2002 (TREMBUREL. 21, Created)			
01-JUN-2002 (TREMBUREL. 21, Last sequence update)			
01-JUN-2002 (TREMBUREL. 21, Last annotation update)			
Flagellar biosynthetic protein.			
FILQ OR ATRU0580 OR AGR_C_1023.			
Agrobacterium tumefaciens (strain C58, ATCC 33970).			
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
Rhizobiaceae; Rhizobium.			
NBBI_TaxID=176299;			
[1]			
RP		SEQUENCE FROM N.A.	
RX		MEDLINE=21608550; PubMed=11743193;	
RA		Wood D.W., Setubal J.C., Kaufl R.D., Monks D.E., Kitajima J.P.,	
RA		Oikura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,	
RA		Chen Y., Paulsen I.T., Eisen J.B., Karp P.D., Bovے D. S.R.,	
RA		Chapman P., Clendening J., Deathridge G., Gillett W., Grant C.,	
RA		Kuttyatin T., Levy R., Li M.-J., McClelland R., Palmieri A.,	
RA		Reymond C., Rouse G., Saenphimimachak C., Wu Z., Romero P., Gordon D.,	
RA		Zhang S., Yoo H., Biddle P., Jung M., Kraspan W., Perry M.,	
RA		Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,	
RA		Chumley F., Tingey S.V., Tomb J.-F., Gordon M., Olson M.V.,	
RA		Nester E.W.,	
RT		"The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";	
RL		Science 294:2317-2323(2001).	
RN		[2]	
RP		SEQUENCE FROM N.A.	
RX		MEDLINE=21608551; PubMed=11743194;	
RA		Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,	
RA		Ouollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Liu F.,	
RA		Houmeli K., Goldstein O., Epp A., Laipasas C., Markelz B.,	
RA		Wolman C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,	
RA		Flanagan C., Crowley C., Gurson J., Lomo C., Sear C., Strub G.,	
RA		Cielo C., Slater S.,	
RT		"Genomic sequence of the plant pathogen and biotechnology agent	
RL		Agrobacterium tumefaciens C58.";	
DR		Science 294:2323-2328(2001).	
DR		EMBL; AE005026; AAC01597.1; -.	
KW		Complete proteome.	
SQ		EMBL; AE007992; AAC086391.1; -.	
Query Match	100.0%	Score 21; DB 16; Length 88;	
Best Local Similarity	100.0%	Score 21; DB 16; Length 88;	
Matches	4;	Conservative	
Qy	1	AAPF	4
Db	65	AAPF	68
RESULT	31		
Q93D9		PRELIMINARY;	PRT;
AC		90 AA.	
09Z3D9;			
01-MAY-1999 (TREMBUREL. 10, Created)			
01-MAY-1999 (TREMBUREL. 10, Last sequence update)			
01-MAY-1999 (TREMBUREL. 10, Last annotation update)			
Hypothetical protein in LEF4-P33 intergenic region.			
Escherichia coli.			
Bacteria; Prokaryota; gamma subdivision; Enterobacteriaceae;			
Escherichia.			
NBBI_TaxID=562;			
[1]			
RESULT	31		
Q93D9		PRELIMINARY;	PRT;
ID		90 AA.	
09Z3D9;			
01-MAY-1999 (TREMBUREL. 10, Created)			
01-MAY-1999 (TREMBUREL. 10, Last sequence update)			
01-MAY-1999 (TREMBUREL. 10, Last annotation update)			
Query Match	100.0%	Score 21; DB 5; Length 90;	
Best Local Similarity	100.0%	Score 21; DB 5; Length 90;	
Matches	4;	Conservative	
Qy	1	AAPF	4
Db	21	AAPF	24
RESULT	32		
Q93NY3		PRELIMINARY;	PRT;
ID		90 AA.	
093NY3;			
01-DEC-2001 (TREMBUREL. 19, Created)			
01-DEC-2001 (TREMBUREL. 19, Last sequence update)			
01-MAR-2002 (TREMBUREL. 20, Last annotation update)			
Acp26Ab protein.			
DR		Acp26AB OR CG9024.	
GS		Drosophila melanogaster (Fruit fly)	
OC		Eukarya; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC		Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
RC		Ephydriidae; Drosophilidae; Drosophila.	
RN		[1]	
RP		SEQUENCE FROM N.A.	
RC		STRAIN=L227, MO13A, AND MO34A;	
RX		MEDLINE=99016087; PubMed=9799260;	
RA		Aquadre M.;	
RT		"Different forces drive the evolution of the Acp26AA and Acp26AB accessory gland genes in the Drosophila melanogaster species complex."	
RT		Genetics 150:1079-1089(1998).	
RL		EMBL; AJ231366; CAB37227.1; -.	
DR		EMBL; AJ231350; CAB37105.1; -.	
DR		EMBL; AJ231352; CAB37199.1; -.	
DR		EMBL; AJ231352; CAB37199.1; -.	
DR		FlyBase; FBgn00202856; Acp26Ab.	
SQ		SEQUENCE 90 AA; 1014 MW; 1FDFFC4DA51F9FBDF CRC64;	
Query Match	90 AA;	Score 90; DB 16; Length 90;	
Best Local Similarity	90 AA;	Score 90; DB 16; Length 90;	
Matches	4;	Conservative	
Qy	1	AAPF	4
Db	21	AAPF	24
RESULT	33		
Q93NY2		PRELIMINARY;	PRT;
ID		90 AA.	
093NY2;			
01-DEC-2001 (TREMBUREL. 19, Created)			
01-DEC-2001 (TREMBUREL. 19, Last sequence update)			
01-MAR-2002 (TREMBUREL. 20, Last annotation update)			
Acp26Ab protein.			
DR		Acp26AB OR CG9024.	
GS		Drosophila melanogaster (Fruit fly)	

Query Match		Score 21; DB 5; Length 90;	
Best Local Similarity 100.0%; Pred. No. 6.8e+02; Mismatches 0; Indels 0; Gaps 0		Score 21; DB 5; Length 90;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 AAPF 4	QY	1 AAPF 4
Db	21 AAPF 24	Db	21 AAPF 24
RESULT 34		RESULT 35	
ID 095NY1	PRELIMINARY;	ID 097184	PRELIMINARY;
AC 095NY1:	PRT; 90 AA.	AC 097184:	PRT; 90 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)		DT 01-MAY-1999 (TREMBLrel. 10, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DR 01-MAR-2002 (TREMBLrel. 20, Last annotation update)		DR 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE ACP26AB protein.		DE ACP26AB protein.	
GN CG9024.		GN ACP26AB OR CG9024.	
OS Drosophila melanogaster (Fruit fly).		OS Drosophila melanogaster (Fruit fly).	
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC Ephydriidae; Drosophilidae; Drosophila.		OC Ephydriidae; Drosophilidae; Drosophila.	
NCBI_TaxID=7277;		NCBI_TaxID=7277;	
RN [1]		RN [1]	
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC STRAIN=VARIOUS STRAINS;		RC STRAIN=LA28;	
RX MEDLINE=99016087; PubMed=9799260;		RX MEDLINE=99016087; PubMed=9799260;	
RA Aguade M;		RA Aguade M;	
RT "Different forces drive the evolution of the Acp26Aa and Acp26Ab accessory gland genes in the Drosophila melanogaster species complex.",		RT "Different forces drive the evolution of the Acp26Aa and Acp26Ab accessory gland genes in the Drosophila melanogaster species complex.",	
RT complex.",		RT complex.",	
RT complex.",		RT complex.",	
RL Genetica 150:1079-1089(1998).		RL Genetica 150:1079-1089(1998).	
DR EMBL: AJ231395; CAB37283; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231351; CAB3197; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231355; CAB37205; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231357; CAB37209; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231360; CAB37215; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231361; CAB37217; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231362; CAB37219; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231364; CAB37223; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231376; CAB37245; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231377; CAB37247; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231384; CAB37261; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
EMBL: AJ231387; CAB37267; 1; -.		EMBL: AJ231367; CAB37229; 1; -.	
EMBL: AJ231390; CAB37273; 1; -.		EMBL: AJ231367; CAB37229; 1; -.	
FlyBase: FBgn0002856; Acp26Ab.		FlyBase: FBgn0002856; Acp26Ab.	
SEQUENCE 90 AA; 10171 MW; 1FDFFC4E8D8F9BDF CRC64;		SEQUENCE 90 AA; 10139 MW; 1FD91C4BD8F9BDF CRC64;	
RN [1]		RN [1]	
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC STRAIN=LA28;		RC STRAIN=LA28;	
RX MEDLINE=99016087; PubMed=9799260;		RX MEDLINE=99016087; PubMed=9799260;	
RA Aguade M;		RA Aguade M;	
RT "Different forces drive the evolution of the Acp26Aa and Acp26Ab accessory gland genes in the Drosophila melanogaster species complex.",		RT "Different forces drive the evolution of the Acp26Aa and Acp26Ab accessory gland genes in the Drosophila melanogaster species complex.",	
RT complex.",		RT complex.",	
RT complex.",		RT complex.",	
RL Genetica 150:1079-1089(1998).		RL Genetica 150:1079-1089(1998).	
DR EMBL: AJ231395; CAB37283; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231351; CAB3197; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231355; CAB37205; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231357; CAB37209; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231360; CAB37215; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231361; CAB37217; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231362; CAB37219; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231364; CAB37223; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231376; CAB37245; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231377; CAB37247; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
DR EMBL: AJ231384; CAB37261; 1; -.		DR EMBL: AJ231367; CAB37229; 1; -.	
EMBL: AJ231387; CAB37267; 1; -.		EMBL: AJ231367; CAB37229; 1; -.	
EMBL: AJ231390; CAB37273; 1; -.		EMBL: AJ231367; CAB37229; 1; -.	
FlyBase: FBgn0002856; Acp26Ab.		FlyBase: FBgn0002856; Acp26Ab.	
SEQUENCE 90 AA; 10171 MW; 1FDFFC4BD8F9BDF CRC64;		SEQUENCE 90 AA; 10139 MW; 1FD91C4BD8F9BDF CRC64;	

Query Match	100.0%	Score 21; DB 5; Length 90;			
Best Local Similarity	100.0%	Pred. No. 6.8e+02;			
Matches	4	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 AAPF 4				
Db	21 AAPF 24				
RESULT	37				
ID	097456	PRELIMINARY;	PRT;	90 AA.	
AC	097456;				
DT	01-MAY-1999	(TREMBREL. 10, Last sequence update)			
DT	01-MAR-2001	(TREMBREL. 16, Last annotation update)			
DE	ACP26AB protein.				
GN	GN				
OS	Drosophila melanogaster (Fruit fly)				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OX				
OC	Ephydriidae; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	{1}				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MA74; LA31; LA106; LA118; MA6; MA31; MA37; MA56; AND MA57; MEDLINE=93016087; PubMed=9799260;				
RA	Aguade M.;				
RT	"Different forces drive the evolution of the Acp26Aa and Acp26Ab accessory gland genes in the <i>Drosophila melanogaster</i> species complex.", J. Mol. Evol. 15(1):1079-1089(1998).				
RT	Genetics 150:1079-1089(1998).				
RL	DR				
DR	EMBL; AJ231401; CAB37629.1; -.				
DR	EMBL; AJ231368; CAB37231.1; -.				
DR	EMBL; AJ231378; CAB37243.1; -.				
DR	EMBL; AJ231381; CAB37255.1; -.				
DR	EMBL; AJ231385; CAB37263.1; -.				
DR	EMBL; AJ231392; CAB37277.1; -.				
DR	EMBL; AJ231394; CAB37281.1; -.				
DR	EMBL; AJ231398; CAB37289.1; -.				
DR	EMBL; AJ231399; CAB37291.1; -.				
DR	EMBL; FBgn0002856; Acp26ab; 191FDC4BD8F9BDF CRC64; SQ				
Query Match	100.0%	Score 21; DB 5; Length 90;			
Best Local Similarity	100.0%	Pred. No. 6.8e+02;	Mismatches 0;	Indels 0;	Gaps 0;
Matches	4	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 AAPF 4				
Db	21 AAPF 24				
RESULT	38				
ID	097460	PRELIMINARY;	PRT;	90 AA.	
AC	097460;				
DT	01-MAY-1999	(TREMBREL. 10, Created)			
DT	01-MAY-1999	(TREMBREL. 10, Last sequence update)			
DT	01-MAR-2001	(TREMBREL. 16, Last annotation update)			
DE	ACP26AB protein.				
GN	GN				
OS	Drosophila melanogaster (Fruit fly)				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OX				
OC	Ephydriidae; Drosophilidae; Drosophila.				
OX	[1]				
RN	SEQUENCE FROM N.A.				
RP	STRAIN=MA50; LA14; LA32; LA60; LA125; MA21; AND MA24;				
RC	MEDLINE=93016087; PubMed=9799260;				
RA	Aguade M.;				
RT	*Different forces drive the evolution of the Acp26Aa and Acp26Ab				
RT	accessory gland genes in the <i>Drosophila melanogaster</i> species complex.", J. Mol. Evol. 15(1):1079-1089(1998).				
RT	Genetics 150:1079-1089(1998).				
RL	DR				
DR	EMBL; AJ231396; CAB37255.1; -.				
DR	EMBL; AJ231363; CAB37231.1; -.				
DR	EMBL; AJ231369; CAB37233.1; -.				
DR	EMBL; AJ231375; CAB37243.1; -.				
DR	EMBL; AJ231383; CAB37255.1; -.				
DR	EMBL; AJ23139; CAB37221.1; -.				
DR	EMBL; AJ231391; CAB37225.1; -.				
DR	FlyBase; FBgn0002856; Acp26Ab.				
SQ	SEQUENCE 90 AA; 10229 MW; 191FC4E8D8F9BDF CRC64;				
Query Match	100.0%	Score 21; DB 5; Length 90;			
Best Local Similarity	100.0%	Pred. No. 6.8e+02;	Mismatches 0;	Indels 0;	Gaps 0;
Matches	4	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 AAPF 4				
Db	21 AAPF 24				
RESULT	39				
ID	097465	PRELIMINARY;	PRT;	92 AA.	
AC	097465;				
DT	01-JUN-2001	(TREMBREL. 17, Created)			
DT	01-JUN-2001	(TREMBREL. 17, Last sequence update)			
DE	ID149.				
GN	ID149.				
OS	Bradyrhizobium japonicum.				
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Bradyrhizobium group; Bradyrhizobium.				
OC	NCBI_TaxID=375;				
RN	{1}				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=110SPC4;				
RX	MEDLINE=2210184; PubMed=11157954;				
RA	Gottschert M., Rothlisberger S., Kundig C., Beck C., Marty R., Hennecke H., Rothlisberger S., Kundig C., Beck C., Marty R., "Potential symbiosis-specific genes uncovered by sequencing a 410-kb DNA region of the <i>Bradyrhizobium japonicum</i> chromosome.", J. Bacteriol. 183:4051-412 (2001).				
RL	DR				
DR	EMBL; AF332012; AAC60755.1; -.				
SQ	SEQUENCE 92 AA; 10033 MW; CC403B2655E98674 CRC64;				
Query Match	100.0%	Score 21; DB 2; Length 92;			
Best Local Similarity	100.0%	Pred. No. 6.9e+02;	Mismatches 0;	Indels 0;	Gaps 0;
Matches	4	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 AAPF 4				
Db	66 AAPF 69				
RESULT	40				
ID	097470	PRELIMINARY;	PRT;	92 AA.	
AC	097470;				
DT	01-FEB-1997	(TREMBREL. 02, Created)			
DT	01-FEB-1997	(TREMBREL. 02, Last sequence update)			
DE	MC class II DQ-beta chain (Fragment).				
GN	GN				
OS	Bos indicus (zebu).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bos.				
OC	NCBI_TaxID=9915;				
RN	{1}				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MA50; LA14; LA32; LA60; LA125; MA21; AND MA24;				
RA	MEDLINE=93016087; PubMed=9799260;				
RT	Aguade M.;				
RT	*Different forces drive the evolution of the Acp26Aa and Acp26Ab				
RT	accessory gland genes in the <i>Drosophila melanogaster</i> species complex.", J. Mol. Evol. 15(1):1079-1089(1998).				
RT	Genetics 150:1079-1089(1998).				

RX MEDLINE=96043218; PubMed=7486255;
RA Marelio K.L., Gallagher A., McKeever D.J., Spooner R.L., Russell G.C.;
RT "Expression of multiple DQB genes in Bos indicus cattle.";
RL Anim. Genet. 26:345-349 (1995).
EMBL: X73348; CAA55903.1; -.
DR InterPro: IPR000353; MHC-II_beta.
DR Pfam: PF00969; MHC-II_beta; 1.
DR ProDom: PD000328; MHC-II_beta; 1.
KW Glycoprotein; MHC-II; Transmembrane.
FT NON_TER 1 1
FT 92 92
SQ SEQUENCE 92 AA; 11175 MW; D82F524E976CF19F CRC64;

Query Match 100.0%; Score 21; DB 7; Length 92;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
Db 79 AAPF 82

Search completed: December 6, 2002, 13:30:08
Job time : 19.5556 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 6, 2002, 13:19:54 ; Search time 26 Seconds
 (without alignments)
 20.500 Million cell updates/sec

Title: US-10-033-526-3

Percent score: 19 AAPL 4

Sequence: AAB69617

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 908470 seqs, 13250520 residues

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:*

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2: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AAL1981.DAT: *

3: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AAL1982.DAT: *

4: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AAL1983.DAT: *

5: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AAL1984.DAT: *

6: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AAL1985.DAT: *

7: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AAL1986.DAT: *

8: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AAL1987.DAT: *

9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AAL1988.DAT: *

10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AAL1990.DAT: *

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17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AAL1997.DAT: *

18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AAL1998.DAT: *

19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AAL1999.DAT: *

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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AAL2001.DAT: *

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AAL2002.DAT: *

AAB69617

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT		1	
ID	AAR46220	ID	AAR46220 standard; Peptide: 4 AA.
XX		XX	
AC	AAR46220;	XX	
DT	04-AUG-1994	XX	(first entry)
DE	Serine protease inhibitor tetrapeptide.	XX	
XX		XX	
KW	Prevention; pschistosomiasis; parasite; infection; prevention; parasitic penetration; skin; cercariae; anti-penetrant.	XX	
OS	Synthetic.	XX	
XX		XX	
FH	Key	Location/Qualifiers	
FT	Modified-site	1 /note= "BG(peptide blocking gp.) attached"	
FT		4 /note= "PI(protease inhibitor), other than chloromethyl ketone," attached"	
FT			
XX			
PN	USS284829-A.		
XX			
PD	08-FEB-1994.		
XX			
PF	26-NOV-1991;	91US-0798565.	
XX			
PR	26-NOV-1991;	91US-0798565.	
XX			
PA	(REGC) UNIV CALIFORNIA.		
XX			
PI	Cohen FE, McKerrow JH.		

XX (GEOR-) GEORGIA TECH RES CORP.
 XX PR 06-NOV-1992; 92US-0973343.
 PT PR 18-AUG-1994; 94US-0292924.
 XX PR 17-OCT-1995; 95US-0541423.
 DR PA (CLRX) CLOROX CO.
 XX PI Leigh SD;
 XX PR WPI; 1997-362936/33.
 XX PR Serine protease from *Streptomyces griseus* ATCC 55178 - with good
 PT stability in presence of urea or guanidine, useful in cleaning
 compositions, including laundry and dishwashing detergents
 PS Example 1; Column 12; 16pp; English.
 XX AW26078 W26096 represent substrates for the serine protease of the
 CC AW26078 W26096 recognise these sequences, but is
 CC invention. The serine protease shown in AW24567. The protease has the
 CC specific for the sequence represented by AW24565 and AW24566
 CC N-terminal and C-terminal sequences represented by AW24565 and AW24566
 CC respectively. The serine protease was isolated from *Streptomyces griseus*
 CC variety alkaliphilus No. 33 (ATCC 5518). The protease has an apparent
 CC molecular weight of 19 kb (by reducing sodium dodecylsulphate
 CC polyacrylamide gel electrophoresis) and improved stability against urea
 CC and guanidine. The protease is inhibited by phenylmethylsulphonyl
 CC fluoride. The serine protease is useful in liquid or granular cleaning
 CC compositions, specifically laundry detergents or additive compositions.
 CC It is also useful in automatic dishwasher detergents, pre-soaks, drain
 CC openers, contact lens cleansers etc. The protease has better activity
 CC against proteinaceous stains than known enzymes and unusually high
 CC stability in the presence of chaotropic agents.
 XX SQ Sequence 4 AA:
 Query Match 100.0%; Score 19; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 1 AAPL 4
 RESULT 4
 AW26060 ID AW26080 standard; peptide: 4 AA.
 XX AC AW26080;
 XX DT 05-NOV-1997 (first entry)
 XX DE Substrate #3 for serine protease.
 XX KW Serine protease; substrate; *Streptomyces griseus*; guanidine; pre-soak;
 KW cleaning composition; laundry detergent; additive composition; enzyme;
 KW dishwasher detergent; drain opener; urea; contact lens cleanser;
 KW proteinaceous stain.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "succinylated"
 FT Modified-site 4
 FT /note= "para-nitroanilidated"
 XX PN US5646028-A.
 XX PD 08-JUL-1997.
 XX PR 18-JUN-1991; 91US-0718303.
 XX PR 18-JUN-1991; 91US-0718303.
 PR (KAO) KAO CORP.

XX Query Match 100.0%; Score 19; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 1 AAPL 4
 RESULT 5
 AW12811 ID AW12811 standard; peptide: 4 AA.
 XX AC AW12811;
 XX DT 21-APR-1997 (first entry)
 XX DE Synthetic substrate #2 for cold-adapted alkali protease.
 XX KW cold-adapted alkali protease; *alteromonas*; urea-denatured haemoglobin;
 KW yolk; casein; p-nitroaniline; detergent; meat softener.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Succinylated
 FT Modified-site 4
 FT /label= p-nitroanilinylated
 XX PN JF08322562-A.
 XX PD 10-DEC-1996.
 XX PF 01-JUN-1995; 95JP-0135056.
 XX PR 01-JUN-1995; 95JP-0135056.
 XX PA (KAOS) KAO CORP.

XX
 DR WPI: 1997-081078/08.
 XX
 XX
 PT Cold-adapted alkali protease - produced by Alteromonas, used in detergents
 PT
 XX
 PS Claim 1; Page 2; 10pp; Japanese.

CC AAW2810-W12812 represent synthetic substrates for the cold-adapted alkali protease of the invention. The alkali protease of the invention is produced by Alteromonas, specifically by Alteromonas species KSM-SP 111 which is isolated from a shellfish in the Antarctic ocean. The enzyme of the invention has an active temperature of 0-70 degrees C, with an optimum of 40 degrees, and with 20% of activity retained at 10 degrees, and 10% maintained at 0 degrees. The pH range of the enzyme is 4-14, with an optimum of 11, but 70% (or higher) of the activity is maintained at pH12. The protease has a molecular weight of 54000, as determined by SDS polyacrylamide gel electrophoresis. The enzyme is capable of acting on casein, urea-denatured haemoglobin, Yolk, and the synthetic substrates represented by these sequences, to yield p-nitroaniline. The enzyme is inhibited by the Hg and Zn metal ions, EDTA, phenylmethanesulphonil fluoride, chymostatin or p-chloromercurybenzoyl acid. Activity of the enzyme is increased 2-7 times by the presence of sodium alkansulphate, sodium alpha-olefinsulphate, sodium polyoxyethylenealkylsulphate, softanol 70H or alpha-sulpho fatty acid ester. The protease can be used as a component of detergents, or as a softener for meat when used at a lower temperature.

XX
 Sequence 4 AA:
 SQ Query Match 100.0%; Score 19; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS QY 1 AAPL 4
 DB 1 AAPL 4

RESULT 6
 ID AAW51756
 TD AAW51756 standard; peptide; 4 AA.
 XX
 AC AAW51756;
 XX
 DT 10-SEP-1998 (first entry)
 XX
 DE Substrate used to assay rotamase activity of 50-54 kDa immunophilin.
 XX
 KW immunophilin; tryptic peptide; C-terminus; FK-506; cyclosporine A; rapamycin; immunosuppressant drug; binding assay.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Succinyl-Ala"
 FT Modified-site 4
 FT /note= "Leu-para-nitroanilide"
 PN US5780307-A.
 XX
 PD 14-JUL-1998.
 XX
 PF 26-JUL-1996; 96US-0686759.
 PR 23-FEB-1994; 94US-0200404.
 PR 02-DEC-1988; 88US-0279176.
 PR 02-MAR-1990; 90US-0487115.
 PR 09-MAY-1990; 90US-0521074.
 PR 22-OCT-1991; 91US-0782761.
 PR 26-FEB-1992; 92US-0841792.

PR 26-JUL-1996; 96US-0686759.
 XX
 PA (SOLID-) SOLDIN S J.
 XX
 PT Soldin SJ;
 XX
 DR WPI: 1998-413070/35.
 XX
 New immunophilin from mammalian lymphoid tissue - used in binding assays for cyclosporine, FK-506 and rapamycin, and for recovering new immuno-suppressants from extracts and cell cultures
 XX
 PS Example 18; Columns 31-32; 56pp; English.
 CC The invention relates to an immunophilin (i.e. a cytosolic immuno-suppressant drug binding protein) that binds specifically to FK-506, cyclosporine A and rapamycin, has molecular weight 34-47 kD (by chromatography), sodium dodecylsulphate/polyacrylamide gel electrophoresis or amino acid analysis) and has isoelectric point (pI) 5.6-7. It is optionally immobilised on a solid support, is used in binding assays for the specified immunosuppressants, and for capturing potential immunosuppressants from microbial extracts or cell cultures, e.g. active metabolites of the specified immunosuppressants or their mammalian homologues. The present sequence represents a peptide substrate which was used to assay the rotamase activity of a 50-54 kDa immunophilin.
 CC
 XX
 Sequence 4 AA:
 SQ Query Match 100.0%; Score 19; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS QY 1 AAPL 4
 DB 1 AAPL 4

RESULT 7
 ID AAW37769
 TD AAW37769 standard; Protein; 4 AA.
 XX
 AC AAW37769;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Amino acid sequence of synthetic chromogenic substrate.
 XX
 KW Subtilisin-type serine protease inhibitor; inhibition; ss; proteolytic activity; extracellular elastolytic serine protease; Aspergillus hyphae; lung; germination; aspergillosis; nasal delivery; chromogenic substrate.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Active-site 1
 FT Modified-site /note= "Suc-Ala"
 FT Modified-site 4
 FT /note= "Leu-pNA"
 XX
 PN US5739283-A.
 XX
 PD 14-APR-1998.
 XX
 PF 07-JUN-1995; 95US-0486895.
 XX
 PR 07-JUN-1995; 95US-0486895.
 XX
 PA (OHIO-) OHIO STATE RES FOUND.
 XX
 PI Ceselski SK, Copelan EA, Kolattukudy PE, Markaryan AN;

XX
 DR WPI; 1998-250492/22.
 XX
 PT Treatment of invasive pulmonary aspergillosis - by nasal administration of composition comprising subtilisin type serine protease inhibitor e.g. streptomyces subtilisin inhibitor, and carrier e.g. phosphate buffered saline.
 XX
 PS Claim 6; columns 17-18; 12pp; English.
 XX
 CC The amino acid sequence is a chromogenic substrate used in the method of invention to develop subtilisin-type serine protease inhibitor (SSI). The SSI inhibits the proteolytic activity of the extracellular elastolytic serine protease produced by aspergillus and reduces the invasion of the lung and tissues surrounding it by the germinating hyphae of aspergillus. It can be used in a drug composition to treat aspergillosis via nasal delivery.
 XX
 SQ Sequence 4 AA:

Query Match	100.0%	Score 19;	DB 19;	Length 4;
Best Local Similarity	100.0%	Pred. No.	7.8e+05;	
Matches	4;	Conservative	0;	Mismatches
QY	1 AAPL 4	Db	1 AAPL 4	

 RESULT 8
 ID AAW39105 standard; peptide; 4 AA.
 XX
 AC AAW39105;
 XX
 DT 08-APR-1998 (first entry)
 DE Calf thymus immunophilin rotamase substrate 6.
 XX
 KW Immunophilin; calf; immunosuppressant drug; FK506; rapamycin; cyclosporin A; rotamase; therapy.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal Suc-dla"
 FT Modified-site 4 /note= "C-terminal Leu-PNA"
 XX
 PN USS698448-A.
 XX
 PD 16-DEC-1997.
 XX
 PF 08-APR-1994; 94US-0224868.
 XX
 PR 23-FEB-1994; 94US-0200404.
 PR 03-DEC-1994; 88US-0229176.
 PR 02-MAR-1990; 90US-047115.
 PR 09-MAY-1990; 90US-0521074.
 PR 22-OCT-1991; 91US-0722761.
 PR 26-FEB-1992; 92US-0841792.
 PR 08-APR-1994; 94US-0224868.
 PA (SOLD) SOLDIN S J.
 XX
 PT Soldin SJ;
 XX
 DR WPI; 1998-051496/05.
 XX
 PT Immunophilin protein that binds immunosuppressant drugs - useful in assays for cyclosporin A, FK506 and rapamycin
 XX

PS Example 18; Column 31; 54pp; English.
 XX
 CC Peptides AAW39100-W39110 represent substrates used in an assay to investigate the rotamase activity of a 10-12 kDa and a 50-52 kDa immunophilin isolated from calf thymus. Immunophilins are proteins capable of binding to immunosuppressant drugs. In this example FK506, rapamycin or cyclosporin. This substrate has a rotamase activity of 0.45 K-obs (min-1) with the 50-52 kDa immunophilin and 0.93 K-obs (min-1) with the 10-12 kDa immunophilin. Immunophilins will have applications for monitoring immunosuppressive therapy and for the capture of potential immunosuppressive drugs from microbial extract, culture media or from mammalian body fluids and tissues.
 XX
 SQ Sequence 4 AA:

Query Match	100.0%	Score 19;	DB 19;	Length 4;
Best Local Similarity	100.0%	Pred. No.	7.8e+05;	
Matches	4;	Conservative	0;	Mismatches
QY	1 AAPL 4	Db	1 AAPL 4	

 RESULT 9
 ID AAY31241
 ID AAY31241 standard; peptide; 4 AA.
 XX
 AC AAY31241;
 XX
 DT 09-NOV-1999 (first entry)
 DE Alpha-aminoalkyl phosphonate derivative peptide 3.
 XX
 KW Alpha-aminoalkyl phosphonate; serine protease inhibitor; anticoagulant; cytostatic; anti-inflammatory; gastrointestinal; endocrine; respiratory; dermatological; chymotrypsin inhibitor; elastase inhibitor; inflammation; trypsin inhibitor; trypsin inhibitor; blood coagulation; pancreatitis; tumour invasion control; emphysema; respiratory distress syndrome; skin blistering.
 XX
 OS Synthetic.
 XX
 PN USS5952307-A.
 XX
 PD 14-SEP-1999.
 XX
 PF 14-AUG-1997; 97US-0907840.
 XX
 PR 14-AUG-1997; 97US-0907840.
 PR 21-JAN-1994; 94US-0184286.
 XX
 PA (GEOR-) GEORGIA TECH R&D CORP.
 XX
 PT Jackson DS, Ni L, Powers JC;
 XX
 DR WPI; 1999-539191/45.
 XX
 PT New aminoalkyl phosphonate derivatives are serine protease inhibitors useful for decreasing blood coagulation and for treating tumour invasion, inflammation, endocrine, respiratory and distress syndrome and skin blistering.
 PT Disclosure; Column 31-32; 18pp; English.
 XX
 CC This invention describes the production of novel alpha-aminoalkyl phosphonate derivatives (I) which have anticoagulant, cytostatic, anti-inflammatory, gastrointestinal, endocrine, respiratory and dermatological activity. The products of the invention are also found to act as serine protease inhibitors, chymotrypsin inhibitors, elastase inhibitors, trypsin inhibitors and trypsin inhibitors. (I) are useful for decreasing blood coagulation, and for controlling tumour invasion, inflammations, pancreatitis, emphysema, respiratory distress syndrome

CC and skin blistering. AAY31239-Y31241 are peptides used to describe the
 CC method of the invention.

XX

SQ Sequence 4 AA;

Qy	1 AAPL 4	Db	1 AAPL 4

RESULT 10

AAB03091 ID AAB03091 standard; peptide; 4 AA.

XX AC AAB03091;

XX DT 10-OCT-2000 (first entry)

XX DE Substrate peptide #2.

XX KW Serine protease; trypsin activity; Trichoderma; bacterial; coagulant; hypertensive; antiinflammatory; leather preparation; silk treatment.

XX OS Synthetic.

XX Key

FT Modified-site	I /note= "Conjugated to succinyl moiety"	FT Modified-site	I /note= "Suc-Ala"
FT 4	/note= "Conjugated to p-nitroaniline (pNA)"	FT 4	/note= "Leu-CO-NR3R4"

XX PA JP200116377-A.

XX PD 25-APR-2000.

XX PF 08-OCT-1998; 98JP-0303263.

XX PR 08-OCT-1998; 98JP-0303263.

XX PA (AMAN) AMANO PHARM KK.

XX DR WPI; 2000-369402/732.

XX A new serine protease and its preparation, used clinically in blood coagulation, hypertension and anti-inflammation - Example 3; Page 5; 9pp; Japanese.

XX PS The invention relates to a novel serine protease from Trichoderma sp. No. 9064. The N-terminus of this protease is given in AAB03085. The novel protease has trypsin-like activity, specifically cleaving peptide chains on the carboxyl side of a basic amino acid (e.g., arginine or lysine). It has a pH optimum of 7-8, and is stable between pH 5 and pH10. It has a temperature optimum of approximately 40 degrees Celsius, and is stable between 40 and 50 degrees Celsius. The invention also relates to a method for the preparation of the novel serine protease, and the use of the protease in protein degradation. The enzyme has coagulant, hypertensive and anti-inflammatory effects. It may also be used in the preparation of leather for raw silk treatment and for the preparation of protein hydrolysate. Sequences AAB03090-B03094 represent tetrapeptides used in the determination of the activity of the novel protease.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 19; DB 21; Length 4; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; AA3 is Asp or Glu, in either the L or D form;

Qy 1 AAPL 4

Db 1 AAPL 4

RESULT 11

AAB97637 ID AAB97637 standard; peptide; 4 AA.

XX AC AAB97637;

XX DT 21-SEP-2001 (first entry)

XX DE Alpha-ketoamide elastolytic proteinase inhibitor peptide.

XX KW Peptide ketoamide; serine protease inhibitor;

XX KW cysteine protease inhibitor; transition state analogue;

XX KW neurodegenerative disease; ischaemia; stroke; Alzheimer's disease;

XX KW anticoagulant; thrombin; adult respiratory distress syndrome;

XX KW emphysema; rheumatoid arthritis; pancreatitis; viral infection;

XX KW muscular dystrophy; myocardial tissue damage; tumour metastasis;

XX KW bone resorption; Schistosoma mansoni; elastolytic protease inhibitor.

XX OS Synthetic.

XX Key

FT Modified-site	I /note= "Conjugated to succinyl moiety"	FT Modified-site	I /note= "Suc-Ala"
FT 4	/note= "Conjugated to p-nitroaniline (pNA)"	FT 4	/note= "Leu-CO-NR3R4"

XX PA JP200116377-A.

XX PD 22-MAY-2001.

XX PF 27-DEC-1996; 96US-0777354.

XX PR 27-DEC-1991; 91US-0815073.

PR 09-SEP-1993; 93US-0118997.

PR 20-MAY-1994; 94US-0246511.

PR 06-OCT-1995; 95US-0539944.

XX PA (GEOR-) GEORGIA TECH RES CORP.

XX PI Powers JC;

XX DR WPI; 2001-440210/47.

XX PT New tripeptide ketoamide derivatives are serine and cysteine protease inhibitors, useful as anticoagulants and for treating neurodegenerative diseases, thrombosis, emphysema and rheumatoid arthritis - Disclosure; Column 18; 24pp; English.

XX PS The invention relates to peptide ketoamide derivatives useful for selectively inhibiting serine proteases and cysteine proteases, and for generally inhibiting all members of these classes of enzymes. The peptide ketoamides are derivatives of substrate peptides of serine and cysteine proteases and act as transition state analogues. The peptides of the invention have the formula M1-Aa1-Aa2-Aa3-CO-NR3R4 where:

M1 is NH₂CO-, NH₂S-, NH₂SO₂-, XNHCO-, X₂NCO-, XNHCS-, XNHCs-, XNCS-, XNHS-

CC XNHSO₂-, X₂NSO₂-, XCO-₂, XCS-₂, XCO₂- or XCO₂;

CC X is 1-10C (fluorooalkyl) (optionally substituted by J), 1-adamantyl, 9-fluorenyl, phenyl or naphthyl (optionally substituted by up to 3 of CC K); or 1-10C alkylphenyl, 1-10C alkylidiphenyl or 1-10C alkylphenoxy (all optionally substituted by K);

CC J is halo, COOH, OH, NO₂, NH₂, 1-10C alkoxy, 1-10C alkylamine, 2-12C dialkylamine, 1-10C alkyl-OCO-, 1-10C alkyl-OCONH- or 1-10C alkylthio;

CC K is halo, 1-10C (perfluoroalkyl), 1-10C alkoxy, NO₂, CN, OH, COOH, NH₂, 1-10C alkylamino, 2-12C dialkylamino, 1-10C acyl, 1-10C alkoxy-CO or 1-10C alkylthio;

CC AA1, AA2 are independently Ala, Val, Leu, Ile, Gly, Ser, Asp or Glu;

CC R₃ is 2-3C alkylphenyl, 3-20C cycloalkylphenyl, 1-20C alkylphenyl
 CC (substituted by up to 3 of K), 3-20C cycloalkylphenyl (substituted by
 CC K), NH-CH₂CH₂(4-hydroxyphenyl) or NH-CH₂CH₂(3-indolyl); and
 CC R₄ = H, 3-20C alkyl, cycloalkyl, 1-20C alkylphenyl (optionally
 CC substituted by up to 3 of K), 3-20C cycloalkylphenyl (optionally
 CC NHC₂CH₂(2-(3-indolyl))
 CC The peptide ketonamides are useful for treating neurodegenerative diseases
 CC (including ischaemia, stroke and Alzheimer's disease), as anticoagulants,
 CC and for treating thrombosis. They are also useful for treating
 CC emphysema, adult respiratory distress syndrome, rheumatoid arthritis,
 CC pancreatitis, viral infections, muscular dystrophy, myocardial tissue
 CC damage, tumour metastasis and bone resorption. The present sequence
 CC represents a Schistosoma mansoni elastolytic protease peptide
 XX SQ sequence 4 AA:
 Query Match 100.0%; Score 19; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 4; Conservati
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 1 AAPL 4
 RESULT 12
 AAB35964 ID AAB35964 standard; peptide: 4 AA.
 XX AC AAB35964;
 XX DT 01-MAR-2001 (first entry)
 DE Elastase cleavable peptide #2.
 XX Polymeric drug conjugate; enzymatically cleavable linker; cardiot;
 KW antiinflammatory; cytostatic; hepatotropic; neuroprotective; cancer;
 KW antibacterial; nephrotropic; immunomodulatory; neoplastic disease;
 KW chronic inflammatory disease; acute inflammatory disease;
 KW cardiac disease; renal disease; liver disease; lung disease;
 KW neurological disease; musculoskeletal disease; immunological disorder;
 KW microbial infection.
 OS Synthetic.
 XX PN WO20064486-A2.
 XX PD 02-NOV-2000.
 XX PF 28-APR-2000; 2000WO-US11670.
 XX PR 99US-011404.
 XX PR 02-NOV-1999; 99US-0163090.
 XX (VERI-) VERITAS MEDICAL TECHNOLOGIES INC.
 XX PI Pachence JM, Belinka BA, Ramani T;
 XX DR WPI: 2001-031659/04.
 XX PS claim 30; page 93; 100pp; English.
 PT Polymeric drug conjugate, for treating diseases associated with organs
 PT e.g. liver or heart, has biologically active agents linked to regular
 PT repeating linear or branched co-polymers by enzymatically cleavable
 PT marker -
 XX The invention relates to a polymeric drug conjugate. The drug conjugate
 CC comprises biologically active agents conjugated via an enzymatically
 CC cleavable linker to a regular repeating linear unit comprising a water
 soluble polymer segment and a multifunctional chemical moiety, or to a
 CC inhibitor.

CC branched polymer comprising two or more water soluble polymer segments
 CC each bound to a common multifunctional chemical moiety. The polymeric
 CC conjugate has antiinflammatory; cytostatic; cardiotrop; hepatotropic;
 CC neuroprotective; antibacterial; nephrotropic; and immunomodulatory
 CC activity. The drug conjugate is useful for alleviating a pathological
 CC condition such as neoplastic diseases, chronic inflammatory diseases,
 CC acute inflammatory diseases, cardiac diseases, renal diseases, liver
 CC diseases, lung diseases, neurological diseases, musculoskeletal diseases
 CC and immunological disorders and various microbial infections by
 CC modulating immunological or hormonal function. The present sequence
 CC represents a peptide which can be used as the enzymatically cleavable
 CC linker in the drug conjugate of the invention.

XX SQ Sequence 4 AA:
 Query Match 100.0%; Score 19; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 4; Conservati
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 1 AAPL 4
 RESULT 13
 AAQ15231 ID AAQ15231 standard; Peptide: 4 AA.
 XX AC AAQ15231;
 XX DT 05-SEP-2002 (first entry)
 XX DE Porphyromonas gingivalis dipeptidylpeptidase-7 substrate peptide 10.
 XX KW Dipeptidylpeptidase-7; DPP-7; amidolytic cleavage; substrate peptide;
 KW DPP-7 inhibitor identification; periodontal disease; gingivitis;
 KW periodontitis.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "The residue is modified with N-succinyl"
 FT Modified-site 4
 FT /note= "The residue is modified with PNA"
 XX PN WO200238742-A2.
 XX PD 16-MAY-2002.
 XX PF 08-NOV-2001; 2001WO-US46782.
 XX PR 08-NOV-2000; 2000US-246327P.
 XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX PI Travis J, Potempa JS, Banbulu A, Bugno M;
 XX DR WPI: 2002-490075/52.
 XX PT Novel isolated dipeptidylpeptidase useful for identifying inhibitor of
 PT the dipeptidylpeptidase for protecting an animal from periodontal
 PT disease caused by porphyromonas gingivalis
 XX PS Example 5; Page 29; 65pp; English.
 XX The invention comprises the amino acid and coding sequence of the
 CC DPP-7 enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the
 CC second and third amino acids from the N-terminal end of a target peptide.
 CC The DPP-7 target peptide has an aliphatic or aromatic residue as a
 CC substituent on the alpha-carbon atom of the second amino acid from the
 CC N-terminal end. The DPP-1 protein and DNA sequences of the invention are

CC useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for
 CC reducing the growth of a bacterium and protecting an animal from a
 CC periodontal disease caused by *Porphyromonas gingivalis* (e.g. gingivitis
 CC or periodontitis). The present amino acid sequence represents a substrate
 CC peptide that was not hydrolysed by the *Porphyromonas gingivalis*
 CC dipeptidylpeptidase-7 (DPP-7) enzyme of the invention.

XX SQ. Sequence 4 AA;

Query Match 100.0%; Score 19; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 1 AAPL 4

Oy 1 AAPL 4
 ID ABB83183 standard; Peptide; 4 AA.
 Db 1 AAPL 4

RESULT 15

ABB83183
 ID ABB83183;
 AC ABB83183;
 XX DE Synthetic peptide #2 used to assay Pral protease activity.
 DT 16-AUG-2002 (first entry)
 KW Pral; protease; enzyme; fungicide; insecticide; serine-peptidase.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1
 FT /note= "N-terminal succinyl"
 FT FT Modified-site 4
 FT /note= "Leu-DNA"
 XX PN WO20024359-A1.
 XX PD 06-JUN-2002.
 XX PF 30-NOV-2001; 2001WO-ES00471.
 XX PR 01-DEC-2000; 2000ES-0002897.
 XX PA (NEWB-) NEWBIOTECHNIC SA.
 PA (UYSB-) UNIV SEVILLA.
 PA (UYSB-) UNIV SALAMANCA.
 XX PI Suarez Fernandez B, Rey Barrera M, Monte Vazquez E.
 PI Lloebell Gonzalez A;
 XX DR WPI; 2002-471330/50.
 XX PS Example 3; Page 26; 51pp; Spanish.

XX The present invention relates to Pral protease from *Trichoderma harzianum*, useful e.g. for
 CC protecting plants against fungal attack, also related nucleic acid -
 XX PS Example 3; Page 26; 51pp; Spanish.

XX The present invention relates to Pral protease from *Trichoderma harzianum* (ABB83181). Pral, a serine-peptidase, catalyses irreversible
 CC inactivation of enzymes and proteins essential for pathogenicity of
 CC fungi. Pral can be used to degrade proteins and peptides, especially
 CC structural components of the cell walls of fungi, insects and arachnids.
 PT Particularly, Pral can be used (optionally in combination with chemical
 CC fungicides) to protect plants, animals, harvested crops and foods against
 CC fungi; to generate protoplasts and yeast extracts; for recovery of
 CC mannosugars; in preparation of wine and (grape) juice; for removal of
 CC dental plaque; in tooth-, denture- and contact lens-cleaning solutions;
 CC to remove biofilms; to treat or clean textiles; as disinfectant and to
 CC prevent contamination of analytical samples. The present peptide was used
 CC in an example from the invention to assay Pral activity.

XX SQ. Sequence 4 AA;

Query Match 100.0%; Score 19; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 1 AAPL 4

RESULT 16

XX The present invention relates to a method of inhibiting the formation of
 CC neurofibrillary tangles in an individual, which involves reducing the
 CC formation of a carboxyl-terminal truncated form of apolipoprotein E
 CC (apoE) in a neurone in the individual. The method is useful for
 CC preventing the formation of neurofibrillary tangles in an individual. The
 XX Claim 24; Page 62; 75pp; English.

XX The present invention relates to a method of inhibiting the formation of
 CC neurofibrillary tangles in an individual, which involves reducing the
 CC formation of a carboxyl-terminal truncated form of apolipoprotein E
 CC (apoE) in a neurone in the individual. The method is useful for
 CC preventing the formation of neurofibrillary tangles in an individual. The
 XX disorder related to apoE in an individual, specifically Alzheimer's
 CC disease, coronary artery disease, head trauma or stroke. The present
 CC sequence is a peptide capable of inhibiting the formation of the
 XX C-terminal truncated form of apoE.

XX Sequence 4 AA;

Query Match 100.0%; Score 19; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

AAR69616
 ID AAR69616 standard; peptide; 8 AA.
 XX
 AC AAR69616;
 XX
 DT 29-AUG-1995 (first entry)
 XX
 DE MHC class I-derived peptide.
 XX
 KW MHC class I; major histocompatibility complex; insulin receptor;
 KW diabetes.
 XX
 OS Synthetic.
 XX
 PN USS385888-A.
 XX
 PD 31-JAN-1995.
 XX
 PF 20-MAR-1987; 87US-0028241.
 XX
 PR 20-MAR-1987; 87US-0028241.
 PR 14-MAR-1989; 89US-0223565.
 PR 01-FEB-1991; 91US-0649471.
 PR 03-MAY-1993; 93US-0057184.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PT Goodenow RS, Olsson L;
 DR WPI; 1995-081582/11.
 XX
 PT Modulating response of cellular insulin receptor to ligand - using Peptide deriv. from MHC class I antigen, partic. to potentiate effect of insulin for treating diabetes
 PT Disclosure; Column 23; 15pp; English.
 XX
 CC Response of an insulin receptor (IR) to a ligand is modulated by contacting mammalian cells having IR on the surface with peptides (given in AAR69608-14) derived from MHC class I antigen. Another peptide provided in the specification is given in AAR69616. Another peptide may be linked to e.g. antibodies or incorporated into
 CC liposomes for administration.
 XX
 SO Sequence 8 AA:
 Query Match 100.0%; Score 19; DB 16; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 5 AAPL 8
 RESULT 18
 AAW07118
 ID AAW07118 standard; peptide; 9 AA.
 XX
 AC AAW07118;
 XX
 DT 23-JAN-1997 (first entry)
 XX
 DE Synthetic peptide used in GalNAc-transferase activity SPA.
 XX
 KW SPA; scintillation proximity assay; antigen; bead coating; capture; antibody; N-acetyl galactosamine transferase; GalNAc transferase; activity; enzyme; O-linked glycosylation.
 XX
 OS Synthetic.
 XX
 PN WO9615258 A1.
 XX
 PD 23-MAY-1996.
 XX
 PR 08-NOV-1995; 95WO-US13483.
 XX
 PR 16-NOV-1994; 94US-0340283.
 XX
 PA (UPJO) UPJOHN CO.
 XX
 PT Elhammer AP;
 XX
 DR WPI; 1996-268220/27.
 XX
 PT Scintillation proximity assay for N-acetyl galactosaminyl activity
 PT - esp. for large scale screening of cpos. for their effect on enzyme
 XX
 PN Claim 14; Page 17; 29pp; English.
 XX
 PD 31-JAN-1995.

xx AAW06985-W07180 are antigenic peptides derived from either the product of the human c-myc oncogene or the FLAG peptide (pRKDDDK).
 cc The peptides are useful for coating beads used in a scintillation proximity assay for N-acetylgalactosamine (GalNAc)-transfase (GNT) activity. The assay involves fewer steps than known assays and is quicker, producing excellent signal-to-noise ratios. The assay is capable of screening large numbers of cpd.s. for their ability to affect GNT activity and is thus useful for identifying inhibitors and promoters of glycosylation (in partic. O-linked glycosylation).

SQ Sequence 9 AA;

Query Match 100.0%; Score 19; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 6 AAPL 9

RESULT 19

AY46545
 ID AY46545 standard; Peptide; 9 AA.

AC AAY46545;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1156.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO945954-A1.
 XX PD 16-SEP-1999.
 XX PF 13-MAR-1998; 98WO-US05039.
 XX PR 13-MAR-1998; 98WO-US05039.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PT Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX DR WPI; 1999-551214/46.

XX New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -

XX Claim 1; Page 76; 150pp; English.
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. The peptides are cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) or prevent viral infections and cancers in mammals (especially humans)

cc e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 cc They can be administered as vaccines to elicit an immune response in
 cc individuals susceptible or otherwise at risk of viral infection or
 cc cancer, or used to treat chronic or acute conditions. They are also
 cc useful diagnostically, and can be used to induce a cytotoxic T cell
 cc response, by contacting a cytotoxic T cell with the peptide e.g. to
 cc produce CTLs ex vivo for infusion back into a patient. The
 cc polynucleotides encoding the immunogenic peptides are also useful
 cc therapeutically and for immunisation as above.

SQ Sequence 9 AA;

Query Match 100.0%; Score 19; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 5 AAPL 8

RESULT 20

AY46769
 ID AY46769 standard; Peptide; 9 AA.

AC AAY46769;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1380.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO945954-A1.
 XX PD 16-SEP-1999.
 XX PF 13-MAR-1998; 98WO-US05039.
 XX PR 13-MAR-1998; 98WO-US05039.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PT Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX DR WPI; 1999-551214/46.

XX New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -

XX Claim 1; Page 84; 150pp; English.
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. The peptides are cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in

CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polyvalent peptides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.

XX Sequence 9 AA;

Query Match 100.0%; Score 19; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;

Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPL 4

Db 2 AAPL 5

RESULT 21

ID AAY46771
 XX AAY46771 standard; Peptide: 9 AA.

AC AAY46771;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1382.
 XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1382.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.

XX OS Synthetic.
 OS Homo sapiens.
 OS Synthetic.
 OS Homo sapiens.

XX PN WO9945954-A1.

XX PD 16-SEP-1999.

XX PF 13-MAR-1998; 98WO-US05039.

XX PR 13-MAR-1998; 98WO-US05039.

XX PA (EPIM-) EPIMMUNE INC.

XX PT Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX DR WPI; 1999-551214/46.

XX PT New immunogenic peptides with HLA binding motif, useful in treatment

PT and diagnosis of cancers and viral diseases

XX PS Claim 1; Page 84; 150pp; English.

XX PS AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2, 1, A1, A3, 2 or A24, 1 or HLA-B or C) and induce a cytotoxic T cell

peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2, 1, A1, A3, 2 or A24, 1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also

CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polyvalent peptides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.

XX Sequence 9 AA;

Query Match 100.0%; Score 19; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;

Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPL 4

Db 2 AAPL 5

RESULT 22

ID AAY47521
 XX AAY47521 standard; Peptide: 9 AA.

AC AAY47521;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2132.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9945954-A1.

XX PD 16-SEP-1999.

XX PF 13-MAR-1998; 98WO-US05039.

XX PR 13-MAR-1998; 98WO-US05039.

XX PA (EPIM-) EPIMMUNE INC.

XX PT Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX DR WPI; 1999-551214/46.

XX PT New immunogenic peptides with HLA binding motif, useful in treatment

PT and diagnosis of cancers and viral diseases

XX PS Claim 1; Page 113; 150pp; English.
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2, 1, A1, A3, 2 or A24, 1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also

CC produce CTLs ex vivo for infusion back into a patient. The
 CC poly nucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.

SQ

Sequence 9 AA;

Query Match 100.0%; Score 19; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 6 AAPL 9

RESULT 23

AY47770 standard; Peptide; 9 AA.

AC AAY47770;
XX

DT 01-DEC-1999 (first entry)

DE Immunogenic peptide having a human leukocyte antigen binding motif 12381.
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.

OS Synthetic.
OS Homo sapiens.

PN WO945954-A1.

PD XX

XX 16-SEP-1999.

PR 13-MAR-1998; 98WO-US05039.

PA 13-MAR-1998; 98WO-US05039.

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

DR XX

XX WPI; 1999-551214/46.

PT New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseasesXX
PS Claim 1; Page 123; 150pp; English.XX
CC AAV45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2, A1, A3, 2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.

CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a Cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC poly nucleotides encoding the immunogenic peptides are also useful

CC therapeutically and for immunisation as above.

SQ

Sequence 9 AA;

Query Match 100.0%; Score 19; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 4 AAPL 7

RESULT 24

RAB48605 standard; Peptide; 9 AA.

AC AAB48605;

DT 28-FEB-2001 (first entry)

DE C-Abl Tyr kinase activity detection probe motif, SEQ ID NO:4.

KW Post-translational modification activity; detection; optical probe;
 KW fluorescence; drug screening; sequence specificity determination;
 KW protease cleavage site; recognition motif; drug discovery;
 KW peptide probe; phosphorylation; tyrosine kinase activity detection;
 KW chymotrypsin cleavage.

OS Synthetic.

PN WO2000066766-A1.

XX PD 09-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12290.

XX PR 05-MAY-1999; 99US-0306542.

XX PA (AURO-) AURORA BIOSCIENCES CORP.

XX PI Pollok BA, Hamman BD, Rodems SM, Makings LR;

XX DR WPI; 2000-665337/64.

PT Engineered optical probe for measuring a post-translational type
 PT modification, comprises a polypeptide with a recognition motif that
 PT modulates the polypeptide cleavage rate by a protease, and a
 PT fluorescent moiety.

XX
PS Example 1; Page 21; 101pp; English.

The invention relates to a engineered optical probe for measuring a post-translational modification activity (e.g., phosphorylation). The probe comprises a non-naturally occurring polypeptide with a recognition motif for the post-translational modification activity, and a protease cleavage site. The probe is attached to a fluorescent moiety. Modification of the polypeptide by the post-translational modification activity results in a modulation of the rate at which a protease cleaves the polypeptide. This is detected by a measurable change in at least one optical property of the optical probe upon cleavage. The invention also includes a recombinant nucleic acid molecule that encodes an optical probe, and vector and host cells comprising this nucleic acid sequence. The invention also relates to a method of determining whether a sample contains a post-translational modification using the probe of the invention: a method of screening a test compound for its ability to modulate a post translational modification activity; a method of determining the sequence specificity of the post-translational activity using a library of probes; systems for spectroscopic measurement utilising a probe of the invention; and therapeutic compositions comprising a modulator of a post-translational activity. The optical probe of the invention is used as an optical sensor of post-translational activities to determine whether a sample contains a post-translational

CC modification, to determine whether a test chemical modulates a post-translational modifying activity, to determine the sequence specificity of a post-translational activity, to identify a therapeutic composition, and in systems for spectroscopic measurements. Compositions containing the probe allow for high throughput and miniaturised screening systems for drug discovery and profiling. Assays using the probe exhibit a large dynamic range, increased sensitivity and allow ratiometric readouts for the detection of post-translational activities. The present sequence represents a tyrosine kinase activity detection probe motif which is cleavable by chymotrypsin.

SQ Sequence

9 AA:

Query Match 100.0%; Score 19; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 AAPL 4

Db 6 AAPL 9

RESULT 25

AAU06934 standard; Peptide; 9 AA.

ID AAU06934

XX AAU06954;

AC AAU06954;

XX DT 24-OCT-2001 (first entry)

XX DE Human MHC molecule HLA-B7 binding 84P2A9 peptide #22.

XX KW 84P2A9-related protein; prostate; testis; tissue; cancer; leukaemia;

KW tumour; kidney; brain; bone; skin; ovary; breast; pancreas; colon; lung;

KW cytosolic; gene therapy; antibody therapy; ribozyme; serum; blood;

XX OS single chain monoclonal antibody; urine.

XX OS Homo sapiens.

XX PN WO200155391-A2.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-US2651.

XX PR 20-JAN-2000; 2000US-0178560.

XX PA (UROG-) UROGENESIS INC.

XX PA Jakobovits A., Afar DEH, Challita-eid PM, Levin E, Mitchell SC;

PI PI Herbert RS;

XX DR WPI; 2001-502631/55.

XX PT New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer -

XX PT treatment of ovarian, breast, lung, colon and prostate cancer -

XX PS Example 8; Page 53; 124pp; English.

XX SQ Sequence

9 AA:

Query Match 100.0%; Score 19; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 AAPL 4

Db 6 AAPL 9

RESULT 26

AAU02213 standard; Peptide; 9 AA.

ID AAU02213

XX AAU02273

AC AAU02273;

XX DT 29-AUG-2001 (first entry)

XX DE HLA binding TAG-16 peptide #49.

XX KW Human; extracellular serine protease; tumour antigen derived gene-16; TAG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;

KW prostate cancer; HLA type.

XX OS Homo sapiens.

XX PN WO200127257-A1.

XX PD 19-APR-2001.

XX PF 13-OCT-2000; 2000WO-US28558.

XX PR 14-OCT-1999; 99US-0418527.

XX PA (UAR-) UNIV ARKANSAS.

XX PI O'Brien TJ, Underwood LJ, Shigemasa K;

XX DR WPI; 2001-273769/2B.

XX PT New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer -

XX PT treatment of ovarian, breast, lung, colon and prostate cancer -

XX PS Example 8; Page 53; 124pp; English.

XX SQ Sequence

9 AA:

Query Match 100.0%; Score 19; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 AAPL 4

Db 4 AAPL 7

CC monitor the level of 84P2A9 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.
CC and in systems for spectroscopic measurements. Compositions containing
CC the probe allow for high throughput and miniaturised screening systems
CC for drug discovery and profiling. Assays using the probe exhibit a large
CC dynamic range, increased sensitivity and allow ratiometric readouts for
CC the detection of post-translational activities. The present sequence for
CC represents a tyrosine kinase activity detection probe motif which is
CC cleavable by chymotrypsin.

SQ Sequence

Query Match 100.0%; Score 19; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPL 4

Db 6 AAPL 9

RESULT 25

AAU06934 standard; Peptide; 9 AA.

ID AAU06934

XX AAU06954;

AC AAU06954;

XX DT 24-OCT-2001 (first entry)

XX DE Human MHC molecule HLA-B7 binding 84P2A9 peptide #22.

XX KW 84P2A9-related protein; prostate; testis; tissue; cancer; leukaemia;

KW tumour; kidney; brain; bone; skin; ovary; breast; pancreas; colon; lung;

KW cytosolic; gene therapy; antibody therapy; ribozyme; serum; blood;

XX OS single chain monoclonal antibody; urine.

XX OS Homo sapiens.

XX PN WO200155391-A2.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-US2651.

XX PR 20-JAN-2000; 2000US-0178560.

XX PA (UROG-) UROGENESIS INC.

XX PA Jakobovits A., Afar DEH, Challita-eid PM, Levin E, Mitchell SC;

PI PI Herbert RS;

XX DR WPI; 2001-502631/55.

XX PT New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer -

XX PT treatment of ovarian, breast, lung, colon and prostate cancer -

XX PS Example 8; Page 53; 124pp; English.

XX SQ Sequence

Query Match 100.0%; Score 19; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPL 4

Db 6 AAPL 9

RESULT 26

AAU02213 standard; Peptide; 9 AA.

ID AAU02213

XX AAU02273

AC AAU02273;

XX DT 29-AUG-2001 (first entry)

XX DE HLA binding TAG-16 peptide #49.

XX KW Human; extracellular serine protease; tumour antigen derived gene-16; TAG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;

KW prostate cancer; HLA type.

XX OS Homo sapiens.

XX PN WO200127257-A1.

XX PD 19-APR-2001.

XX PF 13-OCT-2000; 2000WO-US28558.

XX PR 14-OCT-1999; 99US-0418527.

XX PA (UAR-) UNIV ARKANSAS.

XX PI O'Brien TJ, Underwood LJ, Shigemasa K;

XX DR WPI; 2001-273769/2B.

XX PT New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer -

XX PT treatment of ovarian, breast, lung, colon and prostate cancer -

XX PS Example 8; Page 53; 124pp; English.

XX SQ Sequence

Query Match 100.0%; Score 19; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 AAPL 4

Db 4 AAPL 7

CC The polypeptide sequences represent the 84P2A9-related protein and peptide fragments of the protein. 84P2A9 exhibits prostate and testis specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including leukaemia and tumours of the prostate, testis, kidney, brain, bone, skin, ovary, breast, pancreas, colon and lung. The 84P2A9 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 84P2A9-related protein, and a ribozyme capable of cleaving a polynucleotide having the 84P2A9 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 84P2A9. The sequences can be used in diagnostic methods to

RESULT 27
 ARR96502
 ID AAR96502 standard; peptide; 10 AA.
 XX
 AC AAR96502;
 XX DT 07-MAR-1997 (first entry)
 DE Hepatitis C virus type 4k peptide.
 XX KW Hepatitis C virus; subtype; polymerase chain reaction; amplification;
 KW PCR; primer; probe; antibody; infection.
 OS Synthetic.
 XX
 PN WO9613590-A2.
 XX PD 09-MAY-1996.
 XX PR 23-OCT-1995; 95WO-EP04155.
 XX PR 28-JUN-1995; 95EP-0870076.
 XX PR 21-OCT-1994; 94EP-0870166.
 XX PA (INNO-) INNOGENETICS NV.
 XX PI Maertens G, Stuyver L;
 DR WPI; 1996-251460/25.
 XX PT Acceptor polypeptide for N-acetylgalactosaminyltransferase -
 PT used to develop products for altering glycosylation of proteins
 PT and peptide(s)
 XX PS Claim 1; Page 63; 92pp; English.
 CC A novel synthetic acceptor peptide (I) (AAW16482) for the enzyme
 CC N-acetylgalactosaminyltransferase (GalNACT) (see also AAW16484) can be
 CC used to control glycosylation of a protein or peptide. The
 CC acceptor specificity of bovine colostrum GalNACT (see also AAW16484)
 CC was detd. using a semi-quantitative analysis of the amino acids
 CC surrounding known glycosylation sites in 16 different proteins.
 CC Synthetic acceptor peptides (see also AAW16485-88) were then designed
 CC and the transfer of 3H-acetylgalactosamine to the acceptor peptides
 CC by GalNACT was examined. The results showed that Peptide (I) had
 CC the highest catalytic efficiency of the peptides examined. The
 CC glycosylation of a protein may be controlled by incorporating a
 CC DNA sequence encoding (I) into the gene for the protein, and
 CC exposing the expressed protein to GalNACT.
 XX SQ Sequence 10 AA:
 Query batch 100.0%; Score 19; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3e-02; 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAPL 4
 Db 7 AAPL 10
 SQ Sequence 10 AA:
 RESULT 28
 Query Match 100.0%; Score 19; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAPL 4
 Db 5 AAPL 8
 RESULT 28
 Query Match 100.0%; Score 19; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1169.
 XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9945954-A1.
 DE Acceptor peptide for N-acetylgalactosaminyltransferase.
 PD 16-SEP-1999.

XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PT Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
DR WPI; 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment
XX
and diagnosis of cancers and viral diseases -
PS claim 1; Page 76; 150pp; English.
XX
AAV4390 to AAV48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
known as human leukocyte antigen (HLA)) binding motif. The immunogenic
peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2, 1, A1, A3, 2, or A24, 1 or HLA-B or C) and induce a cytotoxic T cell
response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (Crus) which destroy antigen-bearing cells are
normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce Cris ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
XX
SQ sequence 10 AA:
Query Match 100.0%; Score 19; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+02; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPL 4
Db 5 AAPL 8
RESULT 30
AAU06981
ID AAU06981 standard; Peptide: 10 AA.
AC AAU06981;
XX DT 24-OCT-2001 (first entry)
DE Human MHC molecule HLA-B7 binding 84P2A9 peptide #49.
XX KW 84P2A9-related protein; prostate; testis; tissue; cancer; leukaemia;
KW tumour; kidney; brain; bone; skin; ovary; breast; pancreas;
KW cytostatic; gene therapy; antibody therapy; ribozyme; serum; blood;
KW single chain monoclonal antibody; urine.
XX OS Homo sapiens.
XX PN WO20015391-A2.
XX PD 02-AUG-2001.
XX PR 26-JAN-2001; 2001WO-US02651.
XX PR 26-JAN-2000; 2000WO-018560.

XX
PA (UROG-) UROGENESYS INC.
XX PT Jakobovits A, Afar DEH, Challita-eid PM, Levin E, Mitchell SC;
PT Hubert RS;
XX DR WPI; 2001-502631/55.
XX PT New 84P2A9 gene and its encoded protein, useful for diagnosing and
treating cancer, e.g. leukaemia and cancer of the prostate, testis,
kidney, brain or bone, or for eliciting an immune response -
XX PS Example 12; Page 110; 149pp; English.
CC The polypeptide sequences represent the 84P2A9-related protein and
peptide fragments of the protein. 84P2A9 exhibits prostate and testis
specific expression in normal adult tissue, but it is also aberrantly
expressed in many cancers including leukaemia and tumours of the
CC prostate, testis, liver, brain, bone, skin, ovary, breast, pancreas,
colon and lung. The 84P2A9 polynucleotide, its related protein and
peptide fragments and specific PCR primers are therefore useful for
diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
binds to an 84P2A9-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 84P2A9 coding sequence, are both useful in the
preparation of a composition for treating a patient with a cancer that
CC expresses 84P2A9. The sequences can be used in diagnostic methods to
monitor the level of 84P2A9 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX SQ sequence 10 AA;
Query Match 100.0%; Score 19; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+02; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPL 4
Db 7 AAPL 10
RESULT 31
ID AG94730
XX AG94730 standard; Peptide: 10 AA.
AC AG94730;
XX DT 18-SEP-2001 (first entry)
XX DE Human complementary peptide, SEQ ID NO: 924.
KW Human; complementary peptide; ligand; drug discovery; drug design.
OS Homo sapiens.
XX PN WO200142277-A2.
PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB04776.
XX PR 13-DEC-1999; 99GB-0029464.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX DR WPI; 2001-408419/43.
XX PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -

XX
 PS Example 4; Page 171; 646pp; English.
 XX
 CC The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 19; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Db 5 AAPL 8
 RESULT 32
 AA42595 AARR2595 standard; peptide; 12 AA.
 XX
 AC AARR2595;
 XX
 DT 11-DEC-1994 (first entry)
 XX
 DE Peptide JBL analogous to D-domain portion of IGF-1.
 XX
 KW Insulin-like growth factor-1; IGF-1; receptor; antagonist;
 KW autoprophosphorylation inhibitor; C-domain; D-domain; restenosis;
 KW cancer; metastasis; asthma; cell proliferation; burns; wounds.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FH Disulfide-bond 1.12
 FT XX
 PR WO9323067-A.
 XX
 PA 25-NOV-1993.
 XX
 PR 07-MAY-1993; 93WO-US04329.
 XX
 PR 08-MAY-1992; 92US-0881524.
 XX
 PA (UWE-) UNIV JEFFERSON THOMAS.
 XX
 PT Baserga R, Jameson BA;
 XX
 DR WPI; 1993-386212/48.
 XX
 Compn. contg. peptide(s) corresp. to C or D domains of
 PT insulin-like growth factor - inhibit receptor
 PT auto-phosphorylation and used for treating cell proliferation,
 PT e.g. cancer, restenosis or asthma
 XX
 PS Claims 8, 17; Pages 29, 30; 41pp; English.
 XX
 The invention relates to a pharmaceutical composition and method for
 CC inhibiting cell proliferation, in which the active ingredient
 CC is a synthetic peptide of less than 25 amino acids comprising at
 least a portion of the C- or D-domain of human insulin-like growth
 factor-1. The peptide inhibits IGF-1 induction of auto-
 phosphorylation by IGF-1 receptor. Diseases which the peptide
 CC can be used to treat include restenosis of the coronary arteries
 CC after angioplasty, human neoplasia such as cancer of the prostate,
 CC tumours in pleural and peritoneal cavities and brain metastases,
 CC smooth muscle cell hyperplasia in asthma, burns and wounds, and bone
 CC marrow containing highly proliferating cells.
 CC
 The present peptide, designated JBL, includes residues 61-69 in the
 CC sequence 12 AA;
 Sequence 12 AA;
 Query Match 100.0%; Score 19; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Db 3 AAPL 6
 RESULT 33
 AAWS1870 AAWS1870 standard; peptide; 12 AA.
 XX
 AC AAWS1870;
 XX
 DT 15-SEP-1998 (first entry)
 XX
 DE Peptide sequence which binds to IGF-1 receptor.
 XX
 KW Peptide tail; dicarboxylic acid; marker; chemical coupling; vaccine;
 KW chromatography; immunisation; diagnostic test; nerve reconstruction;
 KW conformationally constrained; diagnosis; growth factor; IGF-1; bFGF.
 XX
 OS Synthetic.
 XX
 PN EP844252-A2.
 XX
 PD 27-MAY-1998.
 XX
 PR 14-NOV-1997; 97EP-0870182.
 XX
 PR 15-NOV-1996; 96US-0030980.
 XX
 PA (REMA/) REMACHE J.
 XX
 PI DeForge D, Remacle J;
 XX
 DR WPI; 1998-274149/25.
 XX
 PT New cyclic peptides used in biotechnology - comprise di:carboxylic
 PT amino acid and tail for coupling to solid supports
 XX
 PS Disclosure; Page 6; 16pp; English.
 XX
 The invention relates to cyclic peptides which comprise a dicarboxylic
 CC amino acid and at least one tail for subsequent coupling on an element
 CC comprising a solid support, a high molecular weight compound, a marker
 CC and/or one or more other similar or different cyclic peptides. The
 CC peptides are used in biotechnology applications, particularly in
 chromatography, immunisation, development of diagnostic tests, vaccines
 CC and pharmaceuticals, for BlaCov ext., for development of combinatorial
 CC libraries of conformationally constrained peptides or for the
 CC development of new biomaterials which allow or improve the binding of
 CC specific antibodies, receptors, ligands, cells and tissues. The
 CC biomaterial may be used for grafting or binding of specific antibodies,
 CC receptors, ligands, cells or tissues and may be used for production or
 CC identification of new or known drugs, vaccines, hormones, interleurons or
 CC cytokines and may be used in the screening of specific cells, in
 CC particular for the diagnosis of tumour cells, which may adhere
 CC differently than normal cells upon the various types of biomaterial. The
 CC biomaterial can be used to allow preferential cells and/or tissues
 CC adhesion on specific parts of the biomaterial in order to guide the
 CC cells and tissue growth along preferential directions, particularly for
 CC specific applications such as nerve reconstruction. The present
 CC sequence represents a peptide which can fix on the IGF-1 receptor and
 CC can advantageously be used as a tailed cyclic peptide.

Sequence	12 AA:	Query Match	100.0%	Score	19;	DB	19;	Length	12;	
		Best Local Similarity	100.0%	Pred.	No.	3.5e+02;	Mismatches	0;	Indels	
QY	1 AAPL 4 111 3 AAPL 6	AAB92048	standard; Peptide; 12 AA.	XX	XX	XX	XX	XX	XX	
Db		AAB92048; AC	AC	XX	XX	XX	XX	XX	XX	
DT	22-JUN-2001 (first entry)	DE	Growth factor peptide SEQ ID NO:1224.	XX	XX	XX	XX	XX	XX	
XX	KW	Protection: endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.	XX	KW	KW	KW	KW	KW	KW	
OS	OS	Homo sapiens.	OS	OS	OS	OS	OS	OS	OS	
XX	PN	WO20069900-A2.	PN	XX	XX	XX	XX	XX	XX	
XX	PD	23-NOV-2000.	PD	XX	XX	XX	XX	XX	XX	
XX	PF	17-MAY-2000; 2000WO-US13576.	PF	XX	XX	XX	XX	XX	XX	
XX	PR	17-MAY-1999; 990US-0134406.	PR	XX	XX	XX	XX	XX	XX	
XX	PR	10-SEP-1999; 990US-0153406.	PR	XX	XX	XX	XX	XX	XX	
XX	PR	15-OCT-1999; 990US-0159783.	PR	XX	XX	XX	XX	XX	XX	
PA	(CONJU-) CONJUCHEM INC.	PA	BRIDON DP, EBRIN AM, MILNER PG, HOLMES DL, THIBAUDEAU K; DR	XX	XX	XX	XX	XX	XX	
XX	PT	WPI; 2001-11-2059/12.	PT	XX	XX	XX	XX	XX	XX	
XX	PT	Modifying and attaching therapeutic peptides to albumin prevents peptide degradation, useful for increasing length of in vivo activity	PT	XX	XX	XX	XX	XX	XX	
XX	PS	Disclosure; Page 595; 733pp; English.	PS	XX	XX	XX	XX	XX	XX	
XX	CC	The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.	CC	CC	CC	CC	CC	CC	CC	
CC	CC	(1) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.	CC	CC	CC	CC	CC	CC	CC	
CC	CC	Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes.	CC	CC	CC	CC	CC	CC	CC	
CC	CC	ABAB9829 to AAB9241 represent peptides which can be used in the exemplification of the present invention.	CC	CC	CC	CC	CC	CC	CC	
CC	CC	QY	1 AAPL 4 111	QY	1 AAPL 4 111	QY	1 AAPL 4 111	QY	1 AAPL 4 111	
SQ	Sequence	12 AA:	Query Match	100.0%	Score	19;	DB	21;	Length	13;
			Best Local Similarity	100.0%	Pred.	No.	3.3e+02;	Mismatches	0;	Indels
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	

Db 4 AAPL 7

RESULT 36

ID AAR38723

XX AAR38723 standard; peptide; 14 AA.

XX AAR38723;

XX DT 09-DEC-1993 (first entry)

DE N-terminal fragment of Megakaryocyte amplifying factor.

XX Megakaryocyte potentiator; Meg-Pot; thrombocytopenia; platelet hypofunction; thrombocyte; interleukin-3; IL-3.

XX PN WO313112-A.

XX PD 08-JUL-1993.

XX 24-DEC-1992; 92WO-JP01689.

XX PR 27-DEC-1991; 91JP-0361522.

PR 31-MAR-1992; 92JP-0122518.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Hattori K, Kojima T, Oh-edo M, Yamaguchi N;

XX DR WPI; 1994-167467/20.

XX PT New mega-karyocyte potentiator - for potential treatment of thrombocytopenia

XX PS Disclosure; Page 49; 74pp; Japanese.

XX CC DNA encoding Meg-Pot has potential use in treatment of thrombocytopenia and low platelet function.

XX SQ Sequence 14 AA;

Query	1 AAPL 4	Db	7 AAPL 10
WPI; 1993-222724/28.			
XX			
Mega-karyocyte amplifier of specified sequence - for treating thrombocytopenia and platelet hypo-funtion			
PT			
XX			
PS Claim 1; Page 16; 23pp; Japanese.			
XX			
CC Megakaryocyte potentiator ("Meg-Pot") amplifies megakaryocytes in vitro in the presence of interleukin-3. The protein elutes in the 40-45% acetonitrile/TFA fraction in reverse phase HPLC, has mol. wt. 32000 (SDS-PAGE) and includes the amino acid sequence AAR38723.			
XX SQ Sequence 14 AA;			
Query Match 100.0%; Score 19; DB 14; Length 14;			
Best Local Similarity 100.0%; Pred. No. 4.1e+02;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 AAPL 4			
Db 7 AAPL 10			

RESULT 37

ID AAR53987

XX AAR53987 standard; peptide; 14 AA.

XX AC AAR53987;

XX DT 08-DEC-1994 (first entry)

DE Meg-Pot N-terminal peptide.

XX Megakaryocyte potentiator; Meg-Pot; thrombocytopenia; platelet.

XX OS Homo sapiens.

XX PN WO9410312-A.

XX PD 11-MAY-1994.

XX PR 25-OCT-1993; 93WO-JP01540.

XX PA (CURA-) CURAGEN CORP.

XX PI Shinkets RA, Leach M;

XX DR WPI; 2001-355949/37.

XX PA Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism -

XX PT Isolated human nucleic acids comprising one or more single nucleotide polymorphisms (SNPs). ABB56531 comprising one or more single nucleotide polymorphisms (SNPs). ABB56531 to ABB56903 represent human peptides encoded by some of the SNP CC oligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides

PR 23-OCT-1992; 92JP-0286153.

PR 11-NOV-1992; 92JP-0301387.

PR 09-DEC-1992; 92JP-0329546.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Hattori K, Kojima T, Oh-edo M, Yamaguchi N;

XX DR WPI; 1994-167467/20.

XX PT New mega-karyocyte potentiator - for potential treatment of thrombocytopenia

XX PS Disclosure; Page 49; 74pp; Japanese.

XX CC DNA encoding Meg-Pot has potential use in treatment of thrombocytopenia and low platelet function.

XX SQ Sequence 14 AA;

Query	1 AAPL 4	Db	7 AAPL 10
ABB56859			
ID ABB56859 standard; Peptide; 14 AA.			
XX			
AC ABB56859;			
XX DT 05-MAR-2002 (first entry)			
XX DE Human SNP related amino acid sequence SEQ ID NO:1424.			
XX KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; immunosuppressive; antinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease; infection; polymorphic protein.			
XX OS Homo sapiens.			
XX PN WO200138586-A2.			
XX PD 31-MAY-2001.			
XX XX			
XX PF 22-NOV-2000; 2000WO-US32311.			
XX PR 24-NOV-1999; 99US-0167383.			
XX PA (CURA-) CURAGEN CORP.			
XX PI Shinkets RA, Leach M;			
XX DR WPI; 2001-355949/37.			
XX PA Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism -			
XX PT Isolated human nucleic acids comprising one or more single nucleotide polymorphisms (SNPs). ABB56531 comprising one or more single nucleotide polymorphisms (SNPs). ABB56531 to ABB56903 represent human peptides encoded by some of the SNP CC oligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides			
XX PS Claim 1; Page 664; 674pp; English.			

Page 19

CC and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism. The pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterised polymorphism are present in individuals. The antibodies may be used in the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples).

	RESULT	40
ABP46386	ABP46386	ID
XX	ABP46386	ID
AC	ABP46386	ID
XX	ABP46386	ID
DT	ABP46386	ID
XX	ABP46386	ID
DE	ABP46386	ID
XX	ABP46386	ID
Human	ABP46386	ID
B1	ABP46386	ID

; 0002 (first entry)
sys binding scFv VH CDR3 SEQ ID 2397

Query Match 100.0%; Score 19; DB 22; Length 14;
 Best Local Similarity 100.0%; pred. No. 4 $1e+02$; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0.
 Qy 1 AAPL 4
 Db 1 AAPL 4

PN	immunosuppress
KW	antiAIDS; vac
KW	systemic lupu
KW	common variab
XX	
OS	
XX	
OS	
Homo sapiens.	
WO200202641-A	

1. progressive; immunoppressive; immunostimulative; immunosuppressive; immunotherapy; medicine; cancer; erythematosus; immunodeficiency

stimulant; immune; autoimmunity; rheumatoid arthritis; deficiency; acquired

nomodulatory; immune disorders; arthritis; CVID; ed immunodeficiencies.

antirheumatic;
immunodeficiency;
AIDS;
syndrome.

RESULT 39
 AAB67038
 ID AAB67038 standard; Peptide; 14 AA.
 XX
 AC
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Human insulin-like growth factor agonist peptide SEQ ID NO: 38.
 XX Human; insulin like growth factor; IGF; agonist; hyperglycaemic disorder;
 KW obesity; neurological disorder; cardiac disorder; renal disorder;
 KW immunological disorder; anabolic disorder.
 XX OS Homo sapiens.
 XX PN WO200078801-A2.
 XX PD 28-DEC-2000.
 XX PR 19-JUN-2000; 2000WO-US17023.
 XX PA 22-JUN-1999; 99US-0337227.
 XX PI (GETH) GENENTECH INC.
 XX Chen YM, Cochran AG, Lowman HB, Skelton NJ;
 XX DR WPI; 2001-112312/12.
 XX PT New peptide for increasing serum and tissue levels of biological active
 PT insulin growth factor -
 XX PS Example 1; Page 54; 75PP; English.
 XX CC The present invention provides the sequences of a number of peptides
 CC which act as human insulin growth factor (IGF) agonists. These can be
 CC used in the treatment of hyperglycaemic, obesity-related, neurological,
 CC cardiac, renal, immunological and anabolic disorders.
 Sequence 14 AA;
 SQ

10-JAN-2002. PPD
 XX
 PR 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-216248P.
 PR 21-MAR-2001; 2001US-217379P.
 PR 25-MAY-2001; 2001US-233499P.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMS-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PT Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX DR WPI; 2002-114799/15.
 XX
 PR Antibodies against B Lymphocyte Stimulating Polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS claim 2; Page 2983; 3148PP; English
 PS XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BiYS) polypeptides. BiYS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antiinflammatory and antiRAbs activity and can be used in vaccines to
 CC inhibit the expression and activity of BiYS. The antibodies bind to BiYS
 CC and so may be used to detect and quantitate the presence of BiYS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BiYS. They may also be
 CC administered to treat diseases associated with aberrant BiYS expression
 CC and activity such as cancer, immune and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP13900-ABP17228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 sequence 14 AA;
 SQ

```

Query Match          100.0%; Score 19; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0;
Indels 0; Gaps 0
QY    1 AAPL 4
      ||||| 
Db    3 AAPL 6

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Quality metric: 100.0%; Score 15; Lb 425; Ua 425; Length 144;
Best Local Similarity 100.0%; Pred. No. 4; Tie 425;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 1 AAPL 4
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Db 9 AAPL 12

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Fri Dec 6 14:08:59 2002

Job time : 27 secs

us-10-033-526-3.mod.rag

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2002, 13:26:14 ; Search time 9,33333 Seconds
(without alignments)
12.610 Million cell updates/sec

Title: US-10-033-526-3
perfect score: 19 AAPL 4
Sequence: APPI

Scoring table: BL0SUM62, Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 294122922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 10%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: ./cpn2-6/ptodata/1/iaa/5B_COMBO.pep:*

3: ./cpn2-6/ptodata/1/iaa/6A_COMBO.pep:*

4: ./cpn2-6/ptodata/1/iaa/6B_COMBO.pep:*

5: ./cpn2-6/ptodata/1/iaa/PCRS_COMBO.pep:*

6: ./cpn2-6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	19	100.0	4 1 US-08-004-6A3C-4	Sequence 4, APPI
2	19	100.0	4 1 US-08-5A4-143A-6	Sequence 1, APPI
3	19	100.0	4 1 US-08-224-888-9	Sequence 6, APPI
4	19	100.0	4 1 US-08-777-208-6	Sequence 9, APPI
5	19	100.0	4 1 US-08-633-633-1	Sequence 6, APPI
6	19	100.0	4 1 US-08-638-575E-1	Sequence 1, APPI
7	19	100.0	4 2 US-08-907-840A-3	Sequence 1, APPI
8	19	100.0	4 2 US-08-967-508-17	Sequence 1, APPI
9	19	100.0	4 3 US-09-069-823-1	Sequence 1, APPI
10	19	100.0	4 4 US-09-578-303-10	Sequence 1, APPI
11	19	100.0	4 4 US-08-888-842-3	Sequence 10, APPI
12	19	100.0	4 8 1 US-08-057-184-11	Sequence 3, APPI
13	19	100.0	8 1 US-08-057-184-11	Sequence 11, APPI
14	19	100.0	8 1 US-08-057-184-12	Sequence 12, APPI
15	19	100.0	9 2 US-08-340-283-143	Sequence 13, APPI
16	19	100.0	9 4 US-08-772-283-29	Sequence 22, APPI
17	19	100.0	9 4 US-09-300-542N-4	Sequence 4, APPI
18	19	100.0	10 3 US-09-105-678A-51	Sequence 51, APPI
19	19	100.0	10 4 US-09-421-208-51	Sequence 51, APPI
20	19	100.0	11 2 US-08-835-231-2	Sequence 2, APPI
21	19	100.0	11 2 US-08-967-506-17	Sequence 17, APPI
22	19	100.0	11 3 US-08-967-506-17	Sequence 17, APPI
23	19	100.0	11 5 PCT-US94-0552-17	Sequence 2, APPI
24	19	100.0	11 5 PCT-US94-0552-17	Sequence 17, APPI
25	19	100.0	12 3 US-08-215-787A-3	Sequence 3, APPI
26	19	100.0	12 5 PCT-US93-04328-3	Sequence 3, APPI
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ALIGNMENTS

RESULT	1	US-08-004-643C-4	;	Sequence 4, APPI
Patent No.	548079	Patent No. 4, Application US/08004643C	;	Sequence 4, APPI
GENERAL INFORMATION:			;	Sequence 4, APPI
APPLICANT:	Gunter Fischer & Gerhard Kllerz		;	Sequence 4, APPI
TITLE OF INVENTION:	Cyclosporine Assay		;	Sequence 4, APPI
NUMBER OF SEQUENCES:	7		;	Sequence 4, APPI
CORRESPONDENCE ADDRESS:	Gunter Fischer et al. c/o G. P. Katona		;	Sequence 4, APPI
STREET:	230 Park Avenue, Room 2200		;	Sequence 4, APPI
CITY:	New York		;	Sequence 4, APPI
STATE:	New York		;	Sequence 4, APPI
ZIP:	10169		;	Sequence 4, APPI
COMPUTER READABLE FORM:			;	Sequence 4, APPI
MEDIUM TYPE:	FLOPPY disk		;	Sequence 4, APPI
COMPUTER:	IBM PC compatible		;	Sequence 4, APPI
OPERATING SYSTEM:	MS-DOS		;	Sequence 4, APPI
SOFTWARE:	conf. to Patentin Release #1.0, Ver.#1.25		;	Sequence 4, APPI
CURRENT APPLICATION NUMBER:	US/08/004-643C		;	Sequence 4, APPI
FILING DATE:	12 January 1993		;	Sequence 4, APPI
CLASSIFICATION:	435		;	Sequence 4, APPI
PRIOR APPLICATION DATA:			;	Sequence 4, APPI
APPLICATION NUMBER:	703-590		;	Sequence 4, APPI
FILING DATE:	20 May 1991		;	Sequence 4, APPI
APPLICATION NUMBER:	398-092		;	Sequence 4, APPI
FILING DATE:	24 August 1989		;	Sequence 4, APPI
APPLICATION NUMBER:	UD WP 601 F/319 577W		;	Sequence 4, APPI
FILING DATE:	07 September 1988		;	Sequence 4, APPI
ATTORNEY/AGENT INFORMATION:			;	Sequence 4, APPI
NAME:	Katona, Gabriel P.		;	Sequence 4, APPI
REGISTRATION NUMBER:	20-829		;	Sequence 4, APPI
REFERENCE/DOCKET NUMBER:	691-003		;	Sequence 4, APPI
TELECOMMUNICATION INFORMATION:			;	Sequence 4, APPI
TELEPHONE:	(212)986-3377		;	Sequence 4, APPI
TELEFAX:	(212)986-6126		;	Sequence 4, APPI
TELEX:			;	Sequence 4, APPI
INFORMATION FOR SEQ ID NO: 4:			;	Sequence 4, APPI
SEQUENCE CHARACTERISTICS:			;	Sequence 4, APPI
LENGTH:	4 amino acid residues		;	Sequence 4, APPI
TYPE:	amino acid		;	Sequence 4, APPI
STRANDEDNESS:	single		;	Sequence 4, APPI
TOPOLOGY:	linear		;	Sequence 4, APPI
;	US-08-004-643C-4		;	Sequence 4, APPI
Query Match Score: 100.0%; Score: 19; DB 1; Length: 4;			;	Sequence 4, APPI
Best Local Similarity: 100.0%; pred. No. 2e+05; Mismatches: 0; Indels: 0; Gaps: 0;			;	Sequence 4, APPI

QY 1 AAPL 4
 QY 1 AAPL 4
 Db 1 AAPL 4

RESULT 2
 US-08-345-820B-1
 Sequence 1, Application US/08345820B
 Patent No. 5618792
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS USEFUL AS INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL ELASTASE
 NUMBER OF SEQUENCES: 4
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-345, 820B
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 STRANDEDNESS: single
 TOPOLogy: unknown
 MOLECULE TYPE: peptide

RESULT 3
 US-08-544-143A-6
 Sequence 5, Application US/08544143A
 Patent No. 5646028
 GENERAL INFORMATION:
 APPLICANT: Leigh, Scott D.
 TITLE OF INVENTION: NOVEL ALKALINE PROTEASE AND USES
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/224, 868
 FILING DATE: 08-APR-1995
 CLASSIFICATION: 436
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/200, 404
 FILING DATE: 23-FEB-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/782, 761
 FILING DATE: 22-OCT-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/487, 115
 FILING DATE: 02-MAR-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/279, 176
 FILING DATE: 02-DEC-1988
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/841, 792
 FILING DATE: 26-FEB-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/521, 074
 FILING DATE: 09-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Bent, Stephen A.
 REGISTRATION NUMBER: 29, 768
 REFERENCE/DOCKET NUMBER: 64688/125/CHRE
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 9001136
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

RESULT 4
 US-08-224-868-9
 Sequence 9, Application US/08224868
 Patent No. 5698448
 GENERAL INFORMATION:
 APPLICANT: Sjodin, Steven J.
 TITLE OF INVENTION: IMMUNOSUPPRESSIVE DRUG BINDING PROTEINS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESS: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/224, 868
 FILING DATE: 08-APR-1995
 CLASSIFICATION: 436
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/200, 404
 FILING DATE: 23-FEB-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/782, 761
 FILING DATE: 22-OCT-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/487, 115
 FILING DATE: 02-MAR-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/279, 176
 FILING DATE: 02-DEC-1988
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/841, 792
 FILING DATE: 26-FEB-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/521, 074
 FILING DATE: 09-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Bent, Stephen A.
 REGISTRATION NUMBER: 29, 768
 REFERENCE/DOCKET NUMBER: 64688/125/CHRE
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 9001136
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

INFORMATION FOR SEQ ID NO: 6:

; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-224-868-9
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 ; Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 4;
 ; Matches 4; Conservative 0; Indels 0; Gaps 0;
 ; QY 1 AAPL 4
 ; Db 1 AAPL 4
 ;
 ; RESULT 5
 ; US-08-77-208-6
 ; Sequence 6, Application US/0877208
 ; Patent No. 5763576
 ; GENERAL INFORMATION:
 ; APPLICANT: Powers, James C.
 ; TITLE OF INVENTION: Tetrapeptide Alpha-Ketocamides
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Deveau, Colton & Marquis
 ; STREET: Two Midtown Plaza, Suite 1400
 ; CITY: Atlanta
 ; STATE: GA
 ; COUNTRY: USA
 ; ZIP: 30309
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM Compatible
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 ; OPERATING SYSTEM: Microsoft Windows 95
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/777,208
 ; FILING DATE: 27-DEC-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/539944
 ; FILING DATE: 06-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Colton, Laurence P.
 ; REGISTRATION NUMBER: 33371
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404) 875-3555
 ; FAX: (404) 875-8505
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; STRANDEDNESS: single
 ; TOPOLogy: unknown
 ; MOLECULE TYPE: Peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Synthetic
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 ; OTHER INFORMATION: /label= 1a
 ; FEATURE: /note= "glutaryl derivative"
 ; NAME/KEY: Modified-site
 ; LOCATION: 4
 ; OTHER INFORMATION: /label= 1b
 ; OTHER INFORMATION: /note= "p-nitro-anilide derivative"
 ; US-08-77-208-6
 ; Query Match 100.0%; Score 19; DB 1; Length 4;
 ; Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 4;
 ; Matches 4; Conservative 0; Indels 0; Gaps 0;
 ; QY 1 AAPL 4
 ; Db 1 AAPL 4
 ;
 ; RESULT 6
 ; US-08-93-653-1
 ; Sequence 1, Application US/08693653
 ; Patent No. 5780439
 ; GENERAL INFORMATION:
 ; APPLICANT: Mendy, Francois
 ; APPLICANT: Kahn, Jean Maurice
 ; APPLICANT: Roger, Loic
 ;
 ; RESULT 7
 ; US-08-98-575E-1
 ; Sequence 1, Application US/08698575E
 ; Patent No. 584585
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS USEFUL AS
 ; NUMBER OF SEQUENCES: 4

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0., Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/698,575E
 FILING DATE:
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/345,820
 FILING DATE:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: single stranded
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-698-575E-1

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 Query Match 100.0%; Score 19; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 AAPL 4

Qy 1 AAPL 4
 Db 1 AAPL 4

US-08-907-840A-3
 Sequence 3 Application US/08907840A
 PATENT NO. 5952307
 GENERAL INFORMATION:
 APPLICANT: Powers, James C.
 TITLE OF INVENTION: Basic Alpha-Aminokalylphosphonate
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Deveau, Colton & Marquis
 STREET: Two Midtown Plaza, Suite 1400
 CITY: Atlanta
 STATE: GA
 COUNTRY: USA
 ZIP: 30309

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Microsoft Windows 95
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/907,840A
 FILING DATE: 14 AUG-1997
 CLASIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/184286
 FILING DATE: 21 JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Colton, Laurence P.
 REGISTRATION NUMBER: 33371
 REFERENCE: 10733-175CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 875-3555
 TELEFAX: (404) 875-8505
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: no
 US-08-907-840A-3

RESULT 9
 Query Match 100.0%; Score 19; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 AAPL 4

Qy 1 AAPL 4
 Db 1 AAPL 4

US-08-765-165-1
 Sequence 1 Application US/08765165
 PATENT NO. 5985233
 GENERAL INFORMATION:
 APPLICANT: Reed, Benjamin J.
 APPLICANT: Sandeman, Richard M.
 APPLICANT: Chandler, David S.
 TITLE OF INVENTION: BIOLOGICAL CONTROL OF INSECTS
 FILE REFERENCE: 08820/002001
 CURRENT APPLICATION NUMBER: US/08/765,165
 EARLIER FILING DATE: 1997-06-27
 EARLIER APPLICATION NUMBER: PCT/AU95/00347
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic substrates
 US-08-765-165-1

Query Match 100.0%; Score 19; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 AAPL 4

Qy 1 AAPL 4
 Db 1 AAPL 4

RESULT 10
 US-09-069-823-1
 Sequence 1 Application US/09069823
 PATENT NO. 6037325
 GENERAL INFORMATION:
 APPLICANT: Gyorkos, Albert C.
 APPLICANT: Spruce, Lyle W.
 TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS
 TITLE OF INVENTION: USEFUL AS INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL
 FILE REFERENCE: 20774.240087
 CURRENT APPLICATION NUMBER: US/09/069,823
 CURRENT FILING DATE: 1998-04-30
 EARLIER APPLICATION NUMBER: 08/345,820
 EARLIER FILING DATE: 1994-11-21
 EARLIER APPLICATION NUMBER: 08/698,575
 EARLIER FILING DATE: 1996-08-15
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Tetrapeptide
 US-09-069-823-1

Query Match 100.0%; Score 19; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 19; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-09-578-303-10
 QY 1 AAPL 4
 Db 1 AAPL 4
 GENERAL INFORMATION:
 APPLICANT: Travis, James
 APPLICANT: Whitworth, S. Troy
 TITLE OF INVENTION: Ant Proteases and Methods of Inhibition
 FILE REFERENCE: 235_001-0101
 CURRENT APPLICATION NUMBER: US/09/578, 303
 CURRENT FILING DATE: 2000-05-25
 PRIORITY FILING DATE: 1999-05-27
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 10
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence:
 OTHER INFORMATION: para-nitroanalide substrate
 NAME/KEY: SITE
 LOCATION: (1)
 OTHER INFORMATION: succinyl end cap
 NAME/KEY: SITE
 LOCATION: (4)
 OTHER INFORMATION: para-nitroanalide end cap
 ;US-09-578-303-10

Query Match 100.0%; Score 19; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 US-08-888-842-3
 QY 1 AAPL 4
 Db 1 AAPL 4
 GENERAL INFORMATION:
 APPLICANT: Lu, Jun Ping
 APPLICANT: Gantley, Lewis C.
 APPLICANT: Yaffe, Michael
 APPLICANT: Fischer, Gunter
 TITLE OF INVENTION: INHIBITORS OF PHOSPHOSERINE AND
 TITLE OF INVENTION: PHOSPHOTHREONINE-PROLINE-SPECIFIC ISOMERASES
 FILE REFERENCE: BIDM97-02PA
 CURRENT APPLICATION NUMBER: US/08/988, 842
 CURRENT FILING DATE: 1997-12-11
 EARLIER APPLICATION NUMBER: 60/058, 164
 EARLIER FILING DATE:
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 6
 TYPE: PRT
 ORGANISM: synthetic nucleotide
 FEATURE:
 NAME/KEY: PHOSPHORYLATION
 LOCATION: (3)...(5)
 ;US-08-888-842-3

Query Match 100.0%; Score 19; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 US-08-857-184-11
 QY 1 AAPL 4
 Db 1 AAPL 4
 GENERAL INFORMATION:
 PATENT NO. 5,385,888
 APPLICANT: Goodenow, Robert S
 APPLICANT: Olsson, Lenart
 TITLE OF INVENTION: Class I MHC Modulation of Surface
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bertram I. Rowland
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/057,184
 FILING DATE: 01-FEB-1991
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 FILING DATE: 01-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertam I
 REGISTRATION NUMBER: 20,015
 REFERENCE/DOCKET NUMBER: A-55115-2/BIR

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1969
 TELEFAX: (415) 398-3249

SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-057-184-12

Query Match 100.0%; Score 19; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 5 AAPL 8

RESULT 15
 US-08-340-283-143

Sequence 143, Application US/08340283

GENERAL INFORMATION:
 APPLICANT: EHammer, Ake P.
 TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
 NUMBER OF SEQUENCES: 205

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
 ADDRESS: (1920-32-1)
 STREET: 301 Henrietta Street
 CITY: Kalamazoo
 STATE: Michigan
 COUNTRY: U.S.A.
 ZIP: 49011

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/340-283
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: STANKE REA, Teresa
 REGISTRATION NUMBER: 30,427

REFERENCE/DOCKET NUMBER: 024916-005

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-340-283-143

Query Match 100.0%; Score 19; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4

RESULT 16
 US-08-772-282-29

Sequence 29, Application US/08772282

GENERAL INFORMATION:
 APPLICANT: SOKOL, Pamela A.
 APPLICANT: KOI, Cora D.
 TITLE OF INVENTION: CONSERVED METALLOPROTEASE EPITOPEs
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS, LLP
 STREET: P. O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22313-1404

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/772-282
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: STANKE REA, Teresa
 REGISTRATION NUMBER: 30,427

REFERENCE/DOCKET NUMBER: 024916-005

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-772-282-29

Query Match 100.0%; Score 19; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 AAPL 7

RESULT 17
US-09-306-542A-4
; Patent No. 6410255
; GENERAL INFORMATION:
; APPLICANT: AURORA BIOSCIENCES CORPORATION
; APPLICANT: POLLOK, Brian
; APPLICANT: HAMMAN, Brian
; APPLICANT: RODENS, Steven
; APPLICANT: MAKINGS, Lewis
; TITLE OF INVENTION: OPTICAL PROBES AND ASSAYS
; FILE REFERENCE: AURO1300
; CURRENT APPLICATION NUMBER: US/09/306,542A
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Optical probe specific motif
US-09-306-542A-4

Query Match 100.0%; Score 19; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 6 AAPL 9

RESULT 18
US-09-105-678A-51
; Sequence 51, Application US/09105678A
; PATENT NO. 6103882
; GENERAL INFORMATION:
; APPLICANT: Sueanga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 1130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-836-075A-185

Query Match 100.0%; Score 19; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 5 AAPL 8

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-51

Query Match 100.0%; Score 19; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 71; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 4 AAPL 7

RESULT 19
US-08-336-075A-185
Sequence 185, Application US/08836075A
PATENT NO. 6180768
; GENERAL INFORMATION:
; APPLICANT: MARRENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-075A-185

Query Match 100.0%; Score 19; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71; 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20
US-09-421-208-51
Sequence 51, Application US/09421208
PATENT NO. 6258561
GENERAL INFORMATION:
APPLICANT: Shigenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
APPLICATION NUMBER: US/09/421, 208
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILED DATE: 27-JUN-1997
APPLICATION NUMBER: US 09/105, 678
FILING DATE: 20-JUN-1998
APPLICATION NUMBER: JP 172118/1997
REGISTRATION NUMBER: 27, 026
REFERENCE NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLogy: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: protein
LOCATION: 4
OTHER INFORMATION: /note = "Xaa = D-Alanine"
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
; US-08-835-231-2
RESULT 21
US-08-935-231-2
Sequence 2, Application US/08835231
PATENT NO. 5861284
GENERAL INFORMATION:
APPLICANT: NISHIMURA, Osamu
APPLICANT: KURUYAMA, Masato
APPLICANT: KOYAMA, No. 5861284uyuki
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY ACTIVE RECOMBINANT CYSTEINE-FREE NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COMPUTER READABLE FORM:

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350, 709
FILED DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838, 857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
REGISTRATION NUMBER: 34, 235
REFERENCE/DOCKET NUMBER: 41614-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: protein
LOCATION: 4
OTHER INFORMATION: /note = "Xaa = D-Alanine"
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
; US-08-835-231-2
RESULT 22
US-08-967-508-17
Sequence 17, Application US/08967508
PATENT NO. 5910570
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammar, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/967,508
 FILING DATE: 13 NOVEMBER 1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/602,830
 FILING DATE: 13 NOVEMBER 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Darrelly Jr., James D.
 REGISTRATION NUMBER: 33,673
 REFERENCE/DOCKET NUMBER: 4755.P.CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 616-833-2210
 TELEFAX: 224401
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-967-508-17

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-967-506-17

Query Match 100.0%; Score 19; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 79; 0; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 111
 Db 7 AAPL 10

RESULT 23
 US-08-967-506-17
 Sequence 17, Application US/08967506
 Patent No. 6096512

GENERAL INFORMATION:
 APPLICANT: The Upjohn Company
 ADDRESS: 301 Henrietta Street
 CITY: Kalamazoo
 STATE: Michigan
 COUNTRY: USA
 ZIP: 49001

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/108,661
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/350,709
 FILING DATE: 07-DEC-1994
 APPLICATION NUMBER: 07-838,857
 FILING DATE: 18-FEB-1992
 APPLICATION NUMBER: JP 024841
 FILING DATE: 19-FEB-1991
 APPLICATION NUMBER: JP 0271438
 FILING DATE: 18-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 41614-FWC
 TELEPHONE: 617-523-6440
 TELEX: 20291-SIRE 2:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO

RESULT 24
 US-09-108-661-2
 Sequence 2, Application US/09108661
 Patent No. 6287805

GENERAL INFORMATION:
 APPLICANT: NISHIMURA, Osamu
 ADDRESS: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/108,661
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/350,709
 FILING DATE: 07-DEC-1994
 APPLICATION NUMBER: 07-838,857
 FILING DATE: 18-FEB-1992
 APPLICATION NUMBER: JP 024841
 FILING DATE: 19-FEB-1991
 APPLICATION NUMBER: JP 0271438
 FILING DATE: 18-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 41614-FWC
 TELEPHONE: 617-523-6440
 TELEX: 20291-SIRE 2:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO

ANTI-SENSE: NO
FEATURE: Protein
NAME/KEY: Protein
LOCATION: 4
OTHER INFORMATION: /note - "xaa = D-Alanine"

FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
; US-09-108-661-2

Query Match Similarity 100.0%; Score 19; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 79; DB 4; Length 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 5 AAPL 8

RESULT 25
PCT-US94-02552-17

Sequence 17, Application PC/TUS9402552
GENERAL INFORMATION:
APPLICANT: Elhammar, Ake P.

APPLICANT: Homa, Fred L.

TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAc:

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: The UpJohn Company, Corp. Intellectual

STREET: 301 Henretta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/02552
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673

REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3139
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
TOPOLOGY: linear

; US-08-219-878A-3

Query Match Similarity 100.0%; Score 19; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 86; DB 4; Length 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 3 AAPL 6

RESULT 27
PCT-US93-04329-3
Sequence 3, Application PC/TUS9304329
GENERAL INFORMATION:
APPLICANT: Bradford A. Jameson and Renato Baserga
TITLE OF INVENTION: IGF-1 Analogs
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04329
FILING DATE: 19930507
CLASSIFICATION:
PRIOR APPLICATION DATA:

RESULT 26
US-08-219-878A-3
; Sequence 3, Application US/08219878A

APPLICATION NUMBER: 07/881,524
 FILING DATE: 08 MAY 92,
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark DeLuca
 REGISTRATION NUMBER: 33,229
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-4399
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12
 TYPE: AMINO ACID
 TOPOLOGY: Linear
 PCT-US93-04329-3

RESULT 28

US-08-256-133-1
 Sequence 1, Application US/08256133
 Patent No. 5498698

GENERAL INFORMATION:

APPLICANT: Yamaguchi, No. 5498698om1

APPLICANT: On-Eda, Masayoshi

APPLICANT: Hattori, Kunihiro

TITLE OF INVENTION: NO. 5498698el Megakaryocyte Potentiator

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: 8110 Gatehouse Road, Suite 500 East
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,133

FILING DATE: 27-JUN-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 230-107P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEFAX: 703-205-8000

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant

MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 IMMEDIATE SOURCE:
 CLONE: HPCYS

FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..14
 OTHER INFORMATION: /label= peptide

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens

US-08-256-133-1

RESULT 29

US-08-426-819A-4
 Sequence 4, Application US/08426819A
 Patent No. 5723318

GENERAL INFORMATION:

APPLICANT: Yamaguchi, No. 5723318om1

APPLICANT: Kojima Teisuo

APPLICANT: On-Eda, Masayoshi

APPLICANT: Hattori, Kunihiro

TITLE OF INVENTION: Genes Coding for Megakaryocyte

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,819A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 230-107P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEFAX: 703-205-8000

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant

MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 IMMEDIATE SOURCE:
 CLONE: HPCYS

FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..14
 OTHER INFORMATION: /label= peptide

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens

US-08-426-819A-4

Query Match 100.0%; Score 19; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 7 AAPL 10

RESULT 30

Query Match 100.0%; Score 19; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 7 AAPL 10

US-09-337-227C-3B
Sequence 38, Application US/09337227C
Patent No. 6420518
GENERAL INFORMATION:
APPLICANT: Chen, Yvonne May-Yee
APPLICANT: Clark, Ross G.
APPLICANT: Cochran, Andrea G.
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
APPLICANT: Skelton, Nicholas J.
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR AGONIST MOLECULES
CURRENT APPLICATION NUMBER: US/09/337-227C
CURRENT FILING DATE: 1999-06-22
PRIORITY NUMBER: US 09/052,888
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: US 08/825,852
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 38
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence 1s synthesized
; Patent No. 6420518
; US-09-337-227C-38
RESULT 31
US-08-256-133-3
Sequence 3, Application US/08256133
; Patent No. 5498698
GENERAL INFORMATION:
APPLICANT: Yamaguchi, No. 5498698omi
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Megakaryocyte Potentiator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,133
FILING DATE: 27-JUN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-256-133-4
Query Match 100.0%; Score 19; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 QY 1111
 Db 8 AAPL 11

RESULT 33
 US-08-256-133-5
 Sequence 5, Application US/08256133
 Patent No. 5498698

GENERAL INFORMATION:
 APPLICANT: Yamaguchi, No. 5498698omi
 APPLICANT: Hattori, Kunihiko
 APPLICANT: Birch, Stewart, Kolasch & Birch
 TITLE OF INVENTION: NO. 5498698el Megakaryocyte Potentiator
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: 8110 Garage Road, Suite 500 East
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22042

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/256,133
 FILING DATE: 27-JUN-1994
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 ATTORNEY/AGENT: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 230-104P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8050
 TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 ORIGIN: Homo sapiens

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 ORIGIN: Homo sapiens

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 ORIGIN: Homo sapiens

NAME/KEY: Peptide
 LOCATION: 1..16
 OTHER INFORMATION: /label= Peptide
 OTHER INFORMATION: /note= "amino terminal peptide of Meg POT, = sequence 1 in
 US-08-256-133-5

Query Match 100.0%; Score 19; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 QY 1111
 Db 9 AAPL 12

RESULT 34
 US-08-426-819A-1
 Sequence 1, Application US/08426819A
 Patent No. 5723318

GENERAL INFORMATION:
 APPLICANT: Yamaguchi, No. 5723318omi
 APPLICANT: Kojima, Tetsuo
 APPLICANT: On-Eda, Masayoshi
 APPLICANT: Hattori, Kunihiko
 TITLE OF INVENTION: Genes Coding for Megakaryocyte
 TITLE OF INVENTION: Potentiator

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747

GENERAL INFORMATION:
 APPLICANT: Yamaguchi, No. 5723318omi
 APPLICANT: Kojima, Tetsuo
 APPLICANT: On-Eda, Masayoshi
 APPLICANT: Hattori, Kunihiko
 TITLE OF INVENTION: Genes Coding for Megakaryocyte
 TITLE OF INVENTION: Potentiator

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747

GENERAL INFORMATION:
 APPLICANT: Yamaguchi, No. 5723318omi
 APPLICANT: Kojima, Tetsuo
 APPLICANT: On-Eda, Masayoshi
 APPLICANT: Hattori, Kunihiko
 TITLE OF INVENTION: Genes Coding for Megakaryocyte
 TITLE OF INVENTION: Potentiator

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747

US-08-735-963-4

Query Match 100.0%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 Db 11 AAPL 14

RESULT 38

US-09-05-057-4

Sequence 4, Application US/09105057

GENERAL INFORMATION:

APPLICANT: Gray, Kevin A.

APPLICANT: Childs, John D.

APPLICANT: Squires, Charles H.

TITLE OF INVENTION: A RHODOCOCCUS FLAVIN REDUCTASE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

CITY: Lexington

STATE: MA

COUNTRY: US

STATE: MA

COUNTRY: US

ZIP: 02421-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/304,214

FILING DATE:

FILING DATE: 23-OCT-1995

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/735,963

ATTORNEY/AGENT INFORMATION:

NAME: Elmore, Carolyn S.

REGISTRATION NUMBER: 37,567

REFERENCE/DOCKET NUMBER: EBC96-0322

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)861-6240

TELEFAX: (781)861-9540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-105-057-4

Sequence 4, Application US/09105057

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;QY 1 AAPL 4
 Db 11 AAPL 14

RESULT 39

US-09-104-214-4

Sequence 4, Application US/09104214

Patent No. 6,743,722

GENERAL INFORMATION:

APPLICANT: Gray, Kevin A.

APPLICANT: Childs, John D.

APPLICANT: Squires, Charles H.

TITLE OF INVENTION: A RHODOCOCCUS FLAVIN REDUCTASE

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend Khourie and Crew

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/124,981A

PATENT NUMBER: 6,537,840

GENERAL INFORMATION:

APPLICANT: Crabtree, Gerald R.

APPLICANT: No. 5837840-throp, Jeffrey P.

TITLE OF INVENTION: N- α -T POLYPEPTIDES AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend Khourie and Crew

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

APPLICATION NUMBER: US/08/124,981A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 5490A-226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US 08-124-981A-26

Query Match 100.0% Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
|||
Db 11 AAPL 14

Search completed: December 6, 2002, 13:31:51
Job time : 10.3333 secs

GenCore version 5.1.3
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Qm protein - protein search, using sw model

Run on: December 6, 2002, 13:30:14 ; Search time 4.88889 Seconds
 13.289 Million cell updates/sec

Title: US-10-033-526-3
 Perfect score: 19
 Sequence: 1 AAPL 4
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 103943 seqs, 1242309 residues
 Total number of hits satisfying chosen parameters: 103943
 Minimum DB seq length: 0
 Maximum DB seq length: 20000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/podata/1/pupbaa/us09_pubcomb.pep: *
 2: /cgn2_6/podata/1/pupbaa/rct_new_pub.pep: *
 3: /cgn2_6/podata/1/pupbaa/us06_pubcomb.pep: *
 4: /cgn2_6/podata/1/pupbaa/us07_new_pub.pep: *
 5: /cgn2_6/podata/1/pupbaa/us07_pubcomb.pep: *
 6: /cgn2_6/podata/1/pupbaa/rctus_pubcomb.pep: *
 7: /cgn2_6/podata/1/pupbaa/rctus_pubcomb.pep: *
 8: /cgn2_6/podata/1/pupbaa/us08_pubcomb.pep: *
 9: /cgn2_6/podata/1/pupbaa/us09_pub.pep: *
 10: /cgn2_6/podata/1/pupbaa/us09_pubcomb.pep: *
 11: /cgn2_6/podata/1/pupbaa/us10_pubcomb.pep: *
 12: /cgn2_6/podata/1/pupbaa/us10_pubcomb.pep: *
 13: /cgn2_6/podata/1/pupbaa/us10_new_pub.pep: *
 14: /cgn2_6/podata/1/pupbaa/us10_pubcomb.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	19	100.0	4	10	US-09-935-744-2 Sequence 2, Appli
2	19	100.0	4	12	US-10-033-526-3 Sequence 3, Appli
3	19	100.0	9	10	US-09-988-019-29 Sequence 29, Appli
4	19	100.0	9	10	US-09-984-018-315 Sequence 315, Appli
5	19	100.0	15	10	US-09-829-549-A-31 Sequence 31, Appli
6	19	100.0	12	10	US-10-001-879-133 Sequence 133, Appli
7	19	100.0	20	10	US-09-864-333-46 Sequence 46, Appli
8	19	100.0	21	10	US-09-813-333-37 Sequence 37, Appli
9	19	100.0	21	10	US-09-813-333-53 Sequence 53, Appli
10	19	100.0	24	10	US-09-864-761-37207 Sequence 37207, A
11	19	100.0	27	10	US-09-60-878-3 Sequence 3, Appli
12	19	100.0	27	10	US-09-864-761-40615 Sequence 40615, A
13	19	100.0	30	10	US-09-864-761-34374 Sequence 34374, A
14	19	100.0	30	10	US-09-864-761-43765 Sequence 43765, A
15	19	100.0	32	10	US-09-821-883-11 Sequence 11, Appli
16	19	100.0	35	10	US-09-864-761-33421 Sequence 33421, A
17	19	100.0	37	9	US-10-108-915-10 Sequence 10, Appli
18	19	100.0	40	10	US-09-864-761-46389 Sequence 46389, A
19	19	100.0	41	8	US-08-424-550B-426 Sequence 426, Appli

ALIGNMENTS

RESULT 1
 US-09-935-744-2
 Sequence 2, Application US/09935744
 ; Patent No. US20020137118A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Inoye, Masayori
 ; ATTORNEY: Shinde, Ujawal
 ; APPLICANT: Fu, Xuan
 ; TITLE OF INVENTION: Biologically Active Protein Folding Intermediates
 ; FILE REFERENCE: 266-723
 ; CURRENT APPLICATION NUMBER: US/09/935,744
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: The sequence is part of a synthetic peptide that is used as a substrate for determining the activation time of a stable crosslinker.
 ; OTHER INFORMATION: d intermediate conformer.
 ; NAME/KEY: MISC_FEATURE
 ; LOCATION: (1)..(4)
 ; OTHER INFORMATION: Sequence is preceded by N-succinyl and followed by p-nitroanil
 ; US-09-935-744-2
 Query Match Best Local Similarity 100.0%; Score 19; DB 10; Length 4;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Oy |||||
 Db 1 AAPL 4
 ; APPLICANT: Robert W. Mailley

RESULT 2
 US-10-033-526-3
 Sequence 3, Application US/10033526
 ; Sequence 3, Application US/10033526
 ; Patent No. US2002014999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert W. Mailley

APPLICANT: Yadong Huang
 TITLE OF INVENTION: Methods of Treating Disorders Related to
 TITLE OF INVENTION: APOE
 FILE REFERENCE: UCAL217
 CURRENT APPLICATION NUMBER: US10/033,526
 CURRENT FILING DATE: 2001-11-02
 PRIOR APPLICATION NUMBER: 60/245,737
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic peptide
 US-10-033-526-3

Query Match 100.0%; Score 19; DB 12; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 4 AAPL 7

RESULT 3
 US-09-980-019-29
 ; Sequence 29, Application US/09988019
 ; Patent No. US20020102277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SOKOL, Pamela A.
 ; KODI, Cora D.
 ; TITLE OF INVENTION: CONSERVED METALLOPROTEASE EPITOPEs
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #11.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/988,019
 ; FILING DATE: 16-NO US20020102277A1-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/772,282
 ; FILING DATE: 20-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STANEK REA, Teresa
 ; REGISTRATION NUMBER: 30,427
 ; REFERENCE/DOCKET NUMBER: 024916-005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 636-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 ; US-09-988-019-29

Query Match 100.0%; Score 19; DB 10; Length 9;

RESULT 4
 US-09-894-018-315
 ; Sequence 31, Application US/09894018
 ; Patent No. US20020119127A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE, Inc.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Chestnut, Robert
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Baker, Denis W
 ; APPLICANT: Newman, Mark
 ; APPLICANT: Brown, David
 ; TITLE OF INVENTION: METOS AND SYSTEM FOR OPTIMIZING
 ; FILE REFERENCE: 39963-20033.00
 ; CURRENT APPLICATION NUMBER: US/09/894,018
 ; CURRENT FILING DATE: 2001-06-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/35568
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/284,221
 ; PRIOR FILING DATE: 1991-12-28
 ; NUMBER OF SEQ ID NOS: 368
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 315
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Transgenic mouse
 ; US-09-894-018-315

Query Match 100.0%; Score 19; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 4 AAPL 7

RESULT 5
 US-09-829-549A-31
 ; Sequence 31, Application US/09829549A
 ; Patent No. US20020052484A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Curators of the University of Missouri
 ; TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
 ; FILE REFERENCE: UMO 1521_1
 ; CURRENT APPLICATION NUMBER: US/09/829,549A
 ; CURRENT FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: US 60/195,785
 ; PRIOR FILING DATE: 2000-04-10
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 31
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)..(15)
 ; OTHER INFORMATION: Random peptide insert
 ; US-09-829-549A-31

Query Match 100.0%; Score 19; DB 10; Length 15;

Best Local Similarity 100.0%; Pred. No. 49; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 9 AAPL 12

RESULT 6
US-10-001-879-133
; Sequence 133, Application US/10001879
; Patent No. US2002012237A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; APPLICANT: Salcedo, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shrijith
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIORITY APPLICATION NUMBER: 60/252,188
; PRIORITY FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SEQ ID NO: 133
; LENGTH: 19
; ORGANISM: Homo sapien

Query Match 100.0%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 7 AAPL 10

RESULT 7
US-09-813-333-46
; Sequence 46, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters FILE REFERENCE: 17939-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIORITY APPLICATION NUMBER: 60/190,834
; PRIORITY FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 53
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis

Query Match 100.0%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 13 AAPL 16

RESULT 9
US-09-813-333-53
; Sequence 53, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters FILE REFERENCE: 17939-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIORITY APPLICATION NUMBER: 60/190,834
; PRIORITY FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 53
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis

Query Match 100.0%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 12 AAPL 15

RESULT 10
US-09-813-333-53
; Sequence 53, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Harrel, David K.
; APPLICANT: Chen, Weisong
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-05-23
; PRIORITY APPLICATION NUMBER: US 60/180,312
; PRIORITY FILING DATE: 2000-02-04

RESULT 8

PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-03-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-03-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 4917
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO 37207
 LENGTH: 24
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AE00659,1
 OTHER INFORMATION: EXPRESSED IN BP474, SIGNAL = 9
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.7
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 18
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.7
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.1
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.4
 US-09-864-761-37207

Query Match 100.0%; Score 19; DB 10; Length 27;
 Best Local Similarity 100.0%; Prod. No. 88; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AAPL 4	Db	19 AAPL 22

RESULT 12
 US-09-864-761-40615
 ; Sequence 40615, Application US/09864761
 ; Patent No. US20020044763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeonica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263,6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30

RESULT 11
 US-09-878-3
 ; Sequence 3, Application US/09060878A
 ; Patient No. US2001006642A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steidler, Lothar
 ; APPLICANT: Renaud, Erik
 ; APPLICANT: Wells, Jeremy Mark
 ; APPLICANT: Le Page, Richard William Falla
 ; TITLE OF INVENTION: Delivery of Biologically Active

PRIOR APPLICATION NUMBER: US 09/774, 203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40615
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021498 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
US-09-864-761-40615

Query Match 100.0%; Score 19; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 88; 0; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAPL 4
Db 1 AAPL 4

RESULT 13
US-09-864-761-34374
; Sequence 34374, Application US/09864761
; PATENT NO. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanezel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aenomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-06-03
; PRIOR APPLICATION NUMBER: GB 24263, 6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234, 687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608, 408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774, 203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34374
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007914.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN BMT74, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.3
; NAME/KEY: unsure
; LOCATION: 22
US-09-864-761-34374

Query Match 100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 98; 0; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAPL 4
Db 25 AAPL 28

RESULT 14
US-09-864-761-43766
; Sequence 43766, Application US/09864761
; PATENT NO. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanezel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aenomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-06-03
; PRIOR APPLICATION NUMBER: GB 24263, 6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234, 687
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: US 09/608, 408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774, 203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 43766
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC005959.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.71
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.73
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.69
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64
; US-09-864-761-43766
Query Match 100.0%; Score 19; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 AAPL 4
; Db 24 AAPL 27
;
RESULT 15
; US-09-821-883-11
; Sequence 11, Application US/09021883
; Patient No. US20020061310A1
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Vidovic, Damir
; APPLICANT: Graddis, Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; FILE REFERENCE: 7636-0022_30
; CURRENT APPLICATION NUMBER: US/09/821, 883
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193, 504
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-821-883-11
Query Match 100.0%; Score 19; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 AAPL 4
; Db 3 AAPL 6
;
Query Match 100.0%; Score 19; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1.e+02;
; QY 1 AAPL 4
; Db 3 AAPL 6
;
RESULT 16

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 1111
27 AAPL 30

RESULT 17

US-10-108-915-10 Application US/10108915

; Sequence 10, Application US/10108915

; Patent No. US2000177204A1

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Shon, Jennie

; APPLICANT: Williams, Mark

; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases

; FILE REFERENCE: BB1286 US NA

; CURRENT APPLICATION NUMBER: US/10/108, 915

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452, 238

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110, 592

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 46

; SEQ ID NO: 10

; LENGTH: 37

; TYPE: PRT

; ORGANISM: Zea mays

; US-10-108-915-10

Query Match 100.0%; Score 19; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 22 AAPL 25

RESULT 18

US-09-864-761-46389

; Sequence 46389, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TIME OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aeonica-2-1

; CURRENT APPLICATION NUMBER: US/09/864, 761

; CURRENT FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: US 60/180, 312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207, 456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632, 366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263, 6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/736, 359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234, 687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608, 408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774, 203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Microsoft Office 97

SEQ ID NO: 46389

SEQUENCE: Annonax Sequence Listing Engine vers. 1.1

LENGTH: 40

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC011505.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EST HUMAN HIT: BP185826.1, EVALUE 7.90e+00

OTHER INFORMATION: SWISSPROT HIT: Q0088082, EVALUE 7.30e-01

Query Match 100.0%; Score 19; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
Db 11 AAPL 14

RESULT 19

US-08-424-550B-426

; Sequence 426, Application US/08424550B

; Patent No. US2002011947A1

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SUFRESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUEHRUFF

; APPLICANT: JAMES C. ECKER

; APPLICANT: SHERI L. BOIJK

; APPLICANT: ITSA K. MUSHAHWAR

; TIME OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

; NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS: ABBOTT LABORATORIES D377/AP6D

ADDRESS: 100 ABBOTT PARK ROAD

STREET: 100 ABBOTT PARK

CITY: ABBOTT PARK

STATE: IL

ZIP: 60064-3500

COMPUTER READABLE FORM

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

Db 36 AAPL 39

RESULT 26

; Sequence 833, Application US/09764869

; Patent No. US2005061521A1

; GENERAL INFORMATION:

; APPLICANT: Rosken et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC07

; CURRENT APPLICATION NUMBER: US/09/764,869

; CURRENT FILING DATE: 2001-01-17

; PRIOR application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 2412

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 833

; LENGTH: 53

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: SITE

; NAME/KEY: SITE

; LOCATION: (50)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (55)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (58)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-869-833

Query Match 100.0%; Score 19; DB 10; Length 63;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; gaps 0;

QY 1 AAPL 4

Db 16 AAPL 19

RESULT 27

; Sequence 33840, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TIME OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeonica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,356

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 242453, 6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

SEQ ID NO: 33840

; LENGTH: 65

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: SITE

; NAME/KEY: SITE

; LOCATION: (50)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (55)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (58)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-864-761-33840

Query Match 100.0%; Score 19; DB 10; Length 63;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; gaps 0;

QY 1 AAPL 4

Db 42 AAPL 45

RESULT 28

; Sequence 7, Application US/09291809C

; Patent No. US20010049831A1

; GENERAL INFORMATION:

; APPLICANT: Detlef Weigel

; APPLICANT: Salk Institute

; TIME OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT

; FILE REFERENCE: SALKINS 026CP1

; CURRENT APPLICATION NUMBER: US/09/291,809C

; CURRENT FILING DATE: 1999-04-14

; PRIOR APPLICATION NUMBER: PCT/0599/08151

; PRIOR FILING DATE: 1999-04-13

; PRIOR APPLICATION NUMBER: 09/060,726

; PRIOR FILING DATE: 1998-04-15

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 7

; LENGTH: 69

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; US-09-291-809C-7

Query Match 100.0%; Score 19; DB 10; Length 69;

Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; gaps 0;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPL 4
    ||| |
Db 2 AAPL 5

RESULT 29
US-09-845-849-7
; Sequence 7, Application US/09845849
; Patent No. US200202395A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
; APPLICANT: WELGEL, Detlef
; APPLICANT: KARDAILLY, Igor
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS_026DVL
; CURRENT APPLICATION NUMBER: US/09/845,849
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-845-849-7

Query Match          100.0%; Score 19; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
    ||| |
Db 2 AAPL 5

RESULT 30
US-09-893-71
; Sequence 71, Application US/09920893
; Patent No. US2002007705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: P2033P1
; CURRENT APPLICATION NUMBER: US/09/820,893
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/5531,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/02,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO: 71
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: xaa equals stop translation
; US-09-820-893-71

Query Match          100.0%; Score 19; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
    ||| |
Db 2 AAPL 5

RESULT 31
US-09-864-761-3659A
; Sequence 3659A, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: US 60/2207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: AnnoMax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 3659A
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007335,2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
; OTHER INFORMATION: EST_HUMAN HIT: BE261817.1, EVALUATION 7.00e+00
; US-09-864-761-3659A

Query Match          100.0%; Score 19; DB 10; Length 72;

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Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAPL 4 Db 28 AAPL 31

RESULT 32
US-10-082-659-9
; Sequence 9, Application US/10082659
; Patent No. US20020168783A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Cohen, Maurice
; APPLICANT: Copitics, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Granados, Edward N.
; APPLICANT: Klass, Michael R.
; APPLICANT: Russell, John C.
; APPLICANT: Stroupe, Stephen D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
; DETECTING DISEASES OF THE PROSTATE
; FILE REFERENCE: 6171.US.P1
; CURRENT APPLICATION NUMBER: US/10/082,659
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/566,876
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-082-659-9

Query Match 100.0%; Score 19; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAPL 4 Db 23 AAPL 26

RESULT 33
US-09-730-617-72
; Sequence 72, Application US/09730617
; Patent No. US20020058279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhiradas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,055
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72

Query Match 100.0%; Score 19; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAPL 4 Db 13 AAPL 16

RESULT 34
US-09-8-20-893-115
; Sequence 115, Application US/09820893
; Patent No. US20020076705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/820,893
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/553,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-820-893-115

Query Match 100.0%; Score 19; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAPL 4 Db 13 AAPL 16

RESULT 35
US-09-730-617-71
; Sequence 71, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhiradas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,055
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71

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; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-730-617-71

Query Match Similarity 100.0%; Score 19; DB 10; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPL 4
Db 23 AAPL 26

RESULT 36
US-09-730-617-73
; Sequence 73, Application US/09730617
; Patent No. US20020068279A1

GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
FILE REFERENCE: 1596-609
CURRENT APPLICATION NUMBER: US/09/730,617
CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 60/169,056
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/169,886
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/169,866
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/170,252
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/175,740
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 73
LENGTH: 85
TYPE: PRT
ORGANISM: Homo sapiens
US-09-730-617-73

Query Match Similarity 100.0%; Score 19; DB 10; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPL 4
Db 23 AAPL 26

RESULT 37
US-09-915-582-62
; Sequence 62, Application US/09915582
; Patent No. US2002020103A1

GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: P5723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; SEQ ID NO: 93
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: .
LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-915-582-62

Query Match Similarity 100.0%; Score 19; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPL 4
Db 33 AAPL 36

RESULT 38
US-09-925-300-1019
; Sequence 1019, Application US/09925300
; Patent No. US20020151681A1

GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 1019
LENGTH: 90
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: .
NAME/KEY: SITE
LOCATION: (44)
ORGANISM: Homo sapiens
LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1019

Query Match Similarity 100.0%; Score 19; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPL 4
Db 66 AAPL 69

RESULT 39
US-09-764-870-533
; Sequence 533, Application US/09764870
; Patent No. US20020042386A1

GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 533
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: .
LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-870-533

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; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (3)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (53)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (92)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-870-533

Query Match 100.0%; Score 19; DB 10; Length 93;
 Best Local Similarity 100.0%; Pred. No. 3. $1.e+02$; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 71 AAPL 74

RESULT 40

US-09-731-872-275

; Sequence 275; Application US-09731872

; Patent No. US20020105604A1

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Bouqueret, Lydie

; APPLICANT: Jober, Sevein

; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

; FILE REFERENCE: 78. US3 REG

; CURRENT APPLICATION NUMBER: US/09/731,872

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,629

; PRIOR FILING DATE: 1999-12-08

; PRIOR APPLICATION NUMBER: US 60/187,470

; PRIOR FILING DATE: 2000-03-06

; NUMBER OF SEQ ID NOS: 482

; SOFTWARE: Patent.pm

; SEQ ID NO 275

; LENGTH: 94

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -25..-1

; US-09-731-872-275

Query Match 100.0%; Score 19; DB 10; Length 94;
 Best Local Similarity 100.0%; Pred. No. 3. $1.e+02$; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4

Db 86 AAPL 89

Search completed: December 6, 2002, 13:42:06

Job time : 4.88889 secs

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Run on:	December 6, 2002, 13:25:59 ; Search time 10.2222 Seconds			
OM protein - protein search, using sw model	(without alignments) 37.618 Million cell updates/sec			
Title:	US-10-033-526-3			
Perfect score:	19			
Sequence:	AAPL 4			
Scoring table:	BLOSUM62			
Gapop:	10.0 , Gapext: 0.5			
Searched:	283224 seqs, 96134422 residues			
Total number of hits satisfying chosen parameters:	283224			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Maximum Match 0%			
Database :	PIR_73;*			
	1: pir1;*			
	2: pir2;*			
	3: pir3;*			
	4: pir4;*			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Length	DB ID	Description
1	19	100.0	18	A49857
2	19	100.0	30	G71359
3	19	100.0	32	T36574
4	19	100.0	34	PC1267
5	19	100.0	36	S78339
6	19	100.0	38	T01577
7	19	100.0	45	PN0592
8	19	100.0	53	E71290
9	19	100.0	60	C82012
10	19	100.0	62	G70988
11	19	100.0	63	E82630
12	19	100.0	66	B81104
13	19	100.0	67	H87216
14	19	100.0	67	E59147
15	19	100.0	67	AB03920
16	19	100.0	72	D81922
17	19	100.0	75	B82158
18	19	100.0	76	A59043
19	19	100.0	76	G98238
20	19	100.0	77	T09311
21	19	100.0	80	AE0572
22	19	100.0	80	T24150
23	19	100.0	80	B95831
24	19	100.0	80	AF2836
25	19	100.0	82	G01978
26	19	100.0	83	C81844
27	19	100.0	83	T35979
28	19	100.0	84	A13550
29	19	100.0	85	A39747

ALIGNMENTS

QY	1 AAPL 4	Db	9 AAPL 12
RESULT 2			
G71359			
hypothetical protein			
C;Species: Treponema pallidum subsp. Pallidum (syphilis spirochete)			
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999			
C;Accession: G71359			
R;Fraser, C.M.; Morris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G			
R;son, J.; Kralak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M			
R;they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.			
Science 281, 375-388, 1998			
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.			
A;Reference number: A71250; MUID:98332770; PMID:965876			
A;Accession: G71359			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-30 <COL>			
A;Cross-references: GB:AB001200; GB:AB000520; NID:93322419; PID: AAC65153.1; PID:9332			
A;Experimental source: strain Nichols			
C;Genetics:			
C;Gene: TP0161			

Query Match Similarity 100.0%; Score 19; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

probable DNA bindi
probable DNA bindi
probable-pyrido-quinoline-
probable export pr
probable export pr
probable export pr
flagellar biosynth
probable export pr
flagellar biosynth
hypothetical prote
hypothetical prote
calmodulin-depende
L-phenylalanine ox
hypothetical prote
conserved Hypothet
hypothetical prote

Db 6 AAPL 9

RESULT 3

T36974 hypothetical protein SCJ11.03 - *Streptomyces coelicolor*
 C;Species: *Streptomyces coelicolor*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T36974
 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1999
 A;Reference number: 221618
 A;Accession: T36974
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-32 <OLI>
 A;Cross-references: EMBL:AL109949; PIDN:CA852888.1; GSPPDB:GN00070; SCOEDB:SCJ11.03
 A;Experimental source: strain A3(2)
 A;Genes:
 A;Gene: SCOEDB:SCJ11.03

Query Match 100.0%; Score 19; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 5 AAPL 8

RESULT 4

PC1267 subtilisin inhibitor 3 - *Streptomyces coelicolor* (fragment)
 C;Species: *Streptomyces coelicolor*
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PC1267
 R;Taguchi, S.; Kikuchi, H.; Kojima, S.; Kumagai, I.; Nakase, T.; Miura, K.; Momose, H.
 Bioact. Biotechnol. Biochem. 57, 522-524, 1993
 A;Title: High frequency of SSI-like protease inhibitors among Streptomyces.
 A;Reference number: PC1260; MUID:93222542; PMID:7763545
 A;Accession: PC1267
 A;Molecule type: protein
 A;Residues: 1-34 <TAG>
 A;Experimental source: strain KCC-S006
 C;Superfamily: plasminostrepin
 C;Keywords: serine protease inhibitor

Query Match 100.0%; Score 19; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 19 AAPL 22

RESULT 5

S78239 Ycf32 protein - *Odontella sinensis* chloroplast
 C;Species: chloroplast *Odontella sinensis*
 C;Accession: S78239; S78293
 R;Kowalik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
 Plant Mol. Biol. Rep. 13, 326-342, 1995
 A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, *Odontella sinensis*
 A;Reference number: S78238
 A;Accession: S78239
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-36 <ROW>
 A;Cross-references: EMBL:Z67753; NID:gi185127; PIDN:CAA91612.1; PID:gi185129
 A;Genetics: 5GEN

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
 A;Note: 5' gene
 A;Accession: S78293
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-36 <KOF>
 A;Cross-references: EMBL:Z67753; NID:gi185127; PIDN:CAA91612.1; PID:gi185129
 A;Genetics: 3GEN
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
 A;Note: 3' gene (C)
 A;Genetics: <GEN1>
 C;Gene: ycf32
 A;Genome: chloroplast
 A;Gene: ycf32'
 A;Genome: chloroplast
 A;Note: gene located on inverted repeat IRB
 C;Superfamily: hypothetical protein ycf32
 C;Keywords: chloroplast

Query Match 100.0%; Score 19; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 9 AAPL 12

RESULT 6

T01677 pseudo-kallikrein - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
 C;Accession: T01677
 R;Evans, B.A.; Drinkwater, C.C.; Richards, R.I.
 J. Biol. Chem. 262, 8027-8034, 1987
 A;Title: Mouse glandular Kallikrein genes: Structure and partial sequence analysis of
 A;Reference number: 155260; MUID:87250386; PMID:3036794
 A;Accession: T01677
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-38 <SYA>
 A;Cross-references: EMBL:M18581; NID:gi198496
 A;Superfamily: trypsin; trypsin homology

Query Match 100.0%; Score 19; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 1 AAPL 4

RESULT 7

PN0592 tyrosine 3-monoxygenase (EC 1.14.16.2) type 1 and 2 - common gibbon (fragment)
 N;Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
 C;Species: Hylobates lar (common gibbon, white-handed gibbon)
 C;Date: 03-Mar-1994 #sequence_revision 07-oct-1994 #text_change 31-Mar-2000
 C;Accession: PN0592
 R;Ichinohe, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
 Biochem. Biophys. Res. Commun. 195, 158-165, 1993
 A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.
 A;Reference number: PN0575; MUID:93371398; PMID:7689834
 A;Accession: PN0592
 A;Molecule type: genomic RNA
 A;Residues: 1-45 <TCH>
 A;Cross-references: GB:L14794
 A;Experimental source: Lymph nodes
 C;Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine bi

C; Superfamily: phenylalanine 4-monoxygenase
 C; Keywords: biotin; monooxygenase; oxidoreductase

Query Match 100.0%; Score 19; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 29 AAPL 32

RESULT 8

E71270 hypothetical protein TP0871 - syphilis spirochete
 C; Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)
 C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C; Accession: E71270
 R; Fraser, C.M.; Morris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDavid, L.; Wedman, J.; Smith, H.O.; Ventris, J.C.; Ley, S.; Stein, L.; Walenz, B.; Evans, R.; Hinde, R.; Churcher, C.; Harris, D.; Gordon, A.; Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A; Reference number: A71250
 A; Accession: E71270
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-53 <COL>
 A; Cross-references: GB:AE001257; GB:AE000520; NID:9323182; PIDN: AAC65846.1; PID:932319
 A; Experimental source: strain Nichols
 A; Gene: TP0871

Query Match

100.0%; Score 19; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 Db 42 AAPL 45

RESULT 9

C82812 hypothetical protein XP0382 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C; Species: *Xylella fastidiosa*
 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000
 C; Accession: C82812
 R; Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis
 A; Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A; Reference number: A82515; MURID:20365717; PMID:10910347
 A; Note: for a complete list of authors see reference number A59328 below
 A; Accession: C82812
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-60 <SIM>
 A; Cross-references: GB:AE003890; GB:AE003849; NID:9105215; PIDN:AAF83192.1; GSPDB:GN001
 A; Experimental source: strain 9a5c
 R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.P.; Carrara, D.M.; Carrer, R.; Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Froehlich, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laichado, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Martins, E.M.F.; Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawakar, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, R.A.; Santelli, R.V.; Sawa M.; Tsunako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; A; Reference number: A59328
 A; Contents: annotation

C; Genetics:
 A; Gene: XF0382

Query Match 100.0%; Score 19; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 34 AAPL 37

RESULT 10

G70588 hypothetical protein Rv1766 - *Mycobacterium tuberculosis* (strain H37RV)
 C; Species: *Mycobacterium tuberculosis*
 C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C; Accession: G70588
 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Skeleton, S.; Squares, S.; Nature, 393, 537-544, 1998
 A; Authors: Stares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A; Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A; Reference number: A70500; MURID:98295987; PMID:9634230
 A; Accession: G70588
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-62 <COL>
 A; Cross-references: GB:Z95890; GB:AL123456; NID:93242245; PIDN: CAB09309.1; PID:631901
 A; Experimental source: strain H37RV
 C; Genetics:
 A; Gene: Rv1766

Query Match

100.0%; Score 19; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 Db 46 AAPL 49

RESULT 11

F82630 hypothetical protein XP1853 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C; Species: *Xylella fastidiosa*
 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000
 C; Accession: F82630
 R; Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis
 A; Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A; Reference number: A82515; MURID:20365717; PMID:10910347
 A; Note: for a complete list of authors see reference number A59328 below
 A; Accession: F82630
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-62 <SIM>
 A; Cross-references: GB:AE004006; GB:AE003849; NID:9106932; PIDN:AAF84659.1; GSPDB:GN
 A; Experimental source: strain 9a5c
 R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.P.; Carrara, D.M.; Carrer, R.; Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Froehlich, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laichado, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Martins, E.M.F.; Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawakar, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, R.A.; Santelli, R.V.; Sawa M.; Tsunako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; A; Reference number: A59328

A:Contents: annotation
C:Genetics:
A;Gene: XF1853

N:Alternate names: epsilon conotoxin TxIX

C:Species: conus textile (cloth-of-gold cone)

C:Accession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Oct-2000

R.Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; She J. Biol. Chem. 274, 36664-36671, 1999

A:Title: The γ -superfamily of conotoxins.

A:Reference number: A59147; MUID:99452958; PMID:10521453

A;Accession: E59147
A:Status: preliminary

A:Status: not compared with conceptual translation

RESULT 12

B81304 Query Match 100.0%; Score 19; DB 2; Length 62;

probable periplasmic protein Cj1021c [imported] - *Campylobacter jejuni* (strain NCTC 1116

C:Species: *Campylobacter jejuni* Tx5a

C:Accession: B81104 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, T.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell G.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp

A:Reference number: A01250; MUID:20150912; PMID:10688204

A:Accession: B81104

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-63 <PAR>

A:Cross-references: GB:AU139077; GB:AU111168; NID:96968444; PIDN:CAB73277.1; PID:9696845

A:Experimental source: prototype O2, strain NCTC 11168

C:Genetics:

A;Gene: Cj1021c

Query Match 100.0%; Score 19; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 11 AAPL 14

RESULT 13
B87276 hypothetical protein CC0225 [imported] - *Caulobacter crescentus*

C:Species: *Caulobacter crescentus*

C:Accession: B87276 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haff, D.H.; Kollar, N.J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Ventler, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: H87249

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-66 <STO>

A:Cross-references: GB:AE005673; NID:913421354; PIDN:AAK22212.1; GSPDB:GN00148

C:Genetics:

A;Gene: CC0225

Query Match 100.0%; Score 19; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 11 AAPL 14

RESULT 14
B59147

conotoxin Tx5.2 precursor [validated] - cone shell (Conus textile)

N:Alternate names: epsilon conotoxin TxIX

C:Species: conus textile (cloth-of-gold cone)

C:Accession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Oct-2000

R.Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; She J. Biol. Chem. 274, 36664-36671, 1999

A:Title: The γ -superfamily of conotoxins.

A:Reference number: A59147; MUID:99452958; PMID:10521453

A;Accession: E59147
A:Status: preliminary

A:Status: not compared with conceptual translation

RESULT 15

AB0396 Query Match 100.0%; Score 19; DB 2; Length 67;

hypothetical protein YPO3260 [imported] - *Yersinia pestis* (strain C092)

C:Species: *Yersinia pestis*

C:Accession: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M

den-Datta, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G

Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell G

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia Pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-67 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92494.1; PID:915981194; GSPDB:GN00175

C:Genetics:

A;Gene: YP03260

Query Match 100.0%; Score 19; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 47 AAPL 50

RESULT 16
 D81922 probable integral membrane protein NMA0779 [imported] - *Neisseria meningitidis* (strain Z
 C; Accession: D81922; C; Species: *Neisseria meningitidis*
 C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C; Accession: A59043; B59043
 C; Species: *Conus geographus* (geography cone)
 C; Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
 C; Accession: A59043; B59043
 R; Craag, A.G.; Norberg, T.; Griffin, D.; Hoeger, C.; Akhtar, M.; Schmidt, K.; Low, W.
 R; Parkhill, J.; Richter, M.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,
 Holroyd, S.; Jaedel, K.; Leather, S.; Moule, S.; Mongali, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A; Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A; Reference number: AB1775; MUID:20222056; PMID:10761919
 A; Accession: D81922
 A; Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB84062.1; PID:9737950
 A; Experimental source: serogroup A, strain 22491
 A; Genetics:
 A; Gene: NMA0779
 Query Match 100.0%; Score 19; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C; Accession: B82758
 C; Species: *Xylella fastidiosa* Consortium of the organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A; Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A; Reference number: AB3515; MUID:2036517; PMID:10910347
 A; Note: For a complete list of authors see reference number A59328 below
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-75 <SIM>
 A; Cross-references: GB:AE003922; GB:AE003849; NID:9105722; PIDN:AAF83639.1; GSPDB:GN001
 A; Experimental source: strain 9a5c
 R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carrasco, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froeh
 chado, M.L.; Kemper, E.L.; Krueger, J.E.; Kuramane, E.E.; Laigr
 A; Authors: Martins, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A; Authors: Martins, E.M.P.; Matsukuma, A.I.; Merck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A
 Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.R.; Santelli, R.V.; Sawak
 A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuhako, M.H.; Vallada, H.; Van Slyns, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A; Reference number: A59328
 A; Content: annotation
 C; Genetics:
 A; Gene: XF0829
 Query Match 100.0%; Score 19; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 58 AAPL 61
 RESULT 18
 A59043 contulakin-G precursor - core shell (*Conus geographus*)
 C; Species: *Conus geographus* (geography cone)
 C; Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
 C; Accession: A59043; B59043
 R; Craag, A.G.; Norberg, T.; Griffin, D.; Hoeger, C.; Akhtar, M.; Schmidt, K.; Low, W.
 a, B.M.; J. Biol. Chem. 274, 13752-13759, 1999
 A; Title: Contulakin-G, an O-glycosylated invertebrate neuropeptidin.
 A; Reference number: A59043; MUID:9253920; PMID:10318778
 A; Accession: A59043
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-76 <CRAL>
 A; Cross-references: GB:AF121108; NID:94808952; PIDN:AAAD30031.1; PID:94808953
 A; Molecule type: protein
 A; Residues: 51-66 <CRAL25>
 C; Keywords: blocked amino end; glycoprotein; neurotoxin; pyroglutamic acid; venom
 F; 1-229;Domain: signal sequence #status predicted <SIG>
 F; 23-50;Domain: amino-terminal propeptide #status predicted <PRO>
 F; 51-66;Product: contulakin-G #status experimental <PAT>
 F; 67-76;Domain: carboxyl-terminal propeptide #status predicted <CPN>
 F; 60;Binding site: carbohydrate (thr) (covalent) #status experimental
 Query Match 100.0%; Score 19; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 16 AAPL 19
 RESULT 19
 G98238 hypothetical protein AGC_L_1719 [imported] - *Agrobacterium tumefaciens* (strain C58, C
 C; Species: *Agrobacterium tumefaciens*
 C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
 C; Accession: G98238
 R; Goodner, B.; Hinkle, G.; Gattinger, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldm
 A.; Liu, F.; Wolam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 234, 2323-2328, 2001
 A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*
 A; Reference number: A97359; PMID:11743194
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-76 <KUR>
 A; Cross-references: GB:AE007870; PIDN:AAK89433.1; PID:915159294; GSPDB:GN00170
 C; Genetics:
 A; Gene: AGC_L_1719
 A; Map Position: linear chromosome
 Query Match 100.0%; Score 19; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 9 AAPL 12
 RESULT 20
 T09231 probable Peroxidase (EC 1.11.1.7) precursor prx10 - spinach (fragment)
 C; Species: *Spinacia oleracea* (spinach)
 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
 C; Accession: T09231
 R; Diocan, T.; Greppin, H.; Simon, P.

submitted to the EMBL Data Library, February 1998
A;Description: CDNA cloning and expression of various peroxidase genes in Spinacia oleracea
A;Reference number: Z16615
A;Accession: T09231
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-77 <DQ>
A;Cross-references: EMBL:Y16777
A;Experimental source: cultivar Nobel; leaf
A;Gene: pxl0
C;Superfamily: peroxidase
C;Keywords: oxidoreductase
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-77/Product: peroxidase pxl0 (fragment) #status predicted <MAT>
Query Match 100.0%; Score 19; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPL 4
Db 59 AAPL 62

RESULT 21
AE0572
hypothetical secreted protein Strv0613 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A;Note: this species has also been called *Salmonella typhi*
C;Accession: AE0572
C;Sequence_revision: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moulton, S.; O'Gaoig, P.
Nature 413, 848-852, 2001
A;Authors: Perry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi C;Reference number: AB0502; PMID:11677608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-78 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05047.1; PID:gi16501823; GSPDB:GN00176
C;Genetics:
A;Gene: STY0013

Query Match 100.0%; Score 19; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 13 AAPL 16

RESULT 22
T24150
hypothetical protein R10H10.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Accession: T24150
C;Sequence_revision: 15-Oct-1999 #text_change 15-Oct-1999
A;Reference number: 219846
A;Accession: T24150
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-80 <WIL>
A;Cross-references: EMBL:Z70686; PIDN:CAA94608.1; GSPDB:GN00022; CESP:R10H10.4
A;Experimental source: clone R10H10
C;Genetics:
A;Gene: CESP:R10H10.4

RESULT 23
B95851
hypothetical protein [imported] - *Sinorhizobium meliloti* (strain 1021) megaplasmid ps
C;Species: *Sinorhizobium meliloti* (strain 1021) megaplasmid ps
C;Accession: B95851
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Her
Proc Natl Acad Sci U.S.A. 98, 9893-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: B95851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <KUR>
A;Cross References: GB:AL591985; PIDN:CAC49474.1; PID:gi15139946; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pea, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keatting, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vanderbord, M.; Vorholt, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A;Reference number: A96039; MUID:21360234; PMID:11474104
A;Contents: annotation
A;Genetics:
A;Gene: Smb20074

Query Match 100.0%; Score 19; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 9 AAPL 12

RESULT 24
AF2836
hypothetical protein Atu2118 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupo
C;Species: *Agrobacterium tumefaciens* (strain C58, Dupo
C;Accession: AF2836
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillett, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AF2836
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <KUR>
A;Cross-references: GB:AE008688; PIDN:ALA43108.1; PID:gi17740580; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2118

A;Map position: circular chromosome

A; Accession: "J35979
A; Status: preliminary; translated from GB/EMBL/DBBJ
A; Molecule type: DNA
A; Cross-references: EMBL:AI035161; PIDN:CAA22740.1; GSPDB:GN00070; SCOECDB:SC9c7.28
A; Experimental source: strain A3(2)
A; Gene: SCOECDB:SC9c7.28

Query Match 100.0%; Score 19; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 48 AAPL 51

RESULT 25

Q01978 calmodulin-dependent protein kinase II gamma F isoform - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1995 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999
C;Accession: G01978
R;Kwiatkowski, A.P.; McCull, J.M.
submitted to the EMBL Data library, July 1995
A; Reference number: G01978

A; Accession: G01978
A; Status: preliminary; translated from GB/EMBL/DBBJ
A; Molecule type: mRNA
A; Residues: 1-62 <XW1>
C;Cross-references: EMBL:U22509; NID:975884; PIDN:AAA75203.1; PID:975885
C;Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology

Query Match 100.0%; Score 19; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 37 AAPL 40

RESULT 26

C81840 hypothetical protein NMA1499 [imported] - Neisseria meningitidis (strain 22491 serogroup C)
C;Species: Neisseria meningitidis
C;Accession: C81840
C;Date: 03-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Hoorde, S.; Jigels, K.; Leather, S.; Moulé, S.; Mungall, K.; Quail, M.A.; Rajandream, M.; Maujean, M.; Goldmann, E.; Selkov, E.; Elzer, P.H.; Hugos, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A., 99, 443-448, 2002
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z22491.
A; Reference number: A81775; MUID:20222556; PMID:10761919
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-83 <PAR>
A; Cross-references: GB:ALI62756; GB:ALI57959; NID:97380091; PIDN:CAB84722.1; PID:9738013
A; Experimental source: serogroup A, strain 22491
A; Genetics:
A; Gene: NMA1499

Query Match 100.0%; Score 19; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 37 AAPL 40

RESULT 27

A39747 hypothetical protein (D-loop region) - minke whale mitochondrial (minke whale, lesser rorqual)
C;Species: mitochondrial Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Accession: A39747
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 07-Dec-1999
R; Hoezel, A.R.; Hancock, J.M.; Dover, G.A.
Mol. Biol. Evol. 8: 475-493, 1991
A;Title: Evolution of the cetacean mitochondrial D-loop region.
A; Reference number: A39747; MUID:92017215; PMID:1717809
A; Accession: A39747
A; Molecule type: DNA
A; Cross-references: GB:M60408; NID:9336457; PIDN:AAA31673.1; PID:9336458
A; Genetics:
A; Gene: mitochondrial
A; Genetic code: SGCI
C;Keywords: mitochondrial

Query Match 100.0%; Score 19; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
Db 37 AAPL 40

RESULT 27

T35979 hypothetical protein SC9c7.28 - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T35979
R; Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A; Reference number: Z21551

Db 52 AAPL 55

RESULT 30
C90666 probable DNA binding protein [imported] - Escherichia coli (strain 0157:H7, substrain R1)
C;Species: Escherichia coli
C;Accession: C90666
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33722.1; PID:913359756; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMO 0509952
C;Genetics:
A;Gene: Ecs0299
C;Superfamily: Escherichia coli prophage cp4-57 regulatory protein alpa

Query Match	100.0%	Score 19;	DB 2;	Length 88;
Best Local Similarity	100.0%	Pred. No.	5.2e+02;	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY 1 AAPL 4
Db 12 AAPL 15

RESULT 31
G85116 probable DNA binding protein [imported] - Escherichia coli (strain 0157:H7, substrain EC)
C;Species: Escherichia coli
C;Accession: G85116
C;Sequence: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lin, A.; Dimaranta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <STO>
A;Cross-references: GB:AE005174; NID:012513050; PIDN:AAG54595.1; GSPDB:GN00145; UNGP:Z03
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0335
C;Superfamily: Escherichia coli prophage cp4-57 regulatory protein alpa

Query Match	100.0%	Score 19;	DB 2;	Length 86;
Best Local Similarity	100.0%	Pred. No.	5.1e+02;	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY 1 AAPL 4
Db 12 AAPL 15

RESULT 32
PC0611 pyrrole-quinoline-quinone protein III - Acinetobacter calcoaceticus (fragment)
C;Species: Acinetobacter calcoaceticus
C;Accession: PC04061
R;Adachi, H.; Tsujimoto, M.
J. Biotech. 118, 55-61, 1995
A;Title: Cloning and expression of dipeptidase from Acinetobacter calcoaceticus ATCC 230
A;Reference number: JC4222; MUID:96115926; PMID:8690717
A;Molecule type: DNA

Db 57 AAPL 60

RESULT 33
C36869 probable export protein fliQ - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: C36869; B64959
R;Malakouti, J.; ElY, B.; Matsumura, P.; Bacteriol. 176, 189-197, 1994
A;Title: Molecular characterization, nucleotide sequence, and expression of the fliQ, A;Reference number: A36869; MUID:94110225; PMID:8282695
A;Accession: C36869
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <HAL>
A;Cross-references: GB:L22182; NID:9347241; PIDN: AAC36860.1; PID:9347244
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Accession: A64720; MUID:9742617; PMID:9278503
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-89 <BLAT>
A;Cross-references: GB:AE00287; GB:U00096; NID:91788257; PIDN: AAC75016.1; PID:917882
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: fliQ
C;Function:
A;Description: required for assembly of the flagellum rivet; may be involved in export
C;Superfamily: flagellar biosynthesis-specific protein
C;Keywords: flagellum; transmembrane protein
F;49-65/Domain: transmembrane #status predicted <TM2>

Query Match	100.0%	Score 19;	DB 1;	Length 89;
Best Local Similarity	100.0%	Pred. No.	5.3e+02;	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY 1 AAPL 4
Db 21 AAPL 24

RESULT 34
S78699 probable export protein fliQ - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: S78699
C;Species: Fan, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.
R;Ohnishi, K.; Bacteriol. 179, 6092-6099, 1997
J. Bacteriol. 179, 6092-6099, 1997
A;Title: The FliQ, FliP, FliQ, and FliR proteins of Salmonella typhimurium: putative
A;Reference number: S78699; MUID:9746436; PMID:9324257
A;Accession: S78699
A;Molecule type: DNA

A; Residues: 1-89 <OHN>
A; Cross-references: EMBL:149021; NID:91066860; PIDN:AB81320_1; PID:g1066864
A; Note: the sequence of residues 27-59 and the corresponding nucleic acid sequence are not identical.
C; Genetics:
A; Gene: fliQ
C; Function:
A; Description: required for assembly of the flagellum rivet; may be involved in export of flagellar biosynthesis-specific protein
C; Superfamily: flagellar biosynthesis-specific protein
C; Keywords: flagellum; transmembrane protein
F; F22-38/Domain: transmembrane #status predicted <TM1>
F; F49-65/Domain: transmembrane #status predicted <TM2>

Query Match 100.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAPL 4
Db 21 AAPL 24

RESULT 35

AB0753 flagellar biosynthetic protein fliQ [imported] - *Salmonella enterica* subsp. *enterica* ser. C; Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A; Note: this species has also been called *Salmonella typhi*
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002
C; Accession: AB0753
R; Parkhill, J.; Dougan, G.; James, K. D.; Thomson, N. R.; Pickard, D.; Wain, J.; Churcher, S.; Threlfall, E. J.; Connor, P.; Cronin, A.; Davis, P.; Davies, R. M.; Dowd, L.; White, N.; Farrar, S.; Moulou, S.; O'Gaora, P.; Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Infantis. Reference number: AB0502; PMID:11677608
A; Accession: AB0753
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-19 <PAR>
A; Cross-references: GB:AL513382; PIDN:CAD05728_1; PID:916503221; GSPDB:GN00176
C; Genetics:
A; Gene: STM2188
C; Superfamily: flagellar biosynthesis-specific protein

Query Match 100.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAPL 4
Db 21 AAPL 24

RESULT 36

AB0221 flagellar biosynthetic protein fliQ [imported] - *Yersinia pestis* (strain c992)
C; Species: *Yersinia pestis*
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C; Accession: AB0221
R; Parkhill, J.; Wren, B. W.; Thomson, N. R.; Titchmarsh, R. W.; Holden, M. T. G.; Prentice, M. B.; deno-Mariage, A. M.; Chillingworth, T.; Cronin, A.; Davies, R. M.; Davis, P.; Dougan, G.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A; Accession number: AB0001; MURB:21470413; PMID:1586360
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-89 <SKO>
A; Cross-references: GB:AE005174; NID:912516056; PIDN:AAG56964_1; GSPDB:GN00145; UMGP:
A; Experimental source: Strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: flio

Query Match 100.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAPL 4
Db 21 AAPL 24

RESULT 37

H90964 probable export protein fliQ [imported] - *Escherichia coli* (strain O157:H7, substrate H90964) #text_change 18-Jul-2001
C; Species: *Escherichia coli*
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Accession: H90964
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C; gasawara, N.; Yasunaga, T.; Kubara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and giga-
A; Reference number: A99629; MUID:2115623; PMID:1258796
A; Accession: H90964
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-89 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAR36111_1; PID:g13362156; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
A; Gene: EC2688
A; Genetics:
C; Superfamily: flagellar biosynthesis-specific protein

Query Match 100.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAPL 4
Db 21 AAPL 24

RESULT 38

H8812 flagellar biosynthesis [imported] - *Escherichia coli* (strain O157:H7, substrate H8812) #text_change 14-Sep-2001
C; Species: *Escherichia coli*
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: H8812
R; Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassner, J. D.; Rose, D. J.; Mayiller, L.; Grotnick, E. J.; Davis, N. W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.; Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: H8812
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-89 <SKO>
A; Cross-references: GB:AE005174; NID:912516056; PIDN:AAG56964_1; GSPDB:GN00145; UMGP:
A; Experimental source: Strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: flio

Query Match 100.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAPL 4
Db 21 AAPL 24

RESULT 39

T31980 hypothetical protein D2062_6 - *Caenorhabditis elegans*
C; Species: *Caenorhabditis elegans*
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Superfamily: flagellar biosynthesis-specific protein

C;Accession: T31980
 R;Tin-Wollam, A.; Wohlmann, P.
 submitted to the EMBL Data Library, July 1997
 A;Description: The sequence of *C. elegans* cosmid D2062.
 A;Reference number: Z22107
 A;Accession: T31980
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-90 <TIN>
 A;Cross-references: EMBL:AF016664; PIDN:AAB66067.1; GSPDB:GN00020; CESP:D2062.6
 A;Experimental source: Strain Bristol NZ; clone D2062
 C;Genetics:
 A;Gene: CESP:D2062.6
 A;Map position: 2

Query Match_h 100.0%; Score 19; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 AAPL 4
Db	44 AAPL 47

RESULT 40

H69198 hypothetical protein MTH74 - Methanobacterium thermoautotrophicum (strain Delta H)
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C;Accession: H69198
 R;Smith, D.R.; Douette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ; Otu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J; Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function and organization
 A;Accession number: A69000; MUID:98037514; PMID:9371463
 A;H69198
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-91 <MTH>
 A;Cross-references: GB:AE000666; NID:g2621094; PIDN:AAB84578.1; PID:g2621108
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH74
 C;Superfamily: Methanobacterium hypothetical protein MTH80

Query Match_h 100.0%; Score 19; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 AAPL 4
Db	48 AAPL 51

Search completed: December 6, 2002, 13:31:02
 Job time : 10.222 secs

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OM protein - protein search, using sw model

Run on: December 6, 2002, 13:20:29 ; Search time 5.5556 Seconds

(Without alignments)
 29.863 Million cell updates/sec

Title: US-10-033-526-3

Perfect score: 19

Sequence: 1 AAPL 4

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs., 41476328 residues

Total number of hits satisfying chosen parameters: 112892
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	19	100.0	30	1	V161_TREPA	083196 treponema p	
2	19	100.0	36	1	PSB1_ODOSI	083195 odontella s	
3	19	100.0	53	1	Y871_TREPA	083841 treponema p	
4	19	100.0	67	1	CXEN_CONTE	P81755 conus texti	
5	19	100.0	75	1	HPT5_RIOFE	P80882 rhodoferax	
6	19	100.0	76	1	CONG_CONGE	093945 conus geogr	
7	19	100.0	81	1	MCH1_HERME	P81511 hidrio medi	
8	19	100.0	89	1	FLIQ_ECOLI	P33134 escherichia	
9	19	100.0	89	1	FLIQ_SALTY	P54701 salmonella	
10	19	100.0	92	1	SL06_CHICK	Q28893 gallus gall	
11	19	100.0	96	1	NULM_PETMA	035541 petromyzon	
12	19	100.0	96	1	YL50_DETRA	093849 deinococcus	
13	19	100.0	107	1	HITA_NEIGO	Q007817 neisseria g	
14	19	100.0	107	1	SS13_STRICO	P28608 streptomyce	
15	19	100.0	109	1	CYPC_STHRA	Q05368 streptomyce	
16	19	100.0	110	1	RLA1_ALFTAL	P49148 alternaria	
17	19	100.0	117	1	NUTP_BEVNU	Q03748 beta vulgar	
18	19	100.0	117	1	YBRA_ECOLI	P09161 escherichia	
19	19	100.0	119	1	LAMP_PERMA	P33577 petromyzon	
20	19	100.0	121	1	FLIO_ECOLI	P22586 escherichia	
21	19	100.0	121	1	RL24_PTRAB	Q9V1U7 pyrococcus	
22	19	100.0	125	1	RLZ7_RICPR	Q3E211 rickettsia	
23	19	100.0	129	1	NITR_AFOCH	P62629 actinobacter	
24	19	100.0	130	1	Y700_TREPA	Q83698 treponema p	
25	19	100.0	132	1	YD69_SCOPA	Q10321 schizosaccharomyces pombe	
26	19	100.0	134	1	CUSA_TENNO	P80683 tenrecio mo	
27	19	100.0	139	1	LAMP_PETMA	P33575 petromyzon	
28	19	100.0	141	1	EXRD_ECOLI	P18784 escherichia	
29	19	100.0	141	1	ZRAB_ECOLI	P22682 escherichia	
30	19	100.0	142	1	EXBD_PSEPU	P05560 pseudomonas	
31	19	100.0	144	1	SSL_PIG	Q9J676 sus scrofa	
32	19	100.0	144	1	SSI_STRAOO	P010-FEB-1996 (Rel. 33, Last sequence update)	
33	19	100.0	144	1	SSI_STRAOO	P28591 streptomyce	

ALIGNMENTS

34	19	100.0	147	1	YEB6_MYCOPN	P75299 mycoplasma
35	19	100.0	149	1	RJ9_MYCOPN	P75500 mycoplasma
36	19	100.0	150	1	EXON_PRVN3	P30660 pseudable
37	19	100.0	150	1	RJ2_MYCOPN	P47339 mycoplasma
38	19	100.0	150	1	TTHV_CHICK	P27731 gallus gallus
39	19	100.0	150	1	TTHV_CROPO	P05245 crocodylus
40	19	100.0	150	1	TPHY_TILRU	P30623 tilapia rug
41	19	100.0	150	1	KR2_MACPN	P75356 mycoplasma
42	19	100.0	151	1	YFR3_ECOLI	P10027 escherichia
43	19	100.0	153	1	NODC_BRASP	P04677 bradyrhizobium
44	19	100.0	155	1	FLIL_SALTY	P26417 salmoneella
45	19	100.0	156	1	CUS5_ARADI	P80518 araneus dia

DE Photosystem II protein Y.
 GN (PSB-Y-A OR PSB-Y-1 OR YCF32.1) AND (PSB-Y-B OR PSB-Y-2 OR YCF32.2).
 OS Odontella sinensis (Marine centric diatom).
 OG Chloroplast.
 OC Bukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 OC Biddulphophycidae; Eupodales; Eupodisceae; Odontella.
 OX NCBI_TaxID=2839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kowallik K.V., Steube B., Schaffran I., Kroth-Pancic P., Freier U.;
 RT "The chloroplast genome of a chlorophyll a+c-containing alga,
 Odontella sinensis";
 RL Plant Mol. Biol. Rep. 13:335-342(1995);
 RT -|- FUNCTION: MANGANESE-BINDING POLYPEPTIDE WITH L-ARGININE
 METABOLIZING ENZYME ACTIVITY. COMPONENT OF THE CORE OF PHOTOSYSTEM
 CC II (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: chloroplast thylakoid membrane.
 CC -|- SIMILARITY: BELONGS TO THE PSY FAMILY.

CC -----
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 CC -----
 CC -----
 DR EMBL; Z67753; CAA91612.1; --.
 DR DOMAIN; 67753; CAA91661.1; --.
 KW Photosystem II; Chloroplast; Transmembrane; Thylakoid.
 FT DOMAIN 1 6 LUMENAL (POTENTIAL).
 FT TRANSMEM 7 23 POTENTIAL.
 FT DOMAIN 24 36 STROMAL (POTENTIAL).
 FT SEQUENCE 36 AA; 3921 MW; 22989D3E7DAE2B63 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 53;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAPL 4
 Db 9 AAPL 12

RESULT 3
 Y871_TREPA STANDARD; PRT; 53 AA.
 ID Y871_TREPA
 AC 083941;
 DT 16-OCT-2001 (Rel. 40, created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Hypothetical protein TP0871.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98332770; PubMed=9665876;

RESULT 4
 CXET_CONTE STANDARD; PRT; 67 AA.
 ID CXET_CONTE
 AC P81755; Q9U6Z7;
 DT 30-MAY-2000 (Rel. 39, created)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Epsilon-conotoxin TxIX precursor (Conotoxin tx5a).
 OS Conus textile (Cloth-of-gold cone).
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6494;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 51-63, AND MASS SPECTROMETRY.
 RC TISSUE=venom duct, and venom;
 MEDLINE=9452558; PubMed=10321453;
 RA Walker C.S., Steele D., Jacobsen R.B., Liraan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Banayopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins";
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steele D., Jacobsen R.B., Liraan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Banayopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=venom duct;
 MEDLINE=21105969; PubMed=11158371;
 RA Conicello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fairnfilber M.;
 RT Mechanisms for evolving hypervariability: the case of conopeptides.";
 OC Mol. Biol. Evol. 18:120-131(2001).
 RN [4]
 RP SEQUENCE OF 51-63, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY
 NMR.
 RC TISSUE=venom;
 MEDLINE=99254114; PubMed=10318957;
 RP SEQUENCE OF 51-63, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY
 NMR.
 RC TISSUE=venom;
 MEDLINE=99254114; PubMed=10318957;
 RA Ricby A.C., Lucas-Meunier E., Kalume D.E., Czerwic E., Hambe B.,
 RA Dahlgqvist I., Fosser P., Baux G., Roepstorff P., Baleja J.D.,
 RA Furie B.C., Furie B., Stenflo J.P.;
 RT "A conotoxin from Conus textile with unusual posttranslational
 RT modifications reduces presynaptic Ca²⁺ influx.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).
 RN [5]
 RP SEQUENCE OF 51-63, AND MASS SPECTROMETRY.
 RC TISSUE=venom;
 RX Published=10579974;
 RA Kalume D.E., Stenflo J.P., Czerwic E., Hambe B., Furie B.C.,
 RA Furie B., Roepstorff P.;
 RT "Structure determination of two conotoxins from Conus textile by a

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RT combination of matrix-assisted laser desorption/ionization mass spectrometry and time-of-flight and electrospray ionization mass spectrometry and biochemical methods".

RT J. Mass Spectrom. 35:145-156(2000).

RL -!- FUNCTION: Acts at presynaptic membranes, blocking the calcium channels. Causes hyperactivity upon intracranially injection into mice. Causes dorsal fins drooping in fish.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- PTM: O-glycan consists of the disaccharide Gal-GalNAc.

CC -!- MASS SPECTROMETRY: MM=1929.4; METHOD=Electrospray.

CC -!- MASS SPECTROMETRY: MM=7849.64; METHOD=MassLab.

CC -!- SIMILARITY: BELONGS TO THE T-SUPERFAMILY OF CONOTOXINS. EPSILON-TYPE FAMILY.

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DR EMBL: AF167177; AAC03687.1; -.

DR DR PDB: 1WCR; 08-JUN-99.

KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor; Vitamin K; Signal; Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylatation; Bromination; 3D-structure.

FT SIGNAL 1 19

FT PROPER 20 50

FT PEPTIDE 51 63

FT PROPEP 64 67

FT DISULFID 52 58

FT DISULFID 53 59

FT MOD_RES 51 51

FT MOD_RES 54 54

FT MOD_RES 57 57

FT MOD_RES 63 63

FT CARBOHYD 60 60

SQ SEQUENCE 67 AA; 7587 MW; 7270505504D6BB3D CRC64;

Query Match 100.0%; Score 19; DB 1; Length 67; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4

Db 61 AAPL 64

RESULT 5

ID HPIIS_RHOFE STANDARD; PRT; 75 AA.

AC P0082; -

DT 01-NOV-1997 (Rel. 35, created)

DT 01-NOV-1997 (Rel. 35, last sequence update)

DT 15-JUN-2002 (Rel. 41, last annotation update)

DE High potential iron-sulfur protein (HiPIP).

GN HiPIP.

OS Rhodofrax fermentans.

OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Rhodofrax.

OX NCBI_TAXID=28066;

RN [1]

RP STRAIN=JMC 7819; MEDLINE=923455; PubMed=9119002; RXNDB=923455; RA Van Driesche G.; Ciulli S.; Hochkoeppler A.; van Beekum J.J.; RT The primary structure of Rhodofrax fermentans high potential iron-sulfur protein, an electron donor to the photosynthetic reaction center.; RT center.; RL Eur. J. Biochem. 24:371-377(1997).

CC -!- FUNCTION: SPECIFIC CLASS OF HIGH-REDOX-POTENTIAL 4Fe-4S FERREDOXINS. FUNCTIONS IN ANAEROBIC ELECTRON TRANSPORT IN MOST PURPLE AND IN SOME OTHER PHOTOSYNTHETIC BACTERIA AND IN AT LEAST ONE GENUS (PARACOCCUS) OF HALOPHILIC, DENITRIFYING BACTERIA.

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- MASS SPECTROMETRY: MM=7849.64; METHOD=Electrospray.

CC -!- SIMILARITY: BELONGS TO THE HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP) FAMILY.

CC HSPB; P00260; ICKU.

DR InterPro IPR000170; Hipot_ironsulf.

DR Pfam; PF01355; HIPIP; 1.

DR PROSITE; PS00596; HIPIP; 1.

KW Electron transport; Iron-sulfur; 4Fe-4S.

FT METAL 38 41

FT METAL 54 54

FT METAL 68 68

FT SEQUENCE 75 AA; 7849 MW; 9FE6C86E62A72D3 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 75; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4

Db 1 AAPL 4

RESULT 6

ID CONG_CONGE STANDARD; PRT; 76 AA.

AC Q9XR5; -

DT 16-OCT-2001 (Rel. 40, created)

DT 16-OCT-2001 (Rel. 40, last sequence update)

DT 15-OCT-2002 (Rel. 41, last annotation update)

DE Contulakin-G precursor.

OS Conus geographus (Geography cone); Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neogastropoda; Conoidea; Conidae; Conus.

RA NCBI_TAXID=6491; RN [1]

RP SEQUENCE FROM N.A., SEQUENCE OF 51-66, AND CHARACTERIZATION.

RC TISSUE=Venom.

RA MEDLINE=99253920; PubMed=0318778; Craig A.G., Norberg T., Griffin D., Hoeger C., Akhtar M., Schmidt K., Low W., Dykert J., Richelson E., Navarro V., Mazella J., Watkins M., Hilliyard D.R., Imperial J., Cruz L.J., Olivera B.M.; RT J. Biol. Chem. 274:13752-13759(1999). RL J. Biol. Chem. 274:13752-13759(1999).

CC -!- FUNCTION: Acts as an agonist of neurotensin receptors.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- PTM: O-glycosylation. The glycosylation seems to enhance the affinity to the neurotensin receptors.

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DR EMBL: AF121108; AAC03031.1; -.

DR G1JCOSS1DB; Q9XR5; -.

KW toxin; Glycoprotein; signal.

FT SIGNAL 1 22

FT SIGNAL 23 48

FT PROPEP 51 66

FT PEPTIDE 67 76

FT MOD_RES 51 51

FT CARBOHYD 60 60

FT PYRROLIDONE CARBOXYLIC ACID.

FT O-LINKED (GALNAc. . .).

FT FTIDCAR_000164.

SQ	SEQUENCE	76 AA;	8261 MW;	D8034EB3C6AARD4 CRC64;	GN	FLQ OR FLAQ OR BJ949 OR Z3039 OR ECS2688.
Query Match		100.0%	Score 19;	DB 1;	Length 76:	OS
Best Local Similarity		100.0%	Pred. No.	2.4e+02		Escherichia coli
Matches	4;	Conservative	0;	NMatches	0;	OC
Qy	1 AAPL 4			Indels	0;	OC
Db	16 AAPL 19			Gaps	0;	OC
RESULT 7	MCP1_HIRME	STANDARD;	PRT;	81 AA.		ESCHERICHIA.
ID	MCP1_HIRME	STANDARD;	PRT;	81 AA.		NCBI_TaxID=562; 83334;
AC	P81511;				RN	[1]
DT	15-JUL-1999	(Rel. 38, Created)			RP	SEQUENCE FROM N.A.
DT	15-JUL-1999	(Rel. 38, Last sequence update)			RC	STRAIN=K12;
DT	15-JUL-1999	(Rel. 38, Last annotation update)			RC	STRAIN=K12 / MG1655;
DE	Metallocarboxypeptidase inhibitor precursor (Lct).				RX	MEDLINE=94110225; PubMed=8282695;
OS	Hirudo medicinalis (Medicinal leech)				RA	Matakooti J., Ely B., Matsunura P.;
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;				RA	"Molecular characterization, nucleotide sequence, and expression of the flq, flip, flaq, and fir genes of Escherichia coli.";
OC	Arachnocoelida; Hirudiniformes; Hirudinidae; Hirudo.				RA	J. Bacteriol. 176:189-197(1994).
OX	NCBL_TaxID=6421;				RL	[2]
RN	SEQUENCE FROM N.A. AND SEQUENCE OF 16-81.				RN	SEQUENCE FROM N.A.
RX	SEQUENCE FROM N.A.				RP	SEQUENCE FROM N.A.
RA	Reverteir D., Vendrell J., Canals F., Horstmann J., Aviles F.X.,				RC	STRAIN=K12;
RA	Fritz H., Sommerhoff C.P.;				RC	STRAIN=K12 / MG1655;
RT	"A carboxypeptidase inhibitor from the medical leech Hirudo medicinalis. Isolation, sequence analysis, cDNA cloning, recombinant expression, and characterization";				RX	MEDLINE=97426117; PubMed=9278503;
RL	J. Biol. Chem. 273:32927-32933(1998).				RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
CC	-i- FUNCTION: TIGHTLY BINDING, COMPETITIVE INHIBITOR OF DIFFERENT TYPES OF PANCREATIC-LIKE CARBOXYPEPTIDASES.				RA	Mau B., Shao Y.;
CC	-i- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE BONDS.				RA	"The complete genome sequence of Escherichia coli K-12.";
CC	-i- MASS SPECTROMETRY: MW=7126; METHOD=MALDI; RANGE=16-81.				RL	Science 277:1453-1474(1997).
CC	CC	CC	CC	CC	RN	[3]
CC	CC	CC	CC	CC	RN	SEQUENCE FROM N.A.
CC	CC	CC	CC	CC	RP	SEQUENCE FROM N.A.
CC	CC	CC	CC	CC	RC	STRAIN=K12;
CC	CC	CC	CC	CC	RC	STRAIN=K12 / MG1655;
CC	CC	CC	CC	CC	RX	MEDLINE=97251358; PubMed=9097040;
CC	CC	CC	CC	CC	RA	Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kilagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Siivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
CC	CC	CC	CC	CC	RA	"A 450-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40,1-150,0 min region on the linkage map.";
CC	CC	CC	CC	CC	RT	RT DNA Res. 3:379-392(1996).
CC	CC	CC	CC	CC	RN	[4]
CC	CC	CC	CC	CC	RN	SEQUENCE FROM N.A.
CC	CC	CC	CC	CC	RP	SEQUENCE FROM N.A.
CC	CC	CC	CC	CC	RC	STRAIN=K12 / EDL933 / ATCC 700927;
CC	CC	CC	CC	CC	RC	STRAIN=O157:H7 / EDL933 / ATCC 700927;
CC	CC	CC	CC	CC	RX	MEDLINE=21074935; PubMed=11206551;
CC	CC	CC	CC	CC	RA	Petra N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posal G., Hackert J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Aranthiaranam T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
CC	CC	CC	CC	CC	RA	"Genome sequence of enterohemorrhagic Escherichia coli 0157:H7";
CC	CC	CC	CC	CC	RL	Nature 409:529-533(2001).
FT	FT	FT	FT	FT	RN	[5]
FT	FT	FT	FT	FT	RP	SEQUENCE FROM N.A.
FT	FT	FT	FT	FT	RC	SEQUENCE FROM N.A.
FT	FT	FT	FT	FT	RC	STRAIN=O157:H7 / RIMD 0509952;
FT	FT	FT	FT	FT	RC	STRAIN=O157:H7 / RIMD 0509952;
FT	FT	FT	FT	FT	RX	MEDLINE=2115231; PubMed=11258796;
FT	FT	FT	FT	FT	RA	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shihagawa H.;
FT	FT	FT	FT	FT	RA	"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
FT	FT	FT	FT	FT	RA	DNA Res. 8:11-22(2001).
FT	FT	FT	FT	FT	RL	-i- FUNCTION: REQUIRED FOR THE ASSEMBLY OF THE RIVET AT THE EARLIEST STAGE OF FLAGELLAR BIOSYNTHESIS.
FT	FT	FT	FT	FT	CC	-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (probable).
FT	FT	FT	FT	FT	CC	-i- SIMILARITY: BELONGS TO THE FLQ/MOPD/SPAO FAMILY.
FT	FT	FT	FT	FT	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

DR Pfam: PF00036; efnand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR Prodrom; PD03407; CABP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CABP; 1.
 KW Mitogen; Cell cycle; Calcium-binding.
 FT CA_BIND; 20; 33; EF_HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND; 61; 72; EF_HAND 2 (HIGH AFFINITY) (POTENTIAL).
 SQ SEQUENCE 92 AA; 10276 MW; 563D65BA7BF7A4 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 2 AAPL 5

RESULT 11
 NULM_PETMA STANDARD; PRT; 96 AA.

ID NULM_PETMA STANDARD; PRT; 96 AA.
 AC Q35541;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
 GN MTND4L OR ND4L OR NAD4L.
 OS Petromyzon marinus (Sea lamprey).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperartia;
 OC Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=9522067; PubMed=7713438;
 RA Lee W.J., Kocher T.D.;
 RT "Complete sequence of a sea lamprey (*Petromyzon marinus*) mitochondrial genome: early establishment of the vertebrate genome organization";
 RL Genetics 139:873-887(1995).
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+)+ ubiquinol.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U11880; AAB08746.1; -.
 DR InterPro; IPR001133; Oxidored4L.
 DR InterPro; IPR003214; Oxidred4L.
 DR Prodrom; PF00420; Oxidred4L.
 DR Prodrom; PD00359; Oxidred4L.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 96 AA; 10392 MW; 4E04282931C8BC8 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 96;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 Db 56 AAPL 59

RESULT 12
 Y150_DEIRA STANDARD; PRT; 96 AA.
 AC Q9RSH4;
 DT 16-OCT-2001 (Rel. 40, Created)

RESULT 13
 HITA_NEIGO STANDARD; PRT; 107 AA.

ID HITA_NEIGO STANDARD; PRT; 107 AA.
 AC Q07817;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HITA protein.
 GN HITA.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F62;
 RA McGee D.J., Srivastava R., Rest R.F.;
 RL Submitted (JUN-1997) to the EMBL/Genbank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE HIT FAMILY.

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CC EMBL; AF003550; AAB61288.1; .

DR HSSP; P4973; iKPC

DR InterPro; IPR01310; HIT.

DR Pfam; PF01230; HIT; L.

DR PRINTS; PR00332; HISTRAD.

DR PROSITE; PS00892; HIT; 1.

SQ SEQUENCE 107 AA; 11612 MW; 131596000912F86B CRC64;

Query Match 100.0%; Score 19; DB 1; Length 107; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4

DB 19 AAPL 22

RESULT 14

SST3_STRCO STANDARD; PRT; 107 AA.

ID SST3_STRCO STANDARD; PRT; 107 AA.

AC P29608; Q9R5B8; .

DT 01-FEB-1993 (Rel. 28, last sequence update)

DT 01-FEB-1994 (Rel. 28, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Subtilisin inhibitor-like protein-3 (SSI-3) (SST3).

OS Streptomyces coelicolor.

OC Actinomycetales; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycetaceae; Streptomyces.

OC Actinomycetales; Streptomyicinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE.

RC STRAIN=KCC 5006;

RX MEDLINE=9419683; PubMed=8143745;

RA Taguchi S., Kojima S., Terabe M., Miura K.-I., Momose H.;

RT "Comparative studies on the primary structures and inhibitory properties of subtilisin-trypsin inhibitors from Streptomyces.";

RL Eur. J. Biochem. 220:911-918(1994).

RN [2]

RP SEQUENCE OF 1-35.

RC STRAIN=KCC 5006;

RX MEDLINE=93146392; PubMed=1490613;

RA Taguchi S., Kojima S., Kumagai I., Ogawara H., Miura K.-I., Momose H.;

RT "Isolation and partial characterization of SSI-like protease inhibitors from streptomyces.";

RL FEMS Microbiol. Lett. 78:293-297(1992).

RN [3]

RP SEQUENCE OF 1-34.

RC STRAIN=KCC 5006;

RX MEDLINE=9322542; PubMed=7763545;

RA Taguchi S., Kikuchi H., Kojima S., Kumagai I., Nakase T., Miura K.-I., Momose H.;

RT "High frequency of SSI-like protease inhibitors among streptomyces.";

RL Biosci. Biotechnol. Biochem. 57:522-524(1993).

CC -!- FUNCTION: INHIBITOR OF SUBTILISIN BPN' AND TRYPSIN.

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: SECRETED.

CC -!- SIMILARITY: BELONGS TO THE SERINE PROTEASE INHIBITORS SSI FAMILY.

DR PROSITE; PS00899; SSI; 1.

DR PIR; S42572; S42572.

FT Serine protease inhibitor. BY SIMILARITY.

FT DISULFID 44 BY SIMILARITY.

FT DISULFID 95 BY SIMILARITY.

FT ACT-SITE 67 REACTIVE BOND (BY SIMILARITY).

FT ACT-SITE 68 REACTIVE BOND (BY SIMILARITY).

SQ SEQUENCE 107 AA; 10924 MW; 711C94BCD94435DE CRC64;

Query Match 100.0%; Score 19; DB 1; Length 107; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4

DB 12 AAPL 15

RESULT 15

CYP_C_STHRA STANDARD; PRT; 109 AA.

ID CYP_C_STHRA STANDARD; PRT; 109 AA.

AC 005368;

DT 01-FEB-1995 (Rel. 31, last created)

DT 01-FEB-1995 (Rel. 31, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Putative polyketide cyclase (Fragment).

GN SCH4.

OS Streptomyces halstedii.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OC Actinomycetales; Streptomyicinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1944.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NRL12281;

RX MEDLINE=93345507; PubMed=8344517;

RA Blanco G., Brian P., Pereira A., Mendez C., Salas J.A., Chater K.F.;

RT "Hybridization and DNA sequence analyses suggest an early evolutionary divergence of related biosynthetic gene sets encoding RT polyketide antibiotics and spore pigments in streptomyces spp.";

RL Gene 130:107-116(1993).

CC -!- FUNCTION: INVOLVED IN DEVELOPMENTALLY REGULATED SYNTHESIS OF A COMPOUND BIOSYNTHETICALLY RELATED TO POLYKETIDE ANTIBIOTICS.

CC WHICH IS ESSENTIAL FOR SPORE COLOR IN STREPTOMYCES HALSTEDII.

CC -!- SIMILARITY: TO POLYKETIDE CYCLASES.

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CC ENBL; L05390; AAA02836; 2; .

DR PIR; PN0640; PN0640.

FT NON_TER 109 AA; 109 MW; 2DC56818A4319950 CRC64;

SQ SEQUENCE 109 AA; 12662 MW; 2DC56818A4319950 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 109; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4

DB 12 AAPL 15

RESULT 16

RAL_AALTAL STANDARD; PRT; 110 AA.

ID RAL_AALTAL STANDARD; PRT; 110 AA.

AC P49148;

DT 01-FEB-1996 (Rel. 33, created)

DT 01-FEB-1996 (Rel. 33, last sequence update)

DT 01-FEB-1996 (Rel. 33, last annotation update)

DT 01-NOV-1997 (Rel. 35, last sequence update)

DE 60S acidic ribosomal protein P1 (Allergen Alt a 12) (Alt a XII).

GN ALTA12.

OS Alternaria alternata.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.

OX NCBI_TaxID=5599;

RN [1]

RT corresponding to the 40.1-50.0 min region on the linkage map.";

RL DNA Res.; 3:379-392(1996);

CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).

CC -!- SIMILARITY: BELONGS TO THE ELIO/MOPB FAMILY.

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CC -----

CC EMBL; L22182; AAC36858; 1; ALT_INIT.

DR EMBL; AE000587; AAC75014; 1; ALT_INIT.

DR EMBL; D90834; BAA15772; 1; ALT_INIT.

DR EMBL; D90835; BAA15778; 1; .

DR EGCGene; EGL1124; filo.

KW Chemotaxis; Flagella; Flagellar rotation; Transmembrane; Complete proteome.

KW TRANSMEM 19 39 POTENTIAL.

FT CONFLICT 15 15 A -> R (IN REF. 1).

FT CONFFLICT 18 18 L -> V (IN REF. 1).

FT SEQUENCE 121 AA; 12670 MW; 0D4B6598308E60F5 CRC64;

Query Match 100.0%; score 19; DB 1; Length 121;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAPL 4 111

Db 15 AAPL 18

RESULT 22

RL7_RICPR STANDARD; PRT; 125 AA.

ID RL7_RICPR

AC 092E1;

DR 30-MAY-2000 (Rel. 39, created)

DT 30-MAY-2000 (Rel. 39, last sequence update)

FT 16-OCT-2001 (Rel. 40, last annotation update)

FT 50S ribosomal protein L7/L12.

DR RP139

RN 01

DE RPL1 OR RP139

OS Rickettsia prowazekii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBL_TaxID=782;

RP {1}

SEQUENCE FROM N.A.

RC STRAIN="Madrid E";

RX MEDLINE=9903499; PubMed=9823893;

RA Andersson S.G.E., Zomorodipour A., Sjöblom T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.;

RT "The genome sequence of Rickettsia prowazekii and the origin of mitochondria", Nature 396:13-140(1998).

CC -!- FUNCTION: SEEMS TO BE INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.

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CC -----

CC EMBL; P02392; 1CFP.

DR InterPro; IPR000206; Ribosomal_L12.

DR Pfam; PF00512; Ribosomal_L12; 1.

DR ProDom; PD01326; Ribosomal_L12; 1.

DR TIGRFAMs; TIGR0055; L12; 1.

KW Ribosomal protein; Complete proteome.

SEQUENCE 125 AA; 13213 MW; 431ED82F25DB867 CRC64;

Query Match 100.0%; score 19; DB 1; Length 125;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAPL 4 111

Db 46 AAPL 49

RESULT 23

NIFFA_AZOCH STANDARD; PRT; 129 AA.

ID NIFFA_AZOCH

AC P56269;

DR 15-JUL-1998 (Rel. 36, Created)

DR 15-JUL-1998 (Rel. 36, Last sequence update)

DR 15-JUL-1998 (Rel. 36, Last annotation update)

DR NIF-specific regulatory protein (Fragment).

GN NIFA.

CC -----

CC EMBL; AJ248284; CAB49252; 1;

DR InterPro; IPR00302; KOW_motif.

DR Pfam; PF00467; KOW; 1.

DR Problem; P001677; Ribosomal_L24; 1.

DR TIGRFAMs; TIGR01080; RPIX_A_E; 1.

DR PROST; PS01108; RIBOSOMAL_L24; 1.

KW Ribosomal protein; Complete proteome.

SEQUENCE 121 AA; 14387 MW; 271DD114AB3F21E67 CRC64;

Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 Azotobacter; NCBI-TaxID=355;

[1] SEQUENCE FROM N/A.
 MEDLINE-89036145; PubMed=3053983;
 Evans D., Jones R., Woodley P., Robson R.;
 RT "Further analysis of nitrogen fixation (*nif*) genes in Azotobacter
 chroococcum: identification and expression in Klebsiella pneumoniae
 of *nifS*, *nifY*, *nifM* and *nifB* genes and localization of *nifE/N*,
nifU, *nifA*- and fixABC-like genes";
 J. Gen. Microbiol. 134: 931-942 (1988);
 -1- FUNCTION: *NifA*, a TRANSCRIPTIONAL ACTIVATOR, IS REQUIRED FOR
 ACTIVATION OF MOST *NIF* OPERONS, WHICH ARE DIRECTLY INVOLVED IN
 NITROGEN FIXATION. *Nifa* INTERACTS WITH SIGMA-54 (BY SIMILARITY).
 -1- SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA-54 FACTOR
 INTERACTION ATP-BANDING DOMAIN.

CC INTERPRO: IPR02197; HTH_FIS.
 DR Interpro; IPR02078; Sig54_interact.
 DR Pfam; PF02954; HTH_B; 1.
 DR TIGR01199; HTH_fis; 1.
 DR PROSTIE; PS00675; SIGMA54_INTERACT_1; PARTIAL.
 DR PROSTIE; PS00676; SIGMA54_INTERACT_2; PARTIAL.
 DR PROSTIE; PS00688; SIGMA54_INTERACT_3; PARTIAL.
 DR PROSTIE; PS00689; SIGMA54_INTERACT_4; 1.
 KW Nitrogen fixation; Transcription regulation; Activator;
 ATP-binding; DNA binding.
 FT NON_TER 1 1 SIGMA-54 FACTOR INTERACTION.
 FT DOMAIN <1 46 H-T-H MOTIF (BY SIMILARITY).
 FT DNA BIND 101 129 H-T-H MOTIF (BY SIMILARITY).
 SQ SEQUENCE 129 AA; 14425 MW; C3D03B18DF96D2 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; NonConservative 0; RT

QY 1 AAPL 4
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OC RT [1]
 OC RN 71 AAPL 74 .

RESULT 24
 Y000_TREPA STANDARD: PRT; 130 AA.
 ID Y7000_TREPA AC 083698;
 DT 16-Oct-2001 (Rel. 40, created)
 DT 16-Oct-2001 (Rel. 40, Last annotation update)
 DT 16-Oct-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein tp0700.
 GN TP0700.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OC NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N/A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RX Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardman J.M., McLeod M.P., Salzberg S.L., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete";
 RL Science 281:375-388(1998).
 CC -----
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 holders.

CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch .
CC	Query Match 100.0%; Score 19; DB 1; Length 130;
CC	Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;
DR	DE Matches 4; Conservative 130 AA; 1404 MW; 0983AFCE31E4868 CRC64; Hypothetical protein; Complete proteome.
KW	SEQUENCE
SY	1 AAPL 4
Db	1111
SY	5 AAPL 8
RESULT	25
YD69_SRHPO	STANDARD;
AC	01-0321;
DT	01-OCT-1995 (Rel. 34, last sequence update)
DT	15-JUN-2002 (Rel. 41, last annotation update)
DE	Very hypothetical protein C17G8.09 in chromosome 1.
GN	SPACING8.09.
OS	Schizosaccharomyces pombe (Fission yeast).
OC	Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
OC	Schizosaccharomycotales; Schizosaccharomycetaceae;
OX	Schizosaccharomyces pombe.
RN	[1]
RP	SEQUENCE FROM N. A.
RC	STRAIN=972;
RX	MEDLINE=21B48401; PUBMED=11859360;
RA	wood V., Gwilliam R., RaJandream M.A., Lyne M., Lyne R., Stewart A.,
RA	Seurots J., Peat R., Hayles J., Baker S., Basham D., Bowman S.,
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G.,
RA	Holroyd S., Hornsby T., Howarth S., Hucke E.J., Hunt S., Jagels K.,
RA	Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch B.,
RA	Rutherford K., Rutters S., Saunders D., Seeger K., Sharp S.,
RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA	Woodward J., Volckaert G., Hert R., Robben J., Gyromorez B.,
RA	Weltjens I., Vansteens E., Kleier M., Schaefer M., Mueller-Huer S.,
RA	Wolff C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA	Borzym K., Langer T., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA	Goffeau A., Cadieu F., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA	Gilbert F., Aves S.J., Xiang Z., Hunt S., Moore K., Hurst S.M.,
RA	Lucas M., Rochet M., Gailardin C., Tallada V.A., Gazzon A., Thoie G.,
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA	Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA	Shipkowski G.V., Ussery D., Barrell B.G., Nurse P.,
RT	The genome sequence of Schizosaccharomyces pombe.;
RL	Nature 415:871-880(2002).
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CC	EMBL: 265795; CAQ93692.1; - .
DR	Hypothetical protein.
SQ	SEQUENCE 132 AA; 15.386 MW; 11233AB9B93D3F6 CRC64;

Query Match 100 %; Score 19; DB 1; Length 132;
 Best Local Similarity 100 %; Pred. No. 4e+02; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 67 AAPL 70

RESULT 26

ID CU3A_TENMO	STANDARD:	PRT:	134 AA.
AC P80633;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Larval cuticle protein A3A (lmp-A3A) (lmp-LCP A3A).			
OS Tenebrio molitor (Yellow mealworm). Mandibulata: Pancrustacea; Hexapoda; Eukaryota: Metazoa: Arthropoda: Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tenebrio.			
OC NCBI_TaxID=7067;			
RN [1]			
RP TISSUE=Cuticle;			
RX MEDLINE=97218698; PubMed=9066122;			
RA Andersen S.O., Rafn K., Roepstorff P.;			
RT "Sequence studies of proteins from larval and pupal cuticle of the yellow meal worm, <i>Tenebrio molitor</i> ." Insect Biochem. Mol. Biol. 27:121-131(1997).			
RL -1- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF TENEBRIOS MOLITOR.			
CC -1- DOMAIN: THE TETRAPEPTIDE (A-A-P-(AVI)) REPEATS FOUND THROUGHOUT THE PROTEIN ARE ALSO PRESENT IN MANY PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES.			
CC -1- MASS SPECTROMETRY: MW=13914.3; METHOD=Electrospray.			
CC -1- SIMILARITY: CONTAINS 1 CUTICLE CONSENSUS DOMAIN.			
DR InterPro:IPR000618; Insect_cuticle.			
DR Pfam:PF00379; Chitin_bind_4; 1.			
DR PRINTS:PR0947; cutICLE.			
DR PROSITE:PS00233; CUTICLE; 1.			
KW Structural protein; Cuticle; 1.			
FT REPEAT 23 1.			
FT REPEAT 26 1.			
SEQUENCE 134 AA; 13976 MW; F6AAAF0644FFE93E CRC64;			

Query Match 100 %; Score 19; DB 1; Length 134;
 Best Local Similarity 100 %; Pred. No. 4.1e+02; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 8 AAPL 11

RESULT 27

ID LAMP_PETM	STANDARD:	PRT:	139 AA.
AC P33575; P33576;			
DT 01-FEB-1994 (Rel. 28, Created)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Lamprin O. precursor (Cartilage matrix protein).			
OS <i>Petromyzon marinus</i> (Sea Lamprey).			
OC Eukaryota: Metazoa: Chordata: Craniata: vertebrata; Hyperoartia; Petromyzontidae; Petromyzontidae; Petromyzon.			
OC NCBI_TaxID=7757;			
RN [1]			
RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-44.			
RC TISSUE=cartilage;			
RX MEDLINE=9312269; PubMed=7678258;			
RA Robson P., Wright G.M., Sitzar E., Maiti A., Rawat M., Youson J.H.,			

Query Match 100 %; Score 19; DB 1; Length 139;
 Best Local Similarity 100 %; Pred. No. 4.2e+02; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 129 AAPL 132

RESULT 28

ID EXBD_ECOLI	STANDARD:	PRT:	141 AA.
AC P18784;			
DT 01-NOV-1990 (Rel. 16, Created)			
DT 01-NOV-1990 (Rel. 16, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Biopolymer transport exbd protein.			
GN EXBD OR B3005 OR Z4358 OR EC3889.			
OS <i>Escherichia coli</i> , and <i>Escherichia coli</i> O157:H7.			
OS <i>Bacteri</i> a: Proteobacteria; gamma subdivision: Enterobacteriaceae;			
OC <i>Escherichia</i> . <i>Escherichia</i> .			
OX NCBI_TaxID=562, 83334;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=K12;			
RX MEDLINE=89359155; PubMed=2670903;			
RA Eick-Helmeich K., Braun V.;			
RT "Import of biopolymers into <i>Escherichia coli</i> : nucleotide sequences of the exbb and exbd genes are homologous to those of the tolQ and tolR genes, respectively." J. Bacteriol. 171:5117-5126(1989).			

Db 37 AAPL 40

RESULT 30

EXBD_PSEPU ID EXBD_PSEPU STANDARD; PRT; 142 AA.

AC Q0506; DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Biopolymer transport exbd protein.

GN EXBD.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WCS358;

RX MEDLINE=93172953; PubMed=8437515;
RA Bitter W., Tommassen J., Weisbeek P.J.;
RT "Identification and characterization of the exB^B, exBD and tonB genes
of Pseudomonas putida WCS358: their involvement in
ferric-pseudooxactin transport.";
RL Mol. Microbiol. 7:117-130 (1993).

CC -!- FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT
TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES.

CC -!- SUBUNIT: THE ACCESSORY PROTEINS EXBB AND EXBD SEEM TO FORM A
COMPLEX WITH TONB.

CC -!- SUBCELLULAR LOCATION: TYPE II membrane protein. Inner membrane
(Probable).

CC -!- SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.

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CC DR EMBL; X70139; CAA49715.1; -.

CC DR PIR; S28443; S28443.

CC DR InterPro; IPR03400; Exbd.

CC DR Pfam; PF02472; Exbd; 1.

CC DR Transport; Protein transport; Transmembrane; Inner membrane.

CC FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).

CC FT TRANSMEM 23 43 POTENTIAL.

CC SQ SEQUENCE 142 AA; 15225 MW; 1430086CBDCB935C CRC64;

Query Match 100.0%; Score 19; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4

Db 37 AAPL 40

RESULT 31

SRE1_PIG ID SRE1_PIG STANDARD; PRT; 144 AA.

AC 097676; DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Sterol regulatory element binding protein-1 (SREBP-1) (Sterol
regulatory element-binding transcription factor 1) (Apocyno-
determination-and differentiation-dependent factor 1) (ADD1)
(Fragment).

DE DE SRBEP1 OR SREBP1.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Sunia; Suidae; Suid.
OC OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=99410873; PubMed=10481259;
RA Ding S.T., McNeel R.L., Mersmann H.J.;

RT "Expression of porcine adipocyte transcripts: tissue distribution and
differentiation in vitro and in vivo.";
RL Comp. Biochem. Physiol. 123B:307-318 (1999).

CC -!- FUNCTION: Transcriptional activator that binds to the sterol
regulatory element1 (SRE-1) (5'-ATCACCCAC-3') Has dual sequence
specificity, binding to both an E-box motif (ATCACGTGA) and to
SRE-1 (5'-ATCACCCAC-3'). Regulates the transcription of genes for
sterol biosynthesis and the LDL receptor gene (By similarity).

CC -!- SUBUNIT: Forms a tight complex with SCAP in the ER membrane.
Efficient DNA binding of the soluble transcription factor fragment
requires dimerization with another BHLH protein.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein that moves from
the endoplasmic reticulum to the Golgi in the absence of sterols
(By similarity).

CC -!- PTM: Under sterol-depleted conditions, SREBPs are cleaved
sequentially by site-1 and site-2 protease. The first cleavage
occurs within the luminal loop and is directly regulated by
sterols. The second cleavage by site-2 protease occurs within the
first transmembrane stretch and liberates the soluble
transcription factor. Cleavage by the cysteine proteases, caspase-3
and caspase-7, is induced during apoptosis, independent of
sterol levels (By similarity).

CC -!- MISCELLANEOUS: SREBPs have to be in a complex with the cleavage-
activating protein (SCAP) to move to the Golgi and be cleaved by
site-1 protease (By similarity).

CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-Helix (BHLH) FAMILY OF
TRANSCRIPTION FACTORS. BHLH ZIP SUBFAMILY.

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CC DR EMBL; AF102873; AAC78685.1; -.

CC DR HSSP; P36956; 1AMG.

CC DR TRANSFAC; T04163; -.

CC DR InterPro; IPR001092; HLM_basic.

CC DR Pfam; PF00010; HLM; 1.

CC DR SMART; SM00353; HLM; 1.

CC DR PROSITE; PS00038; HLM_1; PARTIAL.

CC DR PROSITE; PS50088; HLM_2; 1.

CC DR Transcription regulation; Activator; DNA-binding; Lipid metabolism;

CC KW Cholesterol metabolism; Nuclear protein; Transmembrane;

CC KW Endoplasmic reticulum; Golgi stack.

FT NON_TER 1 DOMAIN <1 >144 CYTOPLASMIC (POTENTIAL).

FT DNA_BIND 96 109 BASIC DOMAIN.

FT DOMAIN 110 >144 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 FT NON_TER 144 AA; 1522 MW; CBAFA77FA2745F1 CRC64;
 SQ

Query Match 100.0%; Score 19; DB 1; Length 144;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 Db 51 AAPL 54

RESULT 32
SSI_STRAO STANDARD; PRT; 144 AA.
 ID SSI_STRAO
 AC P01006
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Subtilisin inhibitor precursor (SSI type).
 GN SSI
 OS Streptomyces alboriseolus.
 OC Actinomycetales; Streptomyceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TAXID=1887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S-3253;
 RX MEDLINE=89278057; PubMed=2732212;
 RA Obata S., Taguchi S., Kumagai T., Miura K.-I.;
 RT "Molecular cloning and nucleotide sequence determination of gene
 encoding Streptomyces subtilisin inhibitor (SSI).";
 RL J. Biotech. 105:367-371(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Miura K.-I., Kumagai T., Obata S., Kojima S., Taguchi S.;
 RT "Partial alteration of a protein Streptomyces subtilisin inhibitor by
 site-directed mutagenesis.";
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:147-149(1988).
 RN [3]
 RP SEQUENCE OF 32-144 FROM N.A.
 RC STRAINS-3253;
 RX MEDLINE=90128271; PubMed=24182228;
 RA Taguchi S., Nishiyama K.-I., Kumagai T., Miura K.-I.;
 RT "Analysis of transcriptional control regions in the Streptomyces
 subtilisin-inhibitor-encoding gene.";
 RL Gene 84:279-286(1989).
 RN [4]
 RP SEQUENCE OF 32-144 FROM N.A.
 RX MEDLINE=93192316; PubMed=8448204;
 RA Ueda Y., Taguchi S., Nishiyama K.-I., Kumagai T., Miura K.-I.;
 RT "Effect of a rare 1-leucine codon, TTA, on expression of a foreign gene
 in Streptomyces lividans.;"
 RL Biochim. Biophys. Acta 1172:262-266(1993).
 RN [5]
 RP SEQUENCE OF 32-144.
 RC STRAIN=S-3253;
 RX MEDLINE=75133116; PubMed=4376147;
 RA Inenaka T., Odani S., Sakai M., Nabeshima Y., Sato S., Miura S.;
 RT "Amino acid sequence of an alkaline proteinase inhibitor
 (Streptomyces subtilisin inhibitor) from Streptomyces alboriseolus
 R. L. Biochem. 76:1191-1209(1974).
 RN REVISIONS TO 142-143.
 RX MEDLINE=80227614; PubMed=6593452;
 RA Sakai M., Odani S., Inenaka T.
 RT "Importance of the carboxyl-terminal four amino acid residues in the
 inhibitory activity of Streptomyces subtilisin inhibitor (with a
 revision of its carboxyl-terminal sequence).";
 RL J. Biochem. 87:891-898(1980).
 RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=79114456; PubMed=63329;
 RA Mitsui Y., Satow Y., Watanabe Y., Hiroto S., Itaka Y.;
 RT "Crystal structures of Streptomyces subtilisin inhibitor and its
 complex with Subtilisin BPN'.";
 RT Nature 277:447-452(1979).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=85033707; PubMed=6387152;
 RA Hiroto S., Aogawa H., Mitsui Y., Itaka Y.;
 RT "Crystal structure at 2.6-A resolution of the complex of subtilisin
 BPN' with streptomyces subtilisin inhibitor";
 RT J. Mol. Biol. 178:389-413(1984).
 RN [9]
 RP MUTAGENESIS OF MET-104.
 RX MEDLINE=90365981; PubMed=1366538;
 RA Obata S., Ohta S., Kumagai T., Miura K.-I.;
 RT "Alteration of the specificity of the Streptomyces subtilisin
 inhibitor by gene engineering";
 RL Biotechnology 8:449-452(1990).
 RN [10]
 RP MUTAGENESIS OF MET-104.
 RX MEDLINE=91349173; PubMed=1908859;
 RA Kojima S., Nishiyama Y., Kumagai T., Miura K.-I.;
 RT "Inhibition of subtilisin BPN' by reaction site P1 mutants of
 Streptomyces subtilisin inhibitor";
 RL J. Biotech. 109:377-382(1991).
 CC -I SUBUNIT: HOMODIMER.
 CC -I SUBCELLULAR LOCATION: Secreted.
 CC -I SIMILARITY: BELONGS TO THE SERINE PROTEASE INHIBITORS SSI FAMILY.
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 CC
 DR D00402; BAA0035; 1;
 DR EMBL; M33133; AAA6821; 1;
 DR EMBL; M33134; AAA6822; 1;
 DR EMBL; X70494; CAA21525; 1;
 DR EMBL; M54887; AAA6827; 1;
 DR PIR; JX0066; XSSMA;
 DR PDB; 2SIC; 15-APR-93.
 DR PRB; 3SS1; 17-AUG-96.
 DR PDB; 2TLD; 15-JUL-92.
 DR InterPro; IPR000691; Srep_subt_inhib.
 DR PRAM; PF00720; SST; 1.
 DR PRINTS; PR00294; SSBTINHTR.
 DR PRODOM; P004028; Strep_subt_inhib; 1.
 DR PROSITE; PS00999; SSI_1.
 KW Serine protease inhibitor; Signal; Repeat; 3D-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 144 SUBTILISIN INHIBITOR.
 FT REPEAT 33 43
 FT DISULFID 65 81
 FT DISULFID 102 132
 FT ACT_SITE 104 105
 FT ACT_SITE 104 116 INTERACTION WITH SUBTILISIN.
 FT SIMILAR 98 116 WITH 12-29 OF BOVINE P.S.I.
 FT SIMILAR 129 132 WITH 32-35 OF BOVINE P.S.I.
 FT MUTAGEN 104 104 M->K, R: ALSO INHIBITS TRYPSIN.
 FT MUTAGEN 104 104 M->Y, N: ALSO INHIBITS CHYMOTRYPSIN.
 FT MUTAGEN 104 104 M->D, E, V, I, G, P: DECREASE IN INHIBITION.
 RT STRAND 42 49
 RT TURN 53 54
 RT STRAND 60 65

FT STRAND 71 73
 FT TURN 75 76
 FT HELIX 77 87
 FT TURN 88 89
 FT TURN 91 92
 FT STRAND 100 103
 FT STRAND 109 116
 FT STRAND 121 128
 FT HELIX 131 135
 FT TURN 136 137
 SQ SEQUENCE 144 AA; 14312 MW; BEAS7ACT7FDCCB8004 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 144;
 Best Local Similarity 100.0%; Pred. No. 4.e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAPL 4
 Db 19 AAPL 22

RESULT 33
 SSL_STRCO ID SSTI_STRCO STANDARD; PRT; 144 AA.
 AC P26591; Q9R644; P26591; Q9R644; (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protease inhibitor precursor (SLPI) (trypsin inhibitor STII) (SILA-3).
 GN STII OR SC00762 OR SCFB1_21C.
 OS Streptomyces coelicolor, and
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinomycetidae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TAXID=1902; 1916;

[1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-85; 87-103 AND 105-143.
 SPECIES=S.lividans;
 MEDLINE=92147677; PubMed=1737780;
 RA Strickler J.E., Berka T.R., Gorniak J., Fornwald J., Keys R.,
 RA Rowland J.J., Rosenblatt M., Taylor D.P.;
 RT "Two novel streptomyces protein protease inhibitors. Purification,
 RT activity, cloning, and expression,"
 RL Biol. Chem. 267:3236-3241(1992).
 RN [2]
 RP SEQUENCE OF 38-144.
 SPECIES=S.lividans; STRAIN=66 / 1326;
 RX MEDLINE=93015780; PubMed=1556971;
 RA Ueda Y., Kojima S., Takeda S., Miura K.-I., Kumagai I.;
 RT "A protease inhibitor produced by Streptomyces lividans 66 exhibits
 RT inhibitory activities toward both subtilisin BPN' and trypsin.";
 RL J. Biochem. 112:204-211(1992).
 RN [3]
 RP SEQUENCE OF 36-71.
 SPECIES=S.lividans; STRAIN=66 / 1326;
 MEDLINE=93225452; PubMed=7763545;

[1]
 RA Taguchi S., Kojima S., Miura K., Momose H.;
 RA "Taxonomic characterization of closely related Streptomyces spp. based
 on the amino acid sequence analysis of protease inhibitor proteins.";
 RA FEMS Microbiol. Lett. 135:169-173(1996).

RQ "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
 RT Nature 417:141-147(2002).
 RN [5]
 RP SEQUENCE OF 38-144 FROM N.A.
 RC SPECIES=S.coelicolor; STRAIN=A3(2);
 RX MEDLINE=9162058; PubMed=8593854;
 RA Taguchi S., Kojima S., Miura K., Momose H.;
 RA "Taxonomic characterization of closely related Streptomyces spp. based
 on the amino acid sequence analysis of protease inhibitor proteins.";
 RA FEMS Microbiol. Lett. 135:169-173(1996).
 RL - I - FUNCTION: STRONG INHIBITORY ACTIVITY TOWARD SUBTILISIN BPN' AND TO A LESSER EXTENT, TO TRYPSIN.
 CC - I - SUBUNIT: HOMODIMER.
 CC - I - SUBCELLULAR LOCATION: Secreted.

CC - I - SIMILARITY: BELONGS TO THE SERINE PROTEASE INHIBITORS SSI FAMILY.

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CC EMBL; M80576; AAA26801 1; -.
 DR EMBL; ALI33171; CAB61542.1; -.
 DR PIR; B42585; B42585.
 DR PIR; JT0619; JT0619.
 DR HSSP; P01006; JSSI.
 DR InterPro; IPR00691; strep_subt_inhib.
 DR Pfam; PF00720; SSI; 1.
 DR PRINTS; PR0214; SSBLINNINHBTR.
 DR PRODOM; PD00428; Strep_subt_inhib; 1.
 DR PS00599; SSI; 1.
 KW Serine protease inhibitor; Signal; Complete proteome.

FT SIGNAL 35 35
 FT CHAIN 36 144 PROTEASE INHIBITOR.
 FT DISLFID 66 81
 FT DISLFID 102 132
 FT ACT_SITE 104 105 REACTIVE BOND.
 SQ SEQUENCE 144 AA; 14313 MW; E748BADE07B4F8B CRC64;

Query Match 100.0%; Score 19; DB 1; Length 144;
 Best Local Similarity 100.0%; Pred. No. 4.e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAPL 4
 Db 56 AAPL 59

RESULT 34
 YEB6_MYCPN ID YEB6_MYCPN STANDARD; PRT; 147 AA.
 AC P75399; P75399;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MN486 (P02_Orf147).
 MPN486 OR Mp256.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TAXID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mycoplasma pneumoniae.
 RX MEDLINE=9710885; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkle E., Li B.-C.,
 RA Hermann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.";
 RT Nucleic Acids Res. 24:4420-4449(1996).

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 CC ---
 DR EMBL; AEG00034; AAB96004_1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 147 AA; 16257 MW;
 DB 0C13A725A8B14C2 CRC64;
 RESULT 35
 RIG_MCPN STANDARD; PRT; 149 AA.
 ID RIG_MCPN
 AC P75540;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L9.
 GN DRN OR MP600.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NEUTRAXID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92365105; PubMed=1323689;
 RA de Wind N., Domén J., Berns A.A.;
 RT "Herpesviruses encode an unusual protein-serine/threonine kinase
 which is nonessential for growth in cultured cells.";
 RL J. Virol. 66:5200-5209 (1992).
 CC ---
 CC -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES ALKALINE EXONUCLEASE
 CC FAMILY.
 CC ---
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 CC ---
 DR EMBL; M94370; AAA017482_1;
 DR PIR; C42744; C42744;
 DR InterPro; IPR001616; Herpes alk exo.
 DR Pfam; PF01771; Herpes alk_exo_1.
 DR Hydrolease; Nuclease; Exonuclease.
 KW ---
 SQ SEQUENCE 150 AA; 15425 MW;
 DB 0433CB1A7CAED734 CRC64;
 RESULT 36
 RIG_MCGE STANDARD; PRT; 150 AA.
 ID RIG_MCGE
 AC P47337;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L9.
 GN DRN OR RIG OR MG093.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NEUTRAXID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAINATCC35350 / G-37;
 MEDLINE=96026366; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult D., C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Smalk K.V., Sandusky M., Fuhrmann J.L.,
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu C., Lucier T.S.,
 RA Peterson S.N., Smith H.O., Hutchinson C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium."
 RL Science 270:397-403 (1995).
 CC ---
 CC -!- SIMILARITY: BELONGS TO THE 23S RNA (BY SIMILARITY).
 CC ---
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 CC ---
 DR EMBL; AB000508; AAB96248_1; -.
 DR P02417; IDRV.
 DR IIPRO; IPR00244; Ribosomal L9.
 DR Pfam; PF01281; Ribosomal_L9; 1.
 DR TIGRFAMS; TIGR00158; L9_1.
 DR PROSITE; PS00511; REBOSMAL_L9; FALSE_NEG.
 KW Ribosomal protein; FRNA-binding; Complete proteome.
 SQ SEQUENCE 149 AA; 17152 MW; EBD94AD27A4FF08DF CRC64;
 RESULT 37
 RIG_MCGE STANDARD; PRT; 150 AA.
 ID RIG_MCGE
 AC P47337;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L9.
 GN DRN OR RIG OR MG093.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NEUTRAXID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAINATCC35350 / G-37;
 MEDLINE=96026366; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult D., C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Smalk K.V., Sandusky M., Fuhrmann J.L.,
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu C., Lucier T.S.,
 RA Peterson S.N., Smith H.O., Hutchinson C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium."
 RL Science 270:397-403 (1995).
 CC ---
 CC -!- SIMILARITY: BELONGS TO THE 19S RNA (BY SIMILARITY).
 CC ---
 RESULT 36

CC -----
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 CC -----
 DR EMBL; X60471; CAA43000.1; .
 DR PIR; S16035; S16035.
 DR PIR; S17827; S17827.
 DR PDB; 1TFP; 10-JUN-96.
 DR InterPro; IPRO00244; Transthyretin.
 DR Pfam; PF00576; Transthyretin; 1.
 DR PRINTS; PR00109; TRANSTHYRETN.
 DR PRODOM; PD003457; Transthyretin; 1.
 DR SMART; SM00095; TR_THY; 1.
 DR PROSITE; PS00768; TRANSTHYRETIN_1; 1.
 DR PROSITE; PS00769; TRANSTHYRETIN_2; 1.
 DR Albumin; Transport; Retinol-binding.
 KW Signal; 3D-structure.
 FT CHAIN 21 150 TRANSTHYRETIN.
 FT BINDING 38 38 THYROID HORMONES (BY SIMILARITY).
 FT BINDING 77 77 THYROID HORMONES (BY SIMILARITY).
 SQ SEQUENCE 150 AA; 16309 MW; 1F82A77699966360 CRC64;
 Query Match 100.0%; Score 19; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Db 36 AAPL 39
 RESULT 38
 THY_CHICK STANDARD; PRT; 150 AA.
 ID THY_CHICK
 AC P27731;
 DT 01-AUG-1992 (Rel. 23, created)
 DT 01-AUG-1992 (Rel. 23, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Transthyretin precursor (Prealbumin) (TBPA).
 GN TTR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC NCBI_TAXID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-40.
 RC STRAIN=White Leghorn; TISSUE=liver;
 RX MEDLINE=92007844; PubMed=1833190;
 RA Duan W., Achen M.G., Richardson S.J., Lawrence M.C.,
 RA Wettenhall R.E.H., Jaworski A., Schreiber G.;
 RT "Isolation, characterization, cDNA cloning and gene expression of an
 avian transthyretin. Implications for the evolution of structure and
 function of transthyretin in vertebrates.",
 RL Eur. J. Biochem. 200:679-687(1991).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=96195657; PubMed=8612621.
 RA Sundelin M., Richardson S.J., Chang L., Pettersson T.M., Schreiber G.,
 RA Blake C.C.F.;
 RT "The crystal structure of transthyretin from chicken.",
 RL Eur. J. Biochem. 235:491-495(1996).
 CC -1- FUNCTION: Thyroid hormone-binding protein. Probably transports
 CC thyroxine from the bloodstream to the brain (By similarity).
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TRANSTHYRETIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; A2223148; CAA11129.1; .
 DR HSSP; P27731; 1TFP.
 DR InterPro; IPRO00825; Transthyretin.
 DR Pfam; PF00576; Transthyretin; 1.
 DR PRINTS; PR00109; TRANSTHYRETN.
 DR SMART; SM00095; TR_THY; 1.
 DR PRODOM; PD003457; Transthyretin; 1.
 DR SMART; SM00095; TR_THY; 1.
 DR PROSITE; PS00769; TRANSTHYRETIN_1; 1.
 DR PROSITE; PS00769; TRANSTHYRETIN_2; 1.
 KW Signal; Albumin; Plasma; Transport; Thyroid hormone; Retinol-binding;
 Vitamin A.

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FT SIGNAL 1 20 POTENTIAL
 FT CHAIN 21 150 TRANSTHYRETIN.
 FT BINDING 38 38 THYROID HORMONES (BY SIMILARITY).
 FT BINDING 77 77 THYROID HORMONES (BY SIMILARITY).
 SQ SEQUENCE 150 AA; 16411 MW; E05DFAA6FBDE22A5 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 20 AAPL 23

Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 AAPL 4
 Db 20 AAPL 23

Search completed: December 6, 2002, 13:28:34
 Job time : 6.55556 secs

RESULT 40

THY_TILRU STANDARD; PRT; 150 AA.

ID -THY_TILRU AC P30623;

DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Transthyretin precursor (Prealbumin) (TBPA).

GN TTR.

OS Tilqua rugosa (Stumpy-tailed skink) (Stumpy-tailed lizard).

OC Lepidosauria; Squamata; Craniata; Vertebrata; Euteleostomi;
 OC Scincidae; Tilqua.

OX NCBI_TaxID=8527;

RN [1]

RP SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING.

RC TISSUE=Brain;

RX MEDLINE=94057100; PubMed=8238627;

RA Achnen M.G., duan W., Pettersson T.M., Harms P.J., Richardson S.J.,
 Lawrence M.C., Wettenhall R.E.H., Aldred A.R., Schreiber G.;
 RT "Transthyretin gene expression in choroid plexus first evolved in
 reptiles";

RL Ann J Physiol 265:R862-R889 (1993)

CC -!- FUNCTION: Thyroid hormone binding protein. Probably transports
 CC thyroxine from the bloodstream to the brain (By similarity).

CC -!- SUBUNIT: Homotetramer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: SYNTHESIZED IN THE CHOROID PLEXUS.

CC -!- SIMILARITY: BELONGS TO THE TRANSTHYRETIN FAMILY.

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DR EMBL; X66697; CAAJ723B; 1; .

DR EMBL; M97509; AACM9620; 1; .

DR PIR; S25531; S25531.

DR HSSP; P27731; 1TFP.

DR Interpro; IPR00895; Transthyretin.

DR Pfam; PF00576; Transthyretin; 1.

DR PRINTS; PR00199; TRANSTHYRETIN.

DR PRODOM; PF00357; Transthyretin; 1.

DR SMART; SM00095; TR.THY; 1.

DR PROSITE; PS00768; TRANSTHYRETIN_1; 1.

DR PROSITE; PS00769; TRANSTHYRETIN_2; 1.

KW albumin; transport; Retinol-binding; vitamin A; Thyroid hormone;

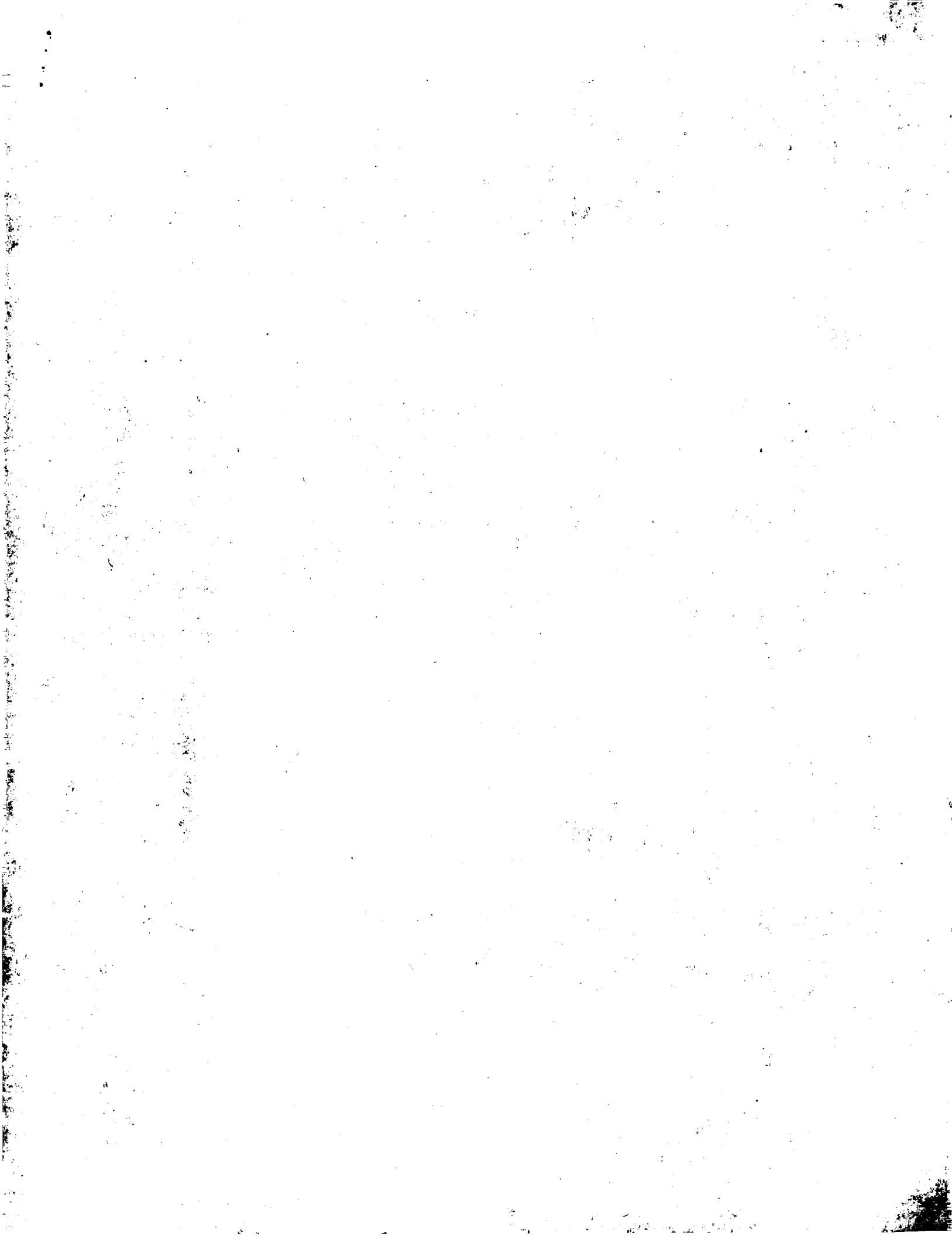
KW Signal.

FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 150 TRANSTHYRETIN.

FT BINDING 38 38 THYROID HORMONES (BY SIMILARITY).
 FT BINDING 77 77 THYROID HORMONES (BY SIMILARITY).

SQ SEQUENCE 150 AA; 16343 MW; 6C88E00949112EE CRC64;

Query Match 100.0%; Score 19; DB 1; Length 150;



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Gencore version 5.1.3

Q9abk2 caulobacter
Q9ppg6 conus texti
Q9l1c5 secale cere
Q43018 prunus dulc
Q81866 heptitis e
Q8abx4 yersinia pe
Q93346 st scrofa
Q9ffin3 arabidopsis
Q8ij0 mycobacteri
Q8s075 oriza sativ
Q9ips8 human enter
Q9ips7 human enter
Q9ips6 human enter
Q9ips5 human enter
Q9ips4 human enter
Q9ips3 human enter
Q9ips2 human enter
Q9ips1 human enter
Q9ips0 human enter
Q9ipr3 human enter
Q9ipr2 human enter
Q9ipr1 human enter
Q9ipr0 human enter

Om protein - protein search, using sw model
Run on: December 6, 2002, 13:25:09 ; Search time 19.5556 Seconds
(without alignments)
42.146 Million cell updates/sec

Title: US-10-033-526-3
Perfect score: 19
Sequence: 1 AAPL 4
Scoring table: BLOSUM62
Gapcost 10.0 , Gapext 0.5
Searched: 671580 seqs, 20604/115 residues
Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPBREMBL_21:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriop:
17: sp_archeap:
18: RN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	14	10 P82332	P82332 pisum sativ
2	19	100.0	16	4 Q9NNE2	Q9nne2 homo sapien
3	19	100.0	18	4 Q9UEB2	Q9ueb2 homo sapien
4	19	100.0	21	4 Q14795	Q14795 homo sapien
5	19	100.0	25	2 Q9RQ9	Q9rq9 vibrio para
6	19	100.0	32	1 Q9RA1	Q9ra1 streptomyce
7	19	100.0	38	16 Q8VKK3	Q8vkk3 mycobacteri
8	19	100.0	5 Q9V69	Q9v69 drosophila	
9	19	100.0	48	16 Q8VE9	Q8ve9 mycobacteri
10	19	100.0	60	16 Q9PC0	Q9pgc0 xylella fas
11	19	100.0	62	16 Q8RK4	Q8rk4 mycobacteri
12	19	100.0	62	16 Q9PC8	Q9pc8 xylella fas
13	19	100.0	63	16 Q9F77	Q9f77 homo sapien
14	19	100.0	63	11 Q922V0	Q922v0 mus musculu
15	19	100.0	63	16 Q9PR9	Q9pr9 campylobact
16	19	100.0	63	17 Q8ZV02	Q8zv02 pyrobaculum

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	14 AA.
1	P82332			
	ID			
	P82332:			
	AC			
	DT	01-JUN-2000 (TREMBL)	14	Created)
	DT	01-JUN-2000 (TREMBL)	14	Last sequence update)
	DT	01-OCT-2000	15	(TREMBL). Last annotation update)
	DE	Unknown protein from 2D-page of thylakoid (SPORI15) (Fragments).		
	OS	pisum sativum (Garden pea)		
	OC	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;		
	OC	Spermatophytina; Magnoliophytina; eudicots; Rosidae;		
	OC	eurosidia 1; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.		
	OX	NCBITaxonID=3888;		
	RN	[1]		
	RP	SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.		
	RC	STRAIN=CV; DE GRACE; TISSUE=LEAF;		
	RX	MEDLINE=2018128; Published=1071520;		
	RA	Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,		
	RA	Adamska I., van Wijk K.J.;		
	RT	"Proteomics of the chloroplast: systematic identification and targeting analysis of luminal and peripheral thylakoid proteins";		
	RL	Plant Cell 12:319-341 (2000).		
	CC	-- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR PERIPHERY.		
	CC	- - DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.		
	CC	- - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS 5.5, ITS MW IS: 27.4 KDA.		
	KW	Chloroplast; Thylakoid membrane.		
	FT	NON_TER	1	
	FT	NON_CONS	6	7
	FT	NON_TER	14	14
	SQ	SEQUENCE	14 AA:	1461 MW: 0803373C937AAB CRC64:

Query Match 100.0%; Score 19; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPL 4 |||||

RESULT 2	DT	01-NOV-1999 (TREMBLrel. 12; Last sequence update)
Q9NN22	PRELIMINARY;	PRT; 16 AA.
ID Q9NN22; AC Q9NN22; DT 01-OCT-2000 (TREMBLrel. 15, Created)	DE	Integrin alpha 2 subunit (Fragment).
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	GN	
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	OS	Homo sapiens (Human).
DE Integrin alpha-2 subunit (Fragment), RTG2.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
OC NCBI_TaxID=9606;	OX	
OS Homo sapiens (Human).	RN	[1]
RA Kuriyama, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	RP	SEQUENCE FROM N.A.
RA Zutter M.M., Santoro S.A., Painter A.S., Tsung Y.L., Gafford A.; RT "The human alpha 2 integrin gene promoter: Identification of positive developmental regulatory elements important for cell-type and density";	RX	
RT blood 92:2382-2388(1998); DR EMBL: AF062039; FT NON-TER 21; SQ SEQUENCE FROM N.A.	RA	J. Biol. Chem. 269:463-469(1994).
RA Kritzik M., Savage B., Nugent D.J., Santoro S., Ruggeri Z.M., Kunicki T.J.; RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles that are associated with differences in platelet alpha2 beta1 density";	DR	EMBL: L24121; AAA16619.2; -.
RT blood 92:2382-2388(1998); DR EMBL: AF062039; FT NON-TER 21; SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;	FT	
Qy 1 AAPL 4	Qy 1 AAPL 4	Score 19; DB 4; Length 21;
RT Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 8 AAPL 11	Score 19; DB 4; Length 21;
Qy 8 AAPL 11	Db 8 AAPL 11	Score 19; DB 4; Length 21;
RESULT 3	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
ID Q9ICB2	PRELIMINARY;	PRT; 18 AA.
ID Q9ICB2; AC Q9ICB2; DT 01-MAY-2000 (TREMBLrel. 13, Created)	DE	Megakaryocyte potentiating factor (Fragment).
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)	OS	Vibrio parahaemolyticus.
DE Homo sapiens (Human); OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.	OC	
OC NCBI_TaxID=670;	OX	
RN [1]	RN	
RP SEQUENCE.	RX	
RA Gildemeister O.S., Zhu B.C., Laine R.A.; RT Chitovirin: a chitin-binding lectin from Vibrio parahaemolyticus.;"	RA	Medline=95210902; Pubmed=7696854;
RL Glycoconj. J. 11:518-526(1994); SQ SEQUENCE 25 AA; 2719 MW; 0CBBADAS711A25CC CRC64;	RL	
Qy 1 AAPL 4	Qy 1 AAPL 4	Score 19; DB 2; Length 25;
RT Best Local Similarity 100.0%; Pred. No. 6.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 4 AAPL 7	Score 19; DB 2; Length 25;
RT Yamaguchi N., Hattori K., Oh-edo M., Kojima T., Imai N., Ochi N.; from a human pancreatic tumor cell line HPC-Y5.;"	Db 4 AAPL 7	Score 19; DB 2; Length 25;
RL J. Biol. Chem. 269:808-819(1994); SQ SEQUENCE 18 AA; 1726 MW; 8F309D27CA1F671 CRC64;	Db 4 AAPL 7	Score 19; DB 2; Length 25;
RESULT 4	DT	01-NOV-1996 (TREMBLrel. 01, Created)
ID Q14595	PRELIMINARY;	PRT; 21 AA.
AC Q14595; OC Actinomycetales; DE Streptomyces; GN Streptomyces.	OC	
OS Streptomyces coelicolor.	OC	
OS Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;	OC	
OS Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.	OC	
OS NCBI_TaxID=1902;	OX	
RN [1]	RN	
RP SEQUENCE FROM N.A.	RP	
RC STRAN=A3(2) / M145;	RC	

RA	Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
RA	Harpur D., Bartram A., Brown S., Chandra G., Chen C.W., Collins M.,	OC	Phygoidea; Drosophilidae; Drosophila.
RA	Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,	OX	NBBI_TaxID:7227;
RA	Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,	RN	[1]
RA	Rabbinkwitsch E., Rajandream M.A., Rutherford K., Rutter S.,	RP	SEQUENCE FROM N.A.
RA	Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,	RC	STRAIN=BERKELEY;
RA	Warren T., Wierzorek A., Woodward J., Barrell B.G., Parkhill J.,	RX	RX
RA	Hopwood D.A.;	RA	NCBI_TaxID=2016006; PubMed=10731132;
RT	*Complete genome sequence of the model actinomycete Streptomyces	RA	NCBI_TaxID=2016006; PubMed=10731132;
RL	coelicolor C3(2).";	RA	NCBI_TaxID=2016006; PubMed=10731132;
DR	Nature 417:141-147 (2002);	RA	NCBI_TaxID=2016006; PubMed=10731132;
EMBL	AEI09949; CAB5288.1; -	RA	NCBI_TaxID=2016006; PubMed=10731132;
KW	Hypothetical protein.	RA	NCBI_TaxID=2016006; PubMed=10731132;
SQ	SEQUENCE 32 AA; 3399 MW; A3RADIC42914D9E2 CRC64;	RA	NCBI_TaxID=2016006; PubMed=10731132;
Query Match	Score 19; DB 16; Length 38;	RA	NCBI_TaxID=2016006; PubMed=10731132;
Best Local Similarity	100.0%; pred. No. 9.3e+02;	RA	NCBI_TaxID=2016006; PubMed=10731132;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RA	NCBI_TaxID=2016006; PubMed=10731132;
QY	1 AAPL 4	RA	NCBI_TaxID=2016006; PubMed=10731132;
Db	5 AAPL 8	RA	NCBI_TaxID=2016006; PubMed=10731132;
RESULT 7		RA	NCBI_TaxID=2016006; PubMed=10731132;
QVKK3	PRELIMINARY; PRT; 38 AA.	RA	NCBI_TaxID=2016006; PubMed=10731132;
ID	OBVKK3	RA	NCBI_TaxID=2016006; PubMed=10731132;
AC	OBVKK3;	RA	NCBI_TaxID=2016006; PubMed=10731132;
DT	01-MAR-2002 (TREMBLrel. 20, Created)	RA	NCBI_TaxID=2016006; PubMed=10731132;
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	RA	NCBI_TaxID=2016006; PubMed=10731132;
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	RA	NCBI_TaxID=2016006; PubMed=10731132;
DE	Hypothetical protein MN0540.	RA	NCBI_TaxID=2016006; PubMed=10731132;
GN	Mycobacterium tuberculosis.	RA	NCBI_TaxID=2016006; PubMed=10731132;
OS	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Mycobacteriaceae; Mycobacterium.	RA	NCBI_TaxID=2016006; PubMed=10731132;
OC	Actinomycetales; Corynebacterineae; Mycobacterium.	RA	NCBI_TaxID=2016006; PubMed=10731132;
OX	NCBI_TaxID=1173;	RA	NCBI_TaxID=2016006; PubMed=10731132;
RN	[1] TAXID=1173;	RA	NCBI_TaxID=2016006; PubMed=10731132;
RP	SEQUENCE FROM N.A.	RA	NCBI_TaxID=2016006; PubMed=10731132;
RC	STRAIN=CDC 1551 / OSHKOSH;	RA	NCBI_TaxID=2016006; PubMed=10731132;
RA	Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,	RA	NCBI_TaxID=2016006; PubMed=10731132;
RA	Peterson J., DeBoy R., Dodson R., Gwynn M.L., Haft D., Hickey E.,	RA	NCBI_TaxID=2016006; PubMed=10731132;
RA	Keltonay J.F., Nelson W.C., Umayam L.A., Ermolovaeva M.D., Salzberg S.L.,	RA	NCBI_TaxID=2016006; PubMed=10731132;
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,	RA	NCBI_TaxID=2016006; PubMed=10731132;
RA	Bishai W.;	RA	NCBI_TaxID=2016006; PubMed=10731132;
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; to the EMBL/GenBank/DDBJ databases.	RA	NCBI_TaxID=2016006; PubMed=10731132;
RL	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.	RA	NCBI_TaxID=2016006; PubMed=10731132;
DR	EBML: AE006954; AAC44763.1; -	RA	NCBI_TaxID=2016006; PubMed=10731132;
DR	TIGR: MT0540; -	RA	NCBI_TaxID=2016006; PubMed=10731132;
DR	HYPOTHETICAL PROTEIN; MT0540; -	RA	NCBI_TaxID=2016006; PubMed=10731132;
DR	EMBL: AE006954; AAC44763.1; -	RA	NCBI_TaxID=2016006; PubMed=10731132;
DR	FBgn0040869; CG151763.	RA	NCBI_TaxID=2016006; PubMed=10731132;
SQ	SEQUENCE 38 AA; 4269 MW; 2B21477D74C98200D CRC64;	RA	NCBI_TaxID=2016006; PubMed=10731132;
Query Match	Score 19; DB 16; Length 38;	RA	NCBI_TaxID=2016006; PubMed=10731132;
Best Local Similarity	100.0%; pred. No. 9.3e+02;	RA	NCBI_TaxID=2016006; PubMed=10731132;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RA	NCBI_TaxID=2016006; PubMed=10731132;
QY	1 AAPL 4	RA	NCBI_TaxID=2016006; PubMed=10731132;
Db	12 AAPL 15	RA	NCBI_TaxID=2016006; PubMed=10731132;
RESULT 9		RA	NCBI_TaxID=2016006; PubMed=10731132;
Q8YKE9	PRELIMINARY; PRT; 48 AA.	RA	NCBI_TaxID=2016006; PubMed=10731132;
ID	Q8YKE9;	RA	NCBI_TaxID=2016006; PubMed=10731132;
AC	Q8YKE9;	RA	NCBI_TaxID=2016006; PubMed=10731132;
DT	01-MAR-2002 (TREMBLrel. 20, Created)	RA	NCBI_TaxID=2016006; PubMed=10731132;
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	RA	NCBI_TaxID=2016006; PubMed=10731132;
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	RA	NCBI_TaxID=2016006; PubMed=10731132;
DE	Hypothetical protein MN0771.	RA	NCBI_TaxID=2016006; PubMed=10731132;
GN	MN0771.	RA	NCBI_TaxID=2016006; PubMed=10731132;
OS	Mycobacterium tuberculosis.	RA	NCBI_TaxID=2016006; PubMed=10731132;
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;	RA	NCBI_TaxID=2016006; PubMed=10731132;
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.	RA	NCBI_TaxID=2016006; PubMed=10731132;
GN	CG15753; protein.	RA	NCBI_TaxID=2016006; PubMed=10731132;
OS	Drosophila melanogaster (Fruit fly).	RA	NCBI_TaxID=2016006; PubMed=10731132;

RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OSKOSH;
 RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Debey R., Dodson R., Gwinn M.L., Haft D., Hickie E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 laboratory strains.",
 RL Submitted (APR 2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE006968; AAK45007.1; -.
 DR TIGR; MT071; -.
 KW Hypothetical protein.
 SQ SEQUENCE 48 AA; 4818 MW; 2AD2B6FF349534CE CRC64;
 Query Match 100.0%; Score 19; DB 16; Length 48;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPL 4
 Db 15 AAPL 18

RESULT 10

QPCCO PRELIMINARY; PRT; 60 AA.
 AC ID 09PGC0
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBrel. 20, Last annotation update)
 DE Hypothetical protein Xf0382.
 GN Xf0382.

OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC *Xylella*.
 OC NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=RASC;

RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bafia G.S., Baptista C.S.,
 RA Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Colauto N.B., Colombo C., Camargo L.E.A., Carraro D.M., Carrer H.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca M.C., Frohne M., Furian L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Honeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krueger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A.J.R., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
 RA Valada H., Van Sluys M.A., Verlouski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "the genome sequence of the plant pathogen *Xylella fastidiosa*.",
 RL Nature 406:151-159 (2000).
 DR EMBL; AE003890; AAC83192.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 60 AA; 6404 MW; BEDA0EA2BD737885 CRC64;

RESULT 11

O8RK84 PRELIMINARY; PRT; 62 AA.
 AC ID 08RK84
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Putative ferredoxin.
 GN MORB.
 OS *Mycobacterium* sp. RPI.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=156204;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RPI;
 RA Poupin P.;
 RT "Cloning and characterization of a gene encoding a cytochrome P450 monooxygenase (Mora) involved in morpholine, piperidine, and pyrrolidine utilization in *Mycobacterium* sp. strain RPI; Isolation and partial characterization of the enzyme.",
 RT Submitted (MAR 2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ310142; CAC84232.1;
 SQ SEQUENCE 62 AA; 6793 MW; 13503FD08A131B80 CRC64;

Query Match 100.0%; Score 19; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
 Db 19 AAPL 22

RESULT 12

QPCCB PRELIMINARY; PRT; 62 AA.
 AC ID 09PCCB
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBrel. 20, Last annotation update)
 DE Hypothetical protein Xf1853.
 GN Xf1853.

OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC *Xylella*.
 OC NCBI_TaxID=2371;

RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=RASC;

RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bafia G.S., Baptista C.S.,
 RA Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Colauto N.B., Colombo C., Camargo L.E.A., Carraro D.M., Carrer H.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca M.C., Frohne M., Furian L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Honeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krueger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

RX	MARQUES M.V., MARTINS E.A.L., MARTINS E.M.F., MATSUKUMA A.Y., MEDLINE=21203559; PubMed=11306812;
RA	Menck C.F.M., Mirucca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Shamsadin R., Jantsan K., Adam I., Engel W.;
RA	Monc D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., "Cloning, organisation, chromosomal localization and expression analysis of the mouse Prag1 gene";
RA	Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A.J., Pesquero J.B., Peixoto B.R., Pereira G.A.G., Pereira H.A.J., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Swasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubakio M.H., Valada H., Van Stuyvesant M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Medians J., Setubal J.C.;
RA	"The genome sequence of the plant pathogen Xylella fastidiosa."; RT
RL	Nature 405:151-159(2000);
DR	EMBL; AE04406; AF08459; KW
KW	Hypothetical protein; Complete proteome; HYPOSEQUENCE
SQ	SEQUENCE 62 AA; 7040 MW; 9456C4B05271D4AF CRC64;
Query Match 100.0%; Score 19; DB 16; Length 62; Best Local Similarity 100.0%; Pred. No. 1.4e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AAPL 4 Db 6 AAPL 9	RESULT 13
Db	SEQUENCE FROM N.A.
PRELIMINARY; PRT; 63 AA.	PRELIMINARY; PRT; 63 AA.
Q9F47 ID 0P6F47 AC 0P6F47; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	Q9F47 ID 0P6F47 AC 0P6F47; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Similar to hypothetical protein MGIC6688.	DE Similar to hypothetical protein MGIC6688.
OS Homo sapiens (human).	OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606; RN [1]	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606; RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;	RC TISSUE=PLACENTA;
RA STRAUSBERG R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	RA STRAUSBERG R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR BC011620; AAH11620_1; SQ SEQUENCE 63 AA; 7143 MW; 9689364527546A CRC64;	DR BC011620; AAH11620_1; SQ SEQUENCE 63 AA; 7143 MW; 9689364527546A CRC64;
Query Match 100.0%; Score 19; DB 4; Length 63; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AAPL 4 Db 2 AAPL 5	Query Match 100.0%; Score 19; DB 11; Length 63; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AAPL 4 Db 51 AAPL 54
RESULT 15	RESULT 15
Q9PNR9 ID Q9PNR9 AC Q9PNR9; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	Q9PNR9 ID Q9PNR9 AC Q9PNR9; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE putative periplasmic protein. GN C11021C.	DE putative periplasmic protein. GN C11021C.
OS Campylobacter jejuni.	OS Campylobacter proteobacteria; epsilon subdivision; Campylobacter group; OC Campylobacter.
OC Campylobacter.	OC Campylobacter.
OX NCBI_TAXID=197; RN [1]	OX NCBI_TAXID=197; RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC STRAIN=NCYC 11168;	RC STRAIN=NCYC 11168;
RA MBDLINE=20150912; PubMed=10688204; parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feilwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Benn C.W.M., Quail M.A., Barrell G.B.; Rutherford K.M., van Viet A.H.M., RA Whitehead S., Barrell B.G.; RT "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences."; RT Nature 403:665-668(2000); RL DR ALI39077; CAI373277.1; -.	RA MBDLINE=20150912; PubMed=10688204; parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feilwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Benn C.W.M., Quail M.A., Barrell G.B.; Rutherford K.M., van Viet A.H.M., RA Whitehead S., Barrell B.G.; RT "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences."; RT Nature 403:665-668(2000); RL DR ALI39077; CAI373277.1; -.
RA Complete proteome.	RA Complete proteome.
SQ SEQUENCE 63 AA; 7609 MW; 3408CB9AD490D11 CRC64;	SQ SEQUENCE 63 AA; 7609 MW; 3408CB9AD490D11 CRC64;
Query Match 100.0%; Score 19; DB 16; Length 63; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AAPL 4 Db 17 AAPL 20	Query Match 100.0%; Score 19; DB 16; Length 63; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AAPL 4 Db 17 AAPL 20
RESULT 16	RESULT 16
Q8ZV02 ID Q8ZV02 AC Q8ZV02; DT 01-MAR-2002 (TREMBLrel. 20, Created) DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	Q8ZV02 ID Q8ZV02 AC Q8ZV02; DT 01-MAR-2002 (TREMBLrel. 20, Created) DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE AMP activated protein kinase gamma 1 (Fragment). GN PRKAG1.	DE AMP activated protein kinase gamma 1 (Fragment). GN PRKAG1.
OS Mus musculus (Mouse); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus. NCBL_TAXID=10909; [1]	OS Mus musculus (Mouse); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus. NCBL_TAXID=10909; [1]
RP SEQUENCE OF 1-0 FROM N.A.	RP SEQUENCE OF 1-0 FROM N.A.
RC STRAIN=129/Sv;	RC STRAIN=129/Sv;

PAB2521A,
GN Pyrobaculum aerophilum.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=IM2 / ATCC 51768 / DSM 7523;
RC
RX PubMed=11792859;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Miller J.H.; "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum"; Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
RL DR EMBL: AE00981; AAL64254; 1; -.
KW HYPOTHETICAL PROTEIN; Complete proteome.
SEQUENCE 63 AA; 6975 MW; DF4893406C8EC2AA CRC64;

Query Match	100.0%	Score 19;	DB 17;	Length 63;
Best Local Similarity	100.0%	Pred. No.	1.5e+03	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY 1 AAPL 4
|||
Db 10 AAPL 13

RESULT 17
Q9ABK2 PRELIMINARY; PRT; 66 AA.
ID Q9ABK2
AC Q9ABK2;
DT 01-JUN-2001 (TREMBUREL. 17, Created)
DT 01-JUN-2001 (TREMBUREL. 17, Last sequence update)
DE Hypothetical protein CC0225.
GN CC0225.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN
SEQUENCE FROM N.A.
RP STRAIN=ATCC 19089 / CB15;
RC MEDLINE=21173698; PubMed=113259647;
RA Nieman W.C., Feltlyium T.V., Laub M.R., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Oita N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phade N.D., Ely B.,
Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolova M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus";
PROC. NATL. ACAD. SCI. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005697; AAC22212.1; -.
KW HYPOTHETICAL PROTEIN; complete proteome.
SQ SEQUENCE 66 AA; 7364 MW; 28EC010054E3C2FB CRC64;

Query Match	100.0%	Score 19;	DB 16;	Length 66;
Best Local Similarity	100.0%	Pred. No.	1.5e+03	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY 1 AAPL 4
|||
Db 11 AAPL 14

RESULT 18
Q9BPG6 PRELIMINARY; PRT; 67 AA.
ID Q9BPG6
AC 01-FEB-1996 (TREMBUREL. 01, Created)
DT 01-FEB-1997 (TREMBUREL. 02, Last sequence update)
DT 01-JUN-2002 (TREMBUREL. 21, Last annotation update)
DE Lipid transfer protein.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;

RESULT 19
Q9LCC5 PRELIMINARY; PRT; 67 AA.
ID Q9LCC5
AC Q9LCC5;
DT 01-OCT-2000 (TREMBUREL. 15, Created)
DT 01-OCT-2000 (TREMBUREL. 15, Last sequence update)
DE TY3 retrotransposon structural protein (Fragment).
GN GAG
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Secale.
OX NCBI_TaxID=4550;
RN
SEQUENCE FROM N.A.
RP RETROTRANSPOSON-TY3 CLASS RETROTRANSPOSON;
RC MEDLINE=20157063; PubMed=1055237;
RA Landdon T., Seago C., Jones R.N., Ougham H., Thomas H., Forster J.W.,
Jenkins G.;
RT "De novo evolution of satellite DNA on the rye B chromosome.";
RL Genetics 154:869-884 (2000).
DR EMBL: AF223161; AAC79935.1; -.
FT NON_TER 67 67
SEQUENCE 67 AA; 7174 MW; AF070B6FBC9C7C8F CRC64;

Query Match	100.0%	Score 19;	DB 10;	Length 67;
Best Local Similarity	100.0%	Pred. No.	1.6e+03	
Matches	4;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY 1 AAPL 4
|||
Db 14 AAPL 17

RESULT 20
Q43018 PRELIMINARY; PRT; 67 AA.
ID Q43018
AC 043018;
DT 01-NOV-1996 (TREMBUREL. 01, Created)
DT 01-FEB-1997 (TREMBUREL. 02, Last sequence update)
DT 01-FEB-1997 (TREMBUREL. 21, Last annotation update)

[1]	RN SEQUENCE FROM N.A.	RX BI S.L., Purdy M.A., McCaustland K.A., Margolis H.S., Bradley D.W.; RC STRAIN=CV; TEXAS;
RA	SueIves M ; Submitted (Ocm-1996) to the EMBL/GenBank/DBJ databases.	RT source during an outbreak in China.;"
RL	DR EMBL: X96115; CAAS476.1; -.	RL Virus Res. 28:123-124(1993);
DR	DR Intertpro: IPR001788; Tryp/alpha/beta, amyl; 1.	DR EMBL: L0816; AA03185; 1; -.
DR	Pfam: PF00234; tryp_alpha/beta, amyl; 1.	FT NON_TER 1 1 .
SQ	SEQUENCE 67 AA; 6909 MW; 88392E48CD4716BB CRC64;	FT NON_TER 67 67 .
Query Match 100.0%; Score 19; DB 10; Length 67;	Best Local Similarity 100.0%; Pred No. 1.6e+03; Mismatches 0;	Matches 4; Conservative 0; Indels 0; Gaps 0;
QY 1 AAPL 4	Db 17 AAPL 20	
RESULT 21		
ID Q81866 PRELIMINARY; PRT; 67 AA.	OBZBX4 PRELIMINARY; PRT; 67 AA.	
AC Q81866; DT 01-NOV-1996 (TREMBLrel. 01, Created)	AC Q8ZBX4; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Poly proline hinge (Fragment).	DE Hypothetical protein YP03260.	
OS Hepatitis E virus.	GN YP03260.	
OC Viruses; ssRNA positive-strand viruses, no DNA stage;	OS Yersinia pestis.	
OC Hepatitis E-like viruses.	OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OX NCBI_TaxID=12461;	OC Yersinia;	
RN [1]	OX NCBI_TaxID=632;	
RP SEQUENCE FROM N.A.	RN	
RX MEDLINE=92024067; PubMed=1926770;	RP SEQUENCE FROM N.A.	
RA Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,	RC STRAIN=CO_92 / BIVAR_ORIENTALIS;	
RA Fry K.E., Reyes G.R.;	RX MEDLINE=2147013; PubMed=11586560;	
RT "Hepatitis E virus (HEV): molecular cloning and sequencing of the	RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,	
RT full-length viral genome."	RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,	
RL Virology 185:120-13(1991).	RA Baker S., Basham D., Bentley S.D., Brooks J., Cerdeno-Taronga A.M.,	
RL	RA Chillingworth T., Cronin A., Davies P., Davis P., Dougan G.,	
RP SEQUENCE FROM N.A.	RA Feltwell T., Hamlin N., Holroyd S., Jacobs K., Karyshev A.V.,	
RX MEDLINE=92261317; PubMed=1584074;	RA Leather S., Moulis S., Oyston P.C.F., Quail M., Rutherford K.,	
RA Uchida T., Shikata T., Ichikawa M., Rikihsia T., Mizuno K., Win K.M.;	RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;	
RA Wang C.-K., Shikata T., Ichikawa M., Rikihsia T., Mizuno K., Win K.M.;	RT Nature 413:523-527(2001).	
RT "Hepatitis E virus: cDNA cloning and expression.";	RL EMBL: AJ414156; CAB92494.1; -.	
RL Microbiol. Immunol. 36:67-79(1993).	KW Hypothetical protein; complete proteome.	
RN [1]	SQ SEQUENCE 67 AA; 7658 MW; 88RAB352AB0CF57E CRC64;	
RP SEQUENCE FROM N.A.	Query Match 100.0%; Score 19; DB 16; Length 67;	
RX MEDLINE=92335009; PubMed=1630924;	Best Local Similarity 100.0%; Pred No. 1.6e+03; Mismatches 0;	
RA Aye T.T., Uchida T., Ma X.Z., Iida F., Shikata T., Zhuang H.,	Matches 4; Conservative 0; Indels 0; Gaps 0;	
RA Win K.M.;	QY 1 AAPL 4	
RT "Complete nucleotide sequence of a hepatitis E virus isolated from the	Db 47 AAPL 50	
RT Xijiang epidemic (1986-1988) of China.";		
RL Nucleic Acids Res. 20:3512-3512(1992).		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=92115700; PubMed=1731327;		
RA Tsarev S.A., Emerson S.U., Revesz G.R., Tsareva T.S., Leegters L.J.,		
RA Malik I.A., Iqbal M., Purcell R.H., "characterization of a prototype of hepatitis E virus.",		
RA Proc. Natl. Acad. Sci. U.S.A. 89:5559-563(1992).		
RN [1]	RESULT 23	
RP SEQUENCE FROM N.A.	Q29346 PRELIMINARY; PRT; 68 AA.	
RX MEDLINE=92217462; PubMed=1589964;	AC Q29346;	
RA Fry K.E., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young I.M.,	DT 01-NOV-1996 (TREMBLrel. 01, Created)	
RA Piatak M., Feldman R.A., Yun K.Y., Purdy M.A., McCausland K.A.,	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
RA Bradley D.W., Reyes G.R.; "Hepatitis E virus (HEV): Strain variation in the nonstructural gene region encoding consensus motifs for an RNA-dependent RNA polymerase and an ATP/GTP binding site.";	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
RT Virus Genes 6:173-183(1992).	DE Fatty acid transporter protein (Fragment).	
RL Virus Genes 6:173-183(1992).	OS Sus scrofa (Pig).	
RN [1]	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RC SEQUENCE FROM N.A.	OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
RN	OX NCBI_TaxID=9823;	
RP SEQUENCE FROM N.A.	Q29346	
RN	TISSUE-SMALL INTESTINE;	

RA MEDLINE=96327607; PubMed=8673129;
 RA Wintero A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 library";
 RL "Mamm. Genome 7:509-517(1996)."
 DR EMBL: F14753; CAA2329.1; -;
 DR InterPro: IPR000566; Lipocin cytFABP.
 DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 68 68 AA; 7419 MW; ACCDFADB0178D8BA CRC64;
 SQ SEQUENCE 68 AA; 7604 MW; 8214FB5BA15DDDF CRC64;

Query Match 100.0%; Score 19; DB 6; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Db 38 AAPL 41

RESULT 24

Q9FLN3 PRELIMINARY; PRT; 68 AA.
 ID Q9FLN3;
 AC 09FLN3;
 DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
 DE EmbCAB62355.1
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis;
 OX NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLOMBIA;
 RX MEDLINE=98290546; PubMed=968582;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asanizu E., Miyajima N.,
 RA Tabata S.,
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 Sequence features of the regions of 1,456,315 bp covered by nineteen
 physically assigned PI and TAC clones.;"
 RT DNA Res. 5:41-54(1998);
 DR EMBL: AB010072; BAB09698.1; -
 SQ SEQUENCE 68 AA; 7479 MW; 1E588234DB8C3DBA CRC64;

Query Match 100.0%; Score 19; DB 10; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Db 5 AAPL 8

RESULT 25

Q8VJ02 PRELIMINARY; PRT; 68 AA.
 ID Q8VJ02;
 AC 08VJ02;
 DT 01-MAR-2002 (TREMBrel. 20, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)
 DE Hypothetical protein MT3573.9.
 GN MT3573.9
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=DC 1551 / OSHKOSH;
 RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Saizberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 laboratory strains."
 DR Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE007161; AAK47923.1; -;
 DR TIGR: MT3573; -;
 KW Hypothetical protein
 SQ SEQUENCE 68 AA; 7604 MW; 8214FB5BA15DDDF CRC64;

Query Match 100.0%; Score 19; DB 16; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Db 62 AAPL 65

RESULT 26

Q8S075 PRELIMINARY; PRT; 69 AA.
 ID Q8S075;
 AC 08S075;
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DE P0678F11.1 protein.
 GN P0678F11.1
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0678F11.1;"
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP003437; BAB86094.1; -
 SQ SEQUENCE 69 AA; 7454 MW; 5A5B882C4C65168 CRC64;

Query Match 100.0%; Score 19; DB 10; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAPL 4
 Db 3 AAPL 6

RESULT 27

Q9IFS8 PRELIMINARY; PRT; 69 AA.
 ID Q9IFS8;
 AC 09IFS8;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Polyprotein (Fragment).
 OS Human enterovirus 71.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Enteroviridae;
 OX NCBI_TaxID=39054;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5033/90;
 RX MEDLINE=2123062; PubMed=11338392;
 RA Chu P.-Y., Lin K.-H., Hwang C.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
 RA Wang J., Shimada Y., Ishiko H.;
 RA "Molecular epidemiology of enterovirus 71 in Taiwan.";

RL Arch. Virol. 146:589-600(2001).
DR EMBL; AB037250; BAB01494.1;
DR InterPro; IPR003138; Pico_P1A.
DR Pfam; PF02225; Pico_P1A; 1.
FT NON_TER
SQ SEQUENCE 69 AA; 7493 MW; 69B04974EE01BD4B CRC64;
Query Match 100.0%; Score 19; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPL 4
Db 65 AAPL 68

RESULT 28
Q9IPS7 PRELIMINARY; PRT; 69 AA.
ID Q9IPS7
AC Q9IPS7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 19, Last annotation update)
DE Polyprotein (Fragment).
OS Human enterovirus 71.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus;
OC NCBI_TaxID=39054;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN#5142/98;
RX MEDLINE=21237062; PubMed=11338392;
RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA Wang J., Shimada Y., Ishiko H.;
RT "Molecular epidemiology of enterovirus 71 in Taiwan.";
RL Arch. Virol. 146:589-600(2001).
DR EMBL; AB037251; BAB01495.1;
DR InterPro; IPR03138; Pico_P1A.
DR Pfam; PF02225; Pico_P1A; 1.
FT NON_TER
SQ SEQUENCE 69 AA; 7493 MW; 69B04974EE01BD4B CRC64;

Query Match 100.0%; Score 19; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPL 4
Db 65 AAPL 68

RESULT 30
Q9IPS5 PRELIMINARY; PRT; 69 AA.
ID Q9IPS5
AC Q9IPS5;
DT 01-OCT-2000 (TREMBLrel. 15, created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE Polyprotein (Fragment).
OS Human enterovirus 71.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus;
OC NCBI_TaxID=39054;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1557/98;
RX MEDLINE=21237062; PubMed=11338392;
RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA Wang J., Shimada Y., Ishiko H.;
RT "Molecular epidemiology of enterovirus 71 in Taiwan.";
RL Arch. Virol. 146:589-600(2001).
DR EMBL; AB037253; BAB01497.1;
DR InterPro; IPR03138; Pico_P1A.
DR Pfam; PF02226; Pico_P1A; 1.
FT NON_TER
SQ SEQUENCE 69 AA; 7493 MW; 69B04974EE01BD4B CRC64;

Query Match 100.0%; Score 19; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPL 4
Db 65 AAPL 68

RESULT 31
Q9IPS4 PRELIMINARY; PRT; 69 AA.
ID Q9IPS4
AC Q9IPS4;
DT 01-OCT-2000 (TREMBLrel. 15, created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Polyprotein (Fragment).
OS Human enterovirus 71.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus;
OC NCBI_TaxID=39054;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN#5142/98;
RX MEDLINE=21237062; PubMed=11338392;
RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA Wang J., Shimada Y., Ishiko H.;
RT "Molecular epidemiology of enterovirus 71 in Taiwan.";
RL Arch. Virol. 146:589-600(2001).
DR EMBL; AB037254; BAB01498.1;
DR InterPro; IPR03138; Pico_P1A.
DR Pfam; PF02226; Pico_P1A; 1.
FT NON_TER
SQ SEQUENCE 69 AA; 7493 MW; 69B04974EE01BD4B CRC64;

Db	65 AAPL 68		RESULT 36	RESULT 38
			Q9IPR9 PRELIMINARY; PRT; 69 AA.	Q9IPR7 PRELIMINARY; PRT; 69 AA.
ID	Q9IPR9		ID Q9IPR7	ID Q9IPR7
AC	Q9IPR9;		AC Q9IPR7;	AC Q9IPR7;
DT	01-OCT-2000	(TREMBREL 15, Created)	DT 01-OCT-2000 (TREMBREL 15, Created)	DT 01-OCT-2000 (TREMBREL 15, Last sequence update)
DT	01-OCT-2000	(TREMBREL 15, Last sequence update)	DT 01-OCT-2000 (TREMBREL 15, Last sequence update)	DT 01-DEC-2001 (TREMBREL 19, Last annotation update)
DE	Polyprotein (Fragment).		DE Polyprotein (Fragment).	DE Polyprotein (Fragment).
OS	Human enterovirus 71.		OS Human enterovirus 71.	OS Human enterovirus 71.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.		OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.	OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
OC	NCBI_TaxID=39054;		OC NCBI_TaxID=39054;	OC NCBI_TaxID=39054;
RN	{1}		RN {1}	RN {1}
RP	SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
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RA	MEDLINE=21237062; PubMed=11338392;		RA MEDLINE=21237062; PubMed=11338392;	RA MEDLINE=21237062; PubMed=11338392;
RA	Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,		RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,	RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA	Wang J., Shimada Y., Ishiko H.; "Molecular epidemiology of enterovirus 71 in Taiwan.";		RA Wang J., Shimada Y., Ishiko H.; "Molecular epidemiology of enterovirus 71 in Taiwan.";	RA Wang J., Shimada Y., Ishiko H.; "Molecular epidemiology of enterovirus 71 in Taiwan.";
RL	Arch. Virol. 146:589-600(2001).		RL Arch. Virol. 146:589-600(2001).	RL Arch. Virol. 146:589-600(2001).
DR	EMBL; AB037229; BAB01503.1; -.		DR EMBL; AB037229; BAB01503.1; -.	DR EMBL; AB037229; BAB01503.1; -.
DR	InterPro; IPR003138; Pico_P1A.		DR InterPro; IPR003138; Pico_P1A.	DR InterPro; IPR003138; Pico_P1A.
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Indels	0;		Indels 0;	Indels 0;
Gaps	0;		Gaps 0;	Gaps 0;
Qy	1 AAPL 4		Qy 1 AAPL 4	Qy 1 AAPL 4
Db	65 AAPL 68		Db 65 AAPL 68	Db 65 AAPL 68
RESULT 37	RESULT 39		RESULT 37	RESULT 39
Q9IPR8	PRELIMINARY; PRT; 69 AA.		Q9IPR8 PRELIMINARY; PRT; 69 AA.	Q9IPR6 PRELIMINARY; PRT; 69 AA.
ID	Q9IPR8		ID Q9IPR6	ID Q9IPR6
AC	Q9IPR8;		AC Q9IPR6;	AC Q9IPR6;
DT	01-OCT-2000 (TREMBREL 15, Created)		DT 01-OCT-2000 (TREMBREL 15, Last sequence update)	DT 01-OCT-2000 (TREMBREL 15, Last sequence update)
DT	01-OCT-2000 (TREMBREL 15, Last sequence update)		DT 01-DEC-2001 (TREMBREL 19, Last annotation update)	DT 01-DEC-2001 (TREMBREL 19, Last annotation update)
DE	Polyprotein (Fragment).		DE Polyprotein (Fragment).	DE Polyprotein (Fragment).
OS	Human enterovirus 71.		OS Human enterovirus 71.	OS Human enterovirus 71.
OS	Polyprotein (Fragment).		OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.	OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
OC	Human enterovirus 71.		OC Human enterovirus 71.	OC Human enterovirus 71.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.		OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.	OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
OC	NCBI_TaxID=39054;		OC NCBI_TaxID=39054;	OC NCBI_TaxID=39054;
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RC	STRAIN=588/98;		RC MEDLINE=21237062; PubMed=11338392;	RC MEDLINE=21237062; PubMed=11338392;
RA	Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,		RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,	RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA	Wang J., Shimada Y., Ishiko H.; "Molecular epidemiology of enterovirus 71 in Taiwan.";		RA Wang J., Shimada Y., Ishiko H.; "Molecular epidemiology of enterovirus 71 in Taiwan.";	RA Wang J., Shimada Y., Ishiko H.; "Molecular epidemiology of enterovirus 71 in Taiwan.";
RL	Arch. Virol. 146:589-600(2001).		RL Arch. Virol. 146:589-600(2001).	RL Arch. Virol. 146:589-600(2001).
DR	EMBL; AB037262; BAB01506.1; -.		DR EMBL; AB037262; BAB01506.1; -.	DR EMBL; AB037262; BAB01506.1; -.
DR	InterPro; IPR003138; Pico_P1A.		DR InterPro; IPR003138; Pico_P1A.	DR InterPro; IPR003138; Pico_P1A.
FT	Pfam; PF02226; PICO_P1A; 1.		FT Pfam; PF02226; PICO_P1A; 1.	FT Pfam; PF02226; PICO_P1A; 1.
SQ	NON_TER 69 AA; 7493 MW; 69B04974EE01BD4B CRC64;		SQ NON_TER 69 AA; 7493 MW; 69B04974EE01BD4B CRC64;	SQ NON_TER 69 AA; 7493 MW; 69B04974EE01BD4B CRC64;
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Best Local Similarity	100.0%; Pred. No. 1.6e+03;		Best Local Similarity 100.0%; Pred. No. 1.6e+03;	Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches	4; Conservative 0; Mismatches 0;		Matches 4; Conservative 0; Mismatches 0;	Matches 4; Conservative 0; Mismatches 0;
Indels	0;		Indels 0;	Indels 0;
Gaps	0;		Gaps 0;	Gaps 0;
Qy	1 AAPL 4		Qy 1 AAPL 4	Qy 1 AAPL 4
Db	65 AAPL 68		Db 65 AAPL 68	Db 65 AAPL 68
RESULT 40	RESULT 40		Q9IPR5	Q9IPR5

ID Q9IIR5 PRELIMINARY; PRT; 69 AA.
AC Q9IIR5;
DT 01-OCT-2000 (TREMBirel. 15, Created)
DT 01-OCT-2000 (TREMBirel. 15, Last sequence update)
DE Polyprotein (Fragment).
OS Human enterovirus 71.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
NCBI_TAXID=39054;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1226/98;
RX MEDLINE=21237062; PubMed=1338392;
RA Chu P.-Y., Lin K.-H., Hwang K.-P., Chou L.-C., Wang C.-F., Shih S.-R.,
RA Wang J., Shimada Y., Ishiko H.;
RT "Molecular epidemiology of enterovirus 71 in Taiwan."
RL Arch. Virol. 146:589-600(2001).
DR EMBL: AB037263; BAB01507.1; -.
DR InterPro: IPR003138; Pico_PIA.
DR Pfam: PF02226; Pico_PIA; 1.
FT NON_TER 69
SQ SEQUENCE 69 AA; 7493 MW; 69B04974FE01BD4B CRC64;

Query Match 100.0%; Score 19; DB 12; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4

Db 65 AAPL 68

Search completed: December 6, 2002, 13:30:09
 Job time : 20.5556 secs

GenCore version 5.1.3					
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Run on: December 6, 2002, 13:19:54 ; Search time 39 Seconds					
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Minimum DB seq length: 0					
Maximum DB seq length: 200000000					
Post-processing: Minimum Match 0%, Maximum Match 100%					
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10: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1991.DAT:*					
11: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1992.DAT:*					
12: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1993.DAT:*					
13: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1994.DAT:*					
14: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1995.DAT:*					
15: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1996.DAT:*					
16: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1997.DAT:*					
17: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1998.DAT:*					
18: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1999.DAT:*					
19: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA2000.DAT:*					
20: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA2001.DAT:*					
21: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA2002.DAT:*					
22: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA2003.DAT:*					
23: /SDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA2004.DAT:*					
RESULTS					
1: AA018046	XX	XX	XX	XX	XX
ID AA018046	standard; peptide: 6 AA.				
AC AA018046;					
DT 30-AUG-2002	(first entry)				
DE C-terminal truncated apoE formation inhibitor peptide #4.					
XX					
OS Synthetic.					
PN W0200238108-A2.					
PD XX					
PD 16-MAY-2002.					
XX					
PF 02-NOV-2001; 2001W0-US551172.					
XX					
PR 03-NOV-2000; 2000US-245737P.					
XX					
PA (GLAD-) GLADSTONE INST J DAVID.					
XX					
PI Huang Y, Mahley RW.					
XX					
DR WPI: 2002-490051/52.					
XX					
PT Inhibiting neurofibrillary tangles formation, useful for treating e.g.					
PT Alzheimer's, coronary artery disease or stroke, by reducing the					
PT Human reciprocal T					
11 29 100.0 397 22 AAG90077	C glutamicum prote				
12 29 100.0 397 22 AAB79052	corynebacterium glt				
13 29 100.0 405 23 AAM1979	Barley biotin synt				
14 29 100.0 410 22 AAB0694	Mouse DEC2a protei				
15 29 100.0 482 22 AABY0692	Human DEC2a protei				
16 29 100.0 484 22 AABY0693	Human DBC2b protei				
17 29 100.0 618 19 AAW2827	Human chromosome X				
18 29 100.0 723 22 ABB2129	Drosophila melanog				
19 29 100.0 747 22 ABBG9083	Drosophila melanog				
20 29 100.0 860 21 AAB33271	Balanus amphitrite				
21 26 89.7 9 18 AAW13821	Specific human leu				
22 26 89.7 9 18 AAW13809	Peptide encoded by				
23 26 89.7 14 23 AAU5695	Propionibacterium				
24 26 89.7 83 22 AAB52233	Eucalyptus granis				
25 26 89.7 138 21 AAB3830	Arabidopsis thalia				
26 26 89.7 159 22 ABG0853	Novel human diago				
27 26 89.7 204 18 AAW33276	S. fradiae tylosin				
28 26 89.7 210 13 AR22377	Even-skipped homeo				
29 26 89.7 325 22 AAG91087	Escherichia coli L				
30 26 89.7 325 22 AAB95630	Arbicidally activ				
31 26 89.7 327 21 AAG33744	An aromatic class				
32 26 89.7 329 21 ABB95120	Arabidopsis thalia				
33 26 89.7 331 22 ABB87703	Novel human diazo				
34 26 89.7 407 23 AAU1957	Arabidopsis thallo				
35 26 89.7 407 23 AAU1958	Drosophila melanog				
36 26 89.7 407 23 AAU0959	Herbically activ				
37 26 89.7 414 22 AAG7989	Drosophila melanog				
38 26 89.7 416 22 ABB95909	Escherichia coli L				
39 26 89.7 431 21 ABB1410	Arbicidally activ				
40 26 89.7 431 23 ABB87703	An aromatic class				
41 26 89.7 431 23 AAU1957	Arabidopsis sp. AT				
42 26 89.7 434 21 AAG33743	Arabidopsis thallo				
43 26 89.7 440 22 ABB65665	Drosophila melanog				
44 26 89.7 460 23 ABB95909	Herbically activ				
45 26 89.7 463 22 ABB59725	Drosophila melanog				
ALIGNMENTS					
RESULT 1					
AA018046	XX	XX	XX	XX	XX
ID AA018046	standard; peptide: 6 AA.				
AC AA018046;					
DT 30-AUG-2002	(first entry)				
DE C-terminal truncated apoE formation inhibitor peptide #4.					
XX					
OS Synthetic.					
PN W0200238108-A2.					
PD XX					
PD 16-MAY-2002.					
XX					
PF 02-NOV-2001; 2001W0-US551172.					
XX					
PR 03-NOV-2000; 2000US-245737P.					
XX					
PA (GLAD-) GLADSTONE INST J DAVID.					
XX					
PI Huang Y, Mahley RW.					
XX					
DR WPI: 2002-490051/52.					
XX					
PT Inhibiting neurofibrillary tangles formation, useful for treating e.g.					
PT Alzheimer's, coronary artery disease or stroke, by reducing the					
PT Human reciprocal T					

PS PT formation of carboxyl-terminal truncated form of apolipoprotein E in a neuron of the individual.

XX
 CC
 CC The present invention relates to a method of inhibiting the formation of neurofibrillary tangles in an individual, which involves reducing the formation of a carboxyl-terminal truncated form of apolipoprotein E (apoE) in a neurone in the individual. The method is useful for inhibiting the formation of neurofibrillary tangles in an individual. The reduction in the formation of carboxyl-terminal truncated apoE treats a disorder related to apoE in an individual, specifically Alzheimer's disease, coronary artery disease, head trauma or stroke. The present sequence is a peptide capable of inhibiting the formation of the C-terminal truncated form of apoE.

CC
 CC SQ Sequence 6 AA;

Query Match	Score	DB	Length	Best Local Similarity	Score	DB	Length	Best Local Similarity	Score	DB	Length	
Qy	1	AAAPPF	6	100.0%	29	DB	23:	100.0%	7.8e+05	Pred.	No.	Gaps
Db	1	AAAPPF	6			Mismatches	0;			Indels	0;	

RESULT 2
 AAU70970
 ID AAU70970 standard; Peptide: 18 AA.
 XX
 AC AAU70970;
 XX
 DT 25-FEB-2002 (first entry)
 DE M. tuberculosis rv1386 protein immunogenic peptide p3.
 KW Tuberculosis; tuberculostatic; antibacterial; vaccine; Rv0284;
 KW Rv0285; Rv0455c; Rv0569; Rv1195; Rv1386; Rv3417; Rv3878; Rv3879;
 KW MT3106_1; OPR13A; Rv0284ct; Mycobacterium bovis; Mycobacterium africanum
 KW BCG vaccine; immunogenic peptide.
 OS Mycobacterium tuberculosis.
 XX
 PN WO200179274-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 19-APR-2001; 2001WO-DK00275.
 PR 19-APR-2000; 2000DK-0000666.
 PR 21-FEB-2001; 2001DK-0000283.
 XX
 PA {STAT-} STATENS SERUM INST.
 XX
 PT Agger EM, Andersen P, Okkels LMM, Weldingh K;
 XX DR WPI; 2002-061970/08.
 XX
 PT New Mycobacterium tuberculosis antigens, useful for diagnosing tuberculosis, and as a vaccine for treating or preventing infections caused by species of tuberculosis complex -
 XX
 PS Example 3; Page 40; 111p; English.

CC The invention relates to a substantially pure polypeptide comprising an amino acid sequence selected from Rv0284, Rv0285, Rv455c, Rv0569, Rv1195, Rv1386, Rv3477, Rv3878, Rv3879, Rv387c or MT3106_1 (also disclosed are OPR13A and Rv0284ct), or their immunogenic portion, nucleic acids encoding them and an amino acid sequence analogue having at least 70% sequence identity to the polypeptide and is immunogenic.

CC The protein is useful in preparing a pharmaceutical composition for diagnosing tuberculosis and in preparing a vaccine against tuberculosis.

CC	caused by virulent mycobacteria. The vaccine or immunogenic/ pharmaceutical composition can be used prophylactically in a subject not infected with a virulent mycobacterium, or therapeutically in a subject already infected with a virulent mycobacterium. The protein is useful for preventing, treating and detecting infections caused by species of CC tuberculosis complex (M. tuberculosis, M. bovis, M. africanum). The nucleic acids may be used for effecting in vivo expression of the antigen, and in diagnostic assays for detecting the presence of CC pathogenic organisms in a sample. The vaccine is an improvement of the living BCG vaccine presently available, where one or more copies of the DNA sequence encoding one or more polypeptide have been incorporated into CC the genome of the microorganism to allow the microorganism to express and secrete the polypeptide. Incorporation of more than one copy of a CC nucleotide sequence enhances the immune response. The present sequence represents an immunogenic peptide derived from an M. CC tuberculosis protein of the invention.
SO	Sequence 18 AA;
Query Match	100.0%; Score 29; DB 23; Length 18;
Best Local Similarity	100.0%; Pred. No. 16;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 AAAAPP 6
Db	9 AAAAPF 14
RESULT 3	
AY11554	
ID AY11554	standard; Protein; 53 AA.
XX	
AC AY11554;	
XX	
DT 16-JUN-1999	(first entry)
XX	
DE Human 5' EST secreted protein SEQ ID NO:206.	
XX	
KW Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haemopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.	
KW	
OS Homo sapiens.	
XX	
PN WO9906439-A2.	
XX	
PD 11-FEB-1999.	
XX	
PF 31-JUL-1998; 98WO-1B01233.	
XX	
PR 01-AUG-1997; 97US-0904468.	
XX	
PA (GEST) GENSET.	
XX	
PI Duclert A, Dumas Milne Edwards J, Lacroix B;	
XX	
DR WPI; 1999-153700/13.	
DR N-PSDB; AAX40272.	
XX	
PT New nucleic acids encoding human secreted proteins - obtained from CDNA Libraries derived from liver, lung, large intestine, colon, thyroid and pancreas tissue	
XX	
PS Claim 27; Page 320-321; 398pp; English.	
XX	
CC AAX40251 to AAX40397 represent 5' expressed sequence tags (ESTs) for human secreted proteins and encode the proteins given in AAY11533 to AAY11679, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They	
CC	

can also be used to develop products for diagnosis and therapy. The

CC proteins obtained may have cytokine activity; cell

CC proliferation/differentiation activity; haemopoiesis regulating

CC activity; tissue growth regulating activity; reproductive hormone

CC regulating activity; chemotactic/ chemokinetic activity; haemostatic and

CC thrombolytic activity; receptor/ ligand activity; anti-inflammatory

CC activity; tumour inhibition activity or other activities. The products

CC can be used in forensic, gene therapy and chromosome mapping procedures.

CC The sequences can also be used for obtaining corresponding promoter

CC sequences. The nucleic acids encoding the signal peptide can be used for

CC directing extracellular secretion of a polypeptide or the insertion of a

CC polypeptide into a membrane, or importing a polypeptide into a cell.

CC series of CD14 mutants were used to localise and characterise an

CC epitope from CD14 specific for the monoclonal antibody 3C-10 (The

CC mutant peptide epitopes are described in AAR8550-97). To characterise

CC the 3C-10 epitope, site directed mutagenesis was used to create a

CC series of cDNAs encoding soluble CD14 having alanine substituted at

CC various positions between amino acids 1-55. The ability of 3C-10 to

CC bind to these mutant proteins was tested using a BIACore biosensor

CC instrument. The epitope was localised to amino acids 7-14 inclusive

CC of CD14.

XX Sequence 55 AA;

Query	Match	Score	DB	Length
Best Local	Similarity	100.0%	Pred. No.	20;
Matches		100.0%	0;	Mismatches
Qy	1 AAAAPF 6		0;	Indels
Db	17 AAAAPF 22		0;	Gaps

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

Query Match Score 29; DB 17; Length 55;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 6; Conservative 0; Mismatches 0;

Indels 0;

Gaps 0;

XX Sequence 55 AA;

CC tuberculosis complex (*M. tuberculosis*, *M. bovis*, *M. africanum*). The
 CC nucleic acids may be used for effeccting expression of the
 CC antigen, and in diagnostic assays for detecting the presence of
 CC pathogenic organisms in a sample. The vaccine is an improvement of the
 CC living BCG vaccine presently available, where one or more copies of the
 CC DNA sequence encoding one or more polypeptide has been incorporated into
 CC the genome of the microorganism to allow the microorganism to express and
 CC secrete the polypeptide. Incorporation of more than one copy of a
 CC nucleotide sequence enhances the immune response. The present
 CC sequence represents an *M. tuberculosis* protein of the invention.

XX Sequence 102 AA;

Query Match 100.0%; Score 29; DB 23; Length 102;

Best Local Similarity 100.0%; Pred. No. 86; Matches 6; Conservative 0; Mismatches 0;

Qy 1 AAAAPP 6

Db 29 AAAAPP 34

RESULT 6

AAU47148

ID AAU47148 standard; Protein; 140 AA.

XX AC

XX DT

XX 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #8044.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

OS WO200181581-A2.

PN 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-200841P.

PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YKW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L maisonneuve J, Zhang Y, Jen S, Carter D; (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX DR WPI; 2001-61674/71.

DR N-PSDB; AAS59537.

PT Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris - Example 1; SEQ ID NO 8343; 1069PP; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperosis and osteomyelitis), uveitis and endophthalmitis.
 CC *P. acnes* is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of *P. acnes* in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for *P. acnes* proteins. These antibodies can be used to
 CC therefore treat *P. acnes* infections. The antibodies may also be used as
 CC diagnostic agents for determining *P. acnes* presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences/.

SQ Sequence 140 AA;

Query Match 100.0%; Score 29; DB 22; Length 140;

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0;

Qy 1 AAAAPP 6

Db 20 AAAAPP 25

RESULT 7

AAW59495

ID AAW59495 standard; Protein; 302 AA.

XX AC

XX DT

XX 08-SEP-1998 (first entry)

DE Human TFE3 5'-RACE fusion product from cell line UOK109.

XX KW PRCC; papillary renal cell carcinoma; TFE3; transcription factor; RACE;

KW fusion protein; translocation; diagnosis; treatment; NonO; p54-nrb.

OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers

PN FT 1..302 /label= "TFE3

FT /note= "partial transcription factor sequence"

XX PN WO9806871-A1.

XX PD 19-FEB-1998.

XX PR 13-AUG-1997; 97WO-GB02209.

XX PR 13-AUG-1996; 96GB-0016986.

XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PI Clark J, Cooper C, Shipley J;

XX DR WPI; 1998-159557/14.

DR N-FSDB; AAV20961.

PT diagnosing papillary renal cell carcinoma by detecting gene
 PT trans-location resulting in fusion of TFE3 gene with some other
 PT gene, also related vectors, transformed cells, specific binding
 PT sequences, peptide(s) encoded by fusions and therapeutic anti-sense
 PT sequences

XX PS Claim 9; Fig 4B; 71PP; English.

This sequence represents a partial transcription factor, TFE3 sequence
 CC from a 5'-RACE product derived from a novel fusion protein
 CC constructed from the NonO protein (also known as p54-nrb) and the
 CC transcription factor TFE3 which is found in cell line UOK109 and used in
 CC a method for the diagnosis, prophylactic and therapeutic treatment of
 CC papillary renal cell carcinoma. The translocation t(X;1) (p11.2;q11.2)
 CC found in papillary renal cell carcinoma (PRCC) associated protein (PRCC)

CC	results in a fusion of the TFE3 gene with a new chromosome 1 gene
CC	designated PRCC (at 1q21.2), resulting in expression of a fusion protein
CC	between the N-terminus of PRCC and almost the whole of the TFE3 gene.
CC	Normal TFE3 transcripts are no longer produced. Two other fusion partners
CC	for TFE3 have also been detected: Nono, from a invx (p11.2; q13.24 or 12)
CC	translocation and the pSF splice factor gene, resulting in t(X;1)
CC	(p11.2;p4). These translocations define a subgroup of PRCC generally
CC	encountered in patients younger than 25.
SQ	sequence 302 AA;
RESULT 8	Query Match 100.0%; Score 29; DB 19; Length 302;
ID AAY08994	Best Local Similarity 100.0%; Pred. No. 2.5e+02;
ID AAY08994	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1	AAAPF 6
OY 1	
Db	137 AAAAPF 142
XX	
RESULT 8	Query Match 100.0%; Score 29; DB 19; Length 302;
ID AAY08994	Best Local Similarity 100.0%; Pred. No. 2.5e+02;
ID AAY08994	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1	AAAPF 6
OY 1	
Db	137 AAAAPF 142
XX	
DE Rice isocitrate dehydrogenase (clone rls6.pk0004.b3).	DE Rice isocitrate dehydrogenase (clone rls6.pk0004.b3).
XX	Rice isocitrate dehydrogenase (clone rls6.pk0004.b3).
KW Isocitrate dehydrogenase; corn; rice; soybean; wheat; transgenic; carbon metabolic pathway; citric acid cycle; ammonia assimilation; herbicide.	KW Isocitrate dehydrogenase; corn; rice; soybean; wheat; transgenic; carbon metabolic pathway; citric acid cycle; ammonia assimilation; herbicide.
XX	OS Oryza sativa.
XX	Key FH
FT Misc-difference 58	Location/Qualifiers
FT /label= unsure	
FT /note= "encoded by GGC"	
XX US6204039-B1.	
XX PD 20-MAR-2001.	
XX XX 19-NOV-1998; 98US-0196520.	
XX PR 02-DEC-1997; 97US-0067388.	
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.	
XX PD 20-MAR-2001.	
XX PT Allen SM, Falco SC;	
XX PN WPI; 2001-280619/29.	
XX DR DR N-PSDB; AACF57652.	
XX PS New plant isocitrate dehydrogenase polynucleotides, for modulating the levels of isocitrate dehydrogenase or citric acid cycle activity in plants, or as genetic tools to enhance or alter carbon or nitrogen metabolic pathways	
XX PT Claim 1; Columns 25-28; 22pp; English.	
XX CC The invention provides nucleic acid sequences encoding corn, rice, soybean and wheat isocitrate dehydrogenases. The nucleic acid sequences are useful for producing or altering the levels of isocitrate dehydrogenase in plants. These are also useful for creating transgenic plants in which the isocitrate dehydrogenase proteins are present at higher or lower levels than normal, or in cell types or developmental stages in which they are not normally found. They are also useful as genetic tools to enhance or alter carbon or nitrogen metabolic pathways, which in turn provide mechanisms for modulating the citric acid cycle and ammonia assimilation in plant cells. The isocitrate dehydrogenase proteins may be used as targets to facilitate design and identification of inhibitors of these enzymes that may be useful as herbicides. The present sequence represents the rice isocitrate dehydrogenase.	
SQ Sequence 362 AA;	
Query Match 100.0%; Score 29; DB 22; Length 362;	Query Match 100.0%; Score 29; DB 22; Length 362;
Best Local Similarity 100.0%; Pred. No. 3e+02;	Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1	AAAPF 6
OY 1	
Db	19 AAAAPF 24
XX AANP2823	
RESULT 10	RESULT 9
Db 19 AAAAPF 24	Db 19 AAAAPF 24
CC Best Local Similarity 100.0%; Pred. No. 3e+02;	CC Best Local Similarity 100.0%; Pred. No. 3e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1	AAAPF 6
OY 1	
Db	19 AAAAPF 24
XX AANP2823	

ID AAW52823 standard; Protein; 389 AA.
 XX
 AC AAW52823;
 XX
 DT 08-SEP-1998 (first entry)
 XX
 DE Human reciprocal TFE3/NonO fusion product from cell line UOK109.
 XX
 KW PRCC; Papillary renal cell carcinoma; TFE3; transcription factor;
 KW fusion protein; translocation; diagnosis; treatment; NonO; p54-nrb.
 XX
 OS Homo sapiens.
 Synthetic.
 XX
 Key Location/Qualifiers
 FH
 FT protein 1..389
 /label= "TFE3
 /note= "reciprocal fusion protein"
 FT Misc-difference 1..295
 /label= "TFE3
 /note= "transcription factor sequence"
 FT Misc-difference 296..389
 /label= NonO
 /note= "also known as p54-nrb"
 XX
 PN WO9806871-A1.
 XX
 PD 19-FEB-1998.
 XX
 PR 13-AUG-1997; 97WO-GB02209.
 XX
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PI Clark J, Cooper C, Shipley J;
 XX
 DR WPI; 1998-159557/14.
 XX
 DR N-PSDB; ARV2059.
 XX
 PT Diagnosing papillary renal cell carcinoma by detecting gene
 PT trans-location - resulting in fusion of TFE3 gene with some other
 PT gene, also related vectors, transformed cells, specific binding
 PT reagents, peptide(s) encoded by fusions and therapeutic anti-sense
 PT sequences
 XX
 PS Claim 9; Fig 3B; 71pp; English.
 XX
 This sequence represents a novel reciprocal fusion protein constructed
 CC from the NonO protein (also known as p54-nrb) and the transcription
 CC factor TFE3 which is found in cell line UOK109 and used in a method for
 CC the diagnosis, prophylactic and therapeutic treatment of papillary renal
 CC cell carcinoma. The translocation t(X;1) (p11.2;q21.2), found in papillary
 CC renal cell carcinoma (PRCC) associated protein (PRCC) results in a fusion
 CC of the TFE3 gene with a new chromosome 1 gene designated PRCC
 CC (at 1q21.2), resulting in expression of a fusion protein between the
 CC N-terminus of PRCC and almost the whole of the TFE3 gene. Normal TFE3
 CC transcripts are no longer produced. Two other fusion partners for TFE3
 CC have also been detected: NonO, from a invX (p11.2; q13.24 or 12);
 CC translocation and the PSF splice factor gene, resulting in t(X;1)
 CC (p11.2;p34). These trans-locations define a subgroup of PRCC generally
 XX
 Sequence 389 AA;

Query Match 100.0%; Score 29; DB 19; Length 389;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; OS Synthetic.

Qy 1 AAAAPP 6
 Db 137 AAAAPP 142

RESULT 11
 AAG90077
 ID AAG90077 standard; Protein; 397 AA.
 XX
 AC AAG90077;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE C glutamicum protein fragment SEQ ID NO: 3831.
 XX
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PT 18-DEC-2000; 2000EP-0127688.
 XX
 PR 16-DEC-1999; 99JP-0377484.
 PR 07-AUG-2000; 2000JP-0153162.
 PR 03-AUG-2000; 2000JP-0280988.
 XX
 PR (KYOW) KYOW HAKKO KOGYO KK.
 XX
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 XX
 PI Tateishi N, Ikeda M, Ozaki A;
 XX
 DR WPI; 2001-376931/40.
 XX
 DR N-PSDB; AAH65296.
 XX
 PT Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 XX
 PS Claim 17; SEQ ID NO: 3831; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described
 CC in the exemplification of the invention.
 Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 European Patent Office.
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 29; DB 22; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; OS Synthetic.

Qy 1 AAAAPP 6
 Db 45 AAAAPP 50

RESULT 12
 AAB79052
 ID AAB79052 standard; Protein; 397 AA.
 XX
 AC AAB79052;
 XX
 DT 30-APR-2001 (first entry)

XX DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:60.
 XX KW Corynebacterium glutamicum; homeostasis; adaptation; HA protein;
 KW fine chemical production; organic acid; proteinoxygenic amino acid;
 KW nonproteinoxygenic amino acid; purine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
 KW diagnosis; Corynebacterium diphtheriae; genetic engineering;
 KW Brevibacterium; environmental condition.

XX OS Corynebacterium glutamicum.
 XX PN WO200100842-A2.
 XX PD 04-JAN-2001.
 XX PF 23-JUN-2000; 2000WO-1B00911.
 XX PR 08-JUL-1999; 990S-0141031.
 XX PR 09-JUL-1999; 990E-01311636.
 XX PR 09-JUL-1999; 990E-0132125.
 XX PR 09-JUL-1999; 990E-0132126.
 XX PR 09-JUL-1999; 990E-0132127.
 XX PR 09-JUL-1999; 990E-0132128.
 XX PR 09-JUL-1999; 990E-0132129.
 XX PR 14-JUL-1999; 990E-0132226.
 XX PR 14-JUL-1999; 990E-1032920.
 XX PR 14-JUL-1999; 990E-1032922.
 XX PR 14-JUL-1999; 990E-1032924.
 XX PR 14-JUL-1999; 990E-1032928.
 XX PR 14-JUL-1999; 990E-1032930.
 XX PR 14-JUL-1999; 990E-1032933.
 XX PR 14-JUL-1999; 990E-1032935.
 XX PR 14-JUL-1999; 990E-1032973.
 XX PR 14-JUL-1999; 990E-1033002.
 XX PR 14-JUL-1999; 990E-1033003.
 XX PR 14-JUL-1999; 990E-1033005.
 XX PR 31-AUG-1999; 990E-1041378.
 XX PR 31-AUG-1999; 990E-1041379.
 XX PR 31-AUG-1999; 990E-1041390.
 XX PR 03-SEP-1999; 990E-1041391.
 XX PA (BADI) BASF AG.
 XX PT Pompejus M, Kroeger B, Schroeder H, zelder O, Haberhauer G;
 XX DR WPI; 2001-061974/07.
 XX N-PSDB; AAF71167.

PT New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, fatty acids, carbohydrates, vitamins or nucleosides, nucleotides, lipids, fatty acids, carboxylic acids, vitamins or enzymes -

XX CC AAF7138 to AAF71357 encode the Corynebacterium glutamicum homeostasis and adaptation (HA) proteins given in AAB79023 to AAB79242. The C. glutamicum HA genes (1) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinoxygenic or nonproteinoxygenic amino acid (preferred), purine or pyrimidine base, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polypeptide or enzyme. The amino acids produced can be lysine, glutamine, glutamate, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (1) or HA proteins encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (1) can be used to map the C. glutamicum genome or can be

CC used as markers for genetically engineered Corynebacterium or Brevibacterium. The HA proteins encoded by the (1) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to different environmental conditions.

SQ Sequence 397 AA;

Query Match 100.0%; Score 29; DB 22; Length 397;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6

Db

45 AAAAPF 50

RESULT 13

ID AAM51979 standard; Protein; 405 AA.

XX

AC AAM51979;

XX

DT 06-FEB-2002 (first entry)

XX

DE Barley biotin synthase protein #2.

XX

KW Barley; biotin synthase; biotin biosynthesis; herbicide; seedling; plant development; clone bshl.pk0005.d10; transgenic plant.

XX

OS Hordeum vulgare.

XX

PN US2001039042-A1.

XX

PD 08-NOV-2001.

XX

PF 19-DEC-2000; 2000US-0740288.

XX

PR 21-DEC-1999; 990S-172929P.

XX

(ALLE,) ALLEN S M.

(KINN,) KINNEY A J.

(MIAO,) MIAO G.

(OROZ,) OROZCO E M.

XX

PT Allen SM, Kinney AJ, Miao G, Orozco EM;

XX

DR WPI; 2002-040723/05.

XX DR N-PSDB; ABA01972.

XX PT New polypeptides, useful as targets for herbicide discovery, and as probes for genetic and physical mapping of genes of which they are

PT part, or creating transgenic plants, comprises biotin synthase

PT polypeptides and encoding Polynucleotides -

XX PS claim 19; Fig 1; 46pp; English.

XX

CC The present invention provides the protein and coding sequences of biotin synthase enzymes from barley, wheat, maize, soybean and the prickly poppy. These sequences can be used to produce transgenic plants which express different levels of the gene, or express it at different times in plant development. They can also be used as a target in the production of herbicides. The present sequence is a barley biotin synthase protein obtained from clone bsh1.pk0005.d10, which was derived from a barley seedling.

XX

SQ Sequence 405 AA;

Query Match 100.0%; Score 29; DB 23; Length 405;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6

Db

45 AAAAPF 50

Db 11 AAAAPF 16

XX PD 01-MAR-2001.

RESULT 14
AAB70694
ID AAB70694 standard; Protein; 410 AA.
XX
AC
XX
AAB70694;
DT 17-MAY-2001 (first entry)
DE Mouse DECC2a protein sequence SEQ ID NO:14.
XX KW DEC2a; DEC2b; bHLH type transcription factor; DEC2; DECl;
KW basic helix loop helix protein; cell differentiation; proliferation.
XX OS Mus musculus.
XX PN WO200114551-A1.
XX PD 01-MAR-2001.
XX PF 19-JUN-2000; 2000WO-JP03991.
XX PR 19-AUG-1999; 99JP-0233286.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Fujimoto K, Shin M, Kato Y;
XX DR WPI; 2001-202935/20.
DR N-PSDB; AAF74767.
XX PS Claim 2; Page 55-59; 83pp; Japanese.
XX CC The present invention describes a basic helix loop helix (bHLH) type
CC transcription factor designated DEC2. DEC2 can be used as a tool in
CC the development of drugs for the treatment and prevention of disorders
CC involving cell differentiation and proliferation. The present sequence
CC represents the specifically claimed human DECC2a protein, as given in the
CC present invention.
XX SQ Sequence 482 AA;
Query Match Best Local Similarity Score Length
Matches 6; Conservative 100.0%; Pred. No. 4e+02; 0; Mismatches 0; Indels 0; Gaps 0;
Db 380 AAAAPF 385

PS Claim 2; Page 77-80; 83pp; Japanese.

XX CC The present invention describes a basic helix loop helix (bHLH) type
CC transcription factor designated DEC2. DEC2 can be used as a tool in
CC the development of drugs for the treatment and prevention of disorders
CC involving cell differentiation and proliferation. The present sequence
CC represents the specifically claimed mouse DECC2a protein, as given in the
CC present invention.

XX SQ Sequence 410 AA;

Query Match 100.0%; Score 29; DB 22; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAPF 6

Db 321 AAAAPF 326

RESULT 15
AAB70692
ID AAB70692 standard; Protein; 482 AA.
XX
AC
XX
AAB70692;
DT 17-MAY-2001 (first entry)
DE Human DECC2a protein sequence SEQ ID NO:2.
XX KW DEC2a; DEC2b; bHLH type transcription factor; DEC2; DECl;
KW basic helix loop helix protein; cell differentiation; proliferation.
XX OS Homo sapiens.
XX PN WO200114551-A1.
XX PD 01-MAR-2001.
XX PF 19-JUN-2000; 2000WO-JP03991.
XX PR 19-AUG-1999; 99JP-0233286.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Fujimoto K, Shin M, Kato Y;
XX DR WPI; 2001-202935/20.
DR N-PSDB; AAF74776.
XX PS Claim 2; Page 69-72; 83pp; Japanese.

XX
 CC The present invention describes a basic helix loop helix (bHLH) type
 CC transcription factor designated DEC2. DEC2 can be used as a tool in
 CC the development of drugs for the treatment and prevention of disorders
 CC involving cell differentiation and proliferation. The present sequence
 CC represents the specifically claimed human DEC2 protein, as given in the
 XX present invention.

SQ Sequence 484 AA;

Query Match 100.0%; Score 29; DB 22; Length 484;
 Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAAAPF 6
 |||||
 Db 382 AAAAPF 387

RESULT 17

RAW52827 ID ABB62129 standard; Protein: 723 AA.
 XX AC ABB62129;
 XX DT 26-MAR-2002 (first entry)

AC ABB62129;
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 13179.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO2001171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-91637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.

XX PT Venter JC, Adams M, Li PWD, Myers EW;

XX DR N-PSDB; ABL06232.

XX DR N-PSDB; ABL06232.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

XX PT WPI; 2001-65860/75.

XX PS Disclosure; SEQ ID NO 13179; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL0511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL7737-ABL702).

CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 723 AA;

Query Match 100.0%; Score 29; DB 22; Length 723;
 Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;

Oy 1 AAAAPF 6
 |||||
 Db 150 AAAAPF 155

RESULT 19

ABB69083 ID ABB69083 standard; Protein: 747 AA.
 XX AC ABB69083;

Query Match 100.0%; Score 29; DB 19; Length 618;

SQ Sequence 618 AA;

Query Match 100.0%; Score 29; DB 19; Length 618;

Best Matches	Local Similarity	Score	Pred. No.	Mismatches	Indels	Gaps	0;
6;	100.0%	29;	5.1e+02;	0;	0;	0;	0;

Best Matches	Local Similarity	Score	Pred. No.	Mismatches	Indels	Gaps	0;
6;	100.0%	29;	6e+02;	0;	0;	0;	0;

XX	26-MAR-2002	(First entry)
XX	22-AUG-2000.	
XX	DE	Drosophila melanogaster polypeptide SEQ ID NO 34041.
XX	KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
OS	OS	Drosophila melanogaster.
XX	PN	WO200171042-A2.
XX	PD	27-SEP-2001.
XX	PP	23-MAR-2001; 2001WO-US02231.
XX	PR	23-MAR-2000; 2000US-191637P.
XX	PR	11-JUL-2000; 2000US-0614150.
XX	PA	(PEKE) PE CORP NY.
XX	PA	Venter JC, Adams M, Li PW, Myers EW;
XX	DR	WPI; 2001-656660/75.
DR	N-PSDB; ABL1386.	
XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
PT	PT	Disclosure; SEQ ID NO 34041; 21pp + Sequence Listing; English.
XX	PS	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0176-ABL3011); expressed DNA sequences (ABB5737-ABB7207). The sequence data for this patent was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX	SQ	Sequence 860 AA;
CC	CC	Query Match 100.0%; Score 29; DB 21; Length 860;
CC	CC	Best Local Similarity 100.0%; Pred. No. 7.1e+02;
CC	CC	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	QY	1 AAAAFF 6
CC	DB	319 AAAAFF 324
XX	RESULT	21
XX	AAW43821	AAW43821 standard; Peptide; 9 AA.
XX	ID	AAW43821;
XX	AC	
XX	XX	20-APR-1998 (first entry)
DT	DE	Specific human leukocyte antigen binding peptide #25.
XX	KW	Human leukocyte antigen; HLA; vaccine; bacterial infection; viral; cytotoxic T-cell; CTL; immunogenic peptide; cancer; poly-alanine. Synthetic.
OS	OS	
XX	PN	W09734617-A1.
XX	PD	25-SEP-1997.
XX	PP	21-MAR-1997; 97WO-US04451.
XX	PR	20-MAR-1997; 97US-0821739.
XX	PR	21-MAR-1996; 96US-0013833.
XX	PA	(CYT-E-) CYTEL CORP.
XX	PI	Cells E, Grey HM, Kubo RT, Sette A;
XX	XX	WPI; 1997-489250/45.
KW	KW	Adhesion/metamorphosis-related protein Bcs-5; barnacle; larva specific; adhesion inhibition; metamorphosis inhibition; compound screening; antifouling composition.
XX	OS	Balanus amphitrite.
XX	JP2000228985-A.	
CC	CC	The present sequence represents a specific example of an immunogenic

CC peptide which was used in a new method of inducing a cytotoxic T cell
 CC (CTL) response against a preselected antigen in a patient. The method
 CC comprises contacting CTLs from the patient with the immunogenic peptide
 CC (containing defined motifs) which binds one of the four HLA MHC products
 CC HLA-A3,2, HLA-A1, HLA-A11 or HLA-A24,1, the peptide having a dissociation
 CC constant (Kd) of less than 5×10^{-7} M. Immunogens are viral, e.g. human
 CC immunodeficiency virus type I (HIV-1), hepatitis B virus (HBV) and
 CC hepatitis C virus (HCV) or cancer antigens and are used in vaccines for
 CC the prevention and treatment of viral infection and cancer. The
 CC immunogens may be administered to the patient as a nucleic acid encoding
 CC the peptide (gene vaccine).

XX Sequence 9 AA;

SQ

Query	Match	Score	DB	Length
Best Local Matches	Similarity 5; Conservative 5;	26; 83.3%	18; Pred. No. 7.8e+05;	9;
Oy	1 AAAPPF 6			
Db	4 AAAAPY 9			

RESULT 22

ID ARW4309

ARW43809 standard; peptide: 9 AA.

XX AC AAW43809;

XX DT 20-APR-1998 (first entry)

XX DE Specific human leukocyte antigen binding peptide #13.

XX KW Human leukocyte antigen; HLA; vaccine; bacterial infection; viral;
 KW cytotoxic T-cell; CTL; immunogenic peptide; cancer; poly-alanine.

XX OS Synthetic.

PN WC9734617-A1.

XX PD 25-SEP-1997.

XX PF 21-MAR-1997; 97W0-US04451.

XX PR 20-MAR-1997; 97HS-0831739.

PR 21-MAR-1996; 96US-0013833.

XX PA (CYTE-) CYTEL CORP.

XX PI Celis E, Grey HM, Kubo RT, Sette A;

XX DR WPI; 1997-489250/45.

XX PT Specific human leukocyte antigen binding peptide - used in vaccines
 PT for the treatment and prevention of e.g. bacterial or viral
 PT infection and cancer

XX PS Claim 19: Page 37; 49pp; English.

XX CC The present sequence represents a specific example of an immunogenic
 CC peptide which was used in a new method of inducing a cytotoxic T cell
 CC (CTL) response against a preselected antigen in a patient. The method
 CC comprises contacting CTLs from the patient with the immunogenic peptide
 CC (containing defined motifs) which binds one of the four HLA MHC products
 CC HLA-A3,2, HLA-A1, HLA-A11 or HLA-A24,1, the peptide having a dissociation
 CC constant (Kd) of less than 5×10^{-7} M. Immunogens are viral, e.g. human
 CC immunodeficiency virus type I (HIV-1), hepatitis B virus (HBV) and
 CC hepatitis C virus (HCV) or cancer antigens and are used in vaccines for
 CC the prevention and treatment of viral infection and cancer. The
 CC immunogens may be administered to the patient as a nucleic acid encoding
 CC the peptide (gene vaccine).

XX Sequence 9 AA;

CC peptide which was used in a new method of inducing a cytotoxic T cell
 CC (CTL) response against a preselected antigen in a patient. The method
 CC comprises contacting CTLs from the patient with the immunogenic peptide
 CC (containing defined motifs) which binds one of the four HLA MHC products
 CC HLA-A3,2, HLA-A1, HLA-A11 or HLA-A24,1, the peptide having a dissociation
 CC constant (Kd) of less than 5×10^{-7} M. Immunogens are viral, e.g. human
 CC immunodeficiency virus type I (HIV-1), hepatitis B virus (HBV) and
 CC hepatitis C virus (HCV) or cancer antigens and are used in vaccines for
 CC the prevention and treatment of viral infection and cancer. The
 CC immunogens may be administered to the patient as a nucleic acid encoding
 CC the peptide (gene vaccine).

XX Sequence 9 AA;

SQ

Query	Match	Score	DB	Length
Best Local Matches	Similarity 83.3%;保守性 5; 比較的 1;	26; 83.3%	18; Pred. No. 7.8e+05;	9;
Oy	1 AAAPPF 6			
Db	4 AAAAPY 9			

RESULT 23

ID AAU99695

AAU99695 standard; Peptide: 14 AA.

XX AC AAU99695;

XX DT 07-OCT-2002 (first entry)

XX DE Peptide encoded by vectors PENTR-D-TOPO and PCDNAGW-DTPO.

XX KW Topoisomerase recognition site; topoisomerase; PCDNAGW(D)-sc;

KW PENTR-DT(sc); PCDNA-DES41; PENTR-D-TOPO; PENTR/SD(D)-TOPO;

KW PCDNA3.2/V5/GMP-TOPO; PCDNAGW-DTPO; recombinational cloning;

XX OS gene targeting; mutation; vector.

XX Synthetic.

XX PN WO200246372-A1.

XX PD 13-JUN-2002.

XX PF 07-DEC-2001; 2001WO-US45773.

XX PR 08-DEC-2000; 2000US-254510P.

PR 11-DEC-2000; 2000US-0732914.

PR 14-SEP-2001; 2001US-318902P.

PR 28-SEP-2001; 2001US-320092P.

PR 27-NOV-2001; 2001US-333124P.

XX PA (INV1-) INVITROGEN CORP.

XX PT Chesnut JD, Carrino J, Leong L, Madden K, Gleeson M, Fan J;

PT Brasch MA, Cheo D, Hartley JL, Byrd DRN, Temple GF;

XX DR WPI; 2002-519462/55.

N-PSDB; ARK8877.

XX PT New isolated nucleic acid molecule comprises one or more recombination
 PT sites and one or more topoisomerase recognition sites and/or one or
 PT more topoisomeres, useful in recombinational cloning

XX PS Example 3; Fig 26; 324p; English.

XX CC The invention relates to an isolated nucleic acid molecule (1)
 CC comprising: (a) one or more recombination sites; and (b) one or more
 CC topoisomerase recognition sites and/or one or more topoisomeres.
 CC Also included are a vector comprising the nucleic acid, a vector chosen
 CC from PCDNAGW(D)-sc, PENTR-D(T)-sc, PCDNA-DES41, PENTR-D-TOPO,
 CC PENTR/SD(D)-TOPO, PCDNA3.2/V5/GMP-TOPO or PCDNA6.2/V5/GMP-TOPO.

CC The invention also relates to a host cell comprising the nucleic acid or vectors and an in vitro method
 CC of cloning a nucleic acid molecule involving: (a) obtaining a first
 CC nucleic acid molecule to be cloned; (b) mixing the first nucleic acid
 CC molecule to be cloned in vitro with a second nucleic acid molecule
 CC comprising at least a first topoisomerase recognition site flanked by at
 CC least a first recombination site, and at least a second topoisomerase
 CC recognition site flanked by at least a second recombination site, where
 CC the first and second recombination sites do not recombine with each
 CC other, and at least one topoisomerase; and (c) incubating the mixture
 CC under conditions such that the first nucleic acid molecule to be cloned
 CC is inserted into the second nucleic acid molecule between the first and
 CC second topoisomerase recognition sites, thereby producing a first product
 CC molecule comprising the first nucleic acid molecule to be cloned between
 CC the first and second recombination sites. The method is useful for

CC cloning a nucleic acid molecule. The nucleic acid (1) is useful in
 CC methods for recombinational cloning and facilitates construction of gene
 CC targeting nucleic acid molecules or vectors which may be used to knockout
 CC or mutate a sequence or gene of interest, particularly genes or sequences
 CC within a host or host cells such as animal, plant, etc. Thus the
 nucleic acid is most preferably used for targeting or mutating a sequence
 CC of gene. The present sequence is the peptide encoded by the 5' end of the
 CC topoisomerase site-containing vectors pENTR/D-TOPO and pcDNAGW-DTOPO.
 XX Sequence 14 AA;

Query Match 89.7%; Score 26; DB 23; Length 14;

Best Local Similarity 83.3%; Pred. No. 51; Mismatches 1; Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 1 AAAAPPF 6
Db 7 AAAAPPF 12

RESULT 24

AAU53233 ID AAU53233 standard; Protein; 83 AA.
XX AC AAU53233;
XX DT 27 FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #14129.

XX SAPHO syndrome; snyovitis; acne; pustulosis; hypertotis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISH;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant;
 OS Propionibacterium acnes.
 XX WO200181581-A2.
 XX PN 01-NOV-2001.
 XX PD 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX PA (CORI-) CORINA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PT l'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPT; 2001-6167747-1.
 DR N-FSDB; AAS59559.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX Example 1; SEQ ID No 14428; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperosis and osteomyelitis), uveitis and endophthalmitis.
 CC acne is also involved in infections of bone, joints and the central
 nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 presence or absence of P. acnes in a patient comprises contacting a
 sample with a binding agent that binds to the proteins of the invention
 and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 83 AA;

Query Match 89.7%; Score 26; DB 22; Length 83;

Best Local Similarity 83.3%; Pred. No. 3e+02; Mismatches 0; Matches 5; Conservative 1; Indels 0; Gaps 0;

QY 1 AAAAPPF 6
Db 8 AAAAPPY 13

RESULT 25

AAB32830 ID AAB32830 standard; Protein; 138 AA.
XX AC AAB32830;
XX DT 25-JAN-2001 (first entry)

DE Eucalyptus grandis transcription factor protein sequence #288.
 XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
 KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
 KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox;
 KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
 KW type 2 Cys2Hs2; CCAAT box element; MYB.

XX OS Eucalyptus grandis.
 XX PN WO200053724-A2.
 XX PR 14-SEP-2000.
 XX PF 09-MAR-2000; 2000WO-US06112.
 XX PR 11-MAR-1999; 99US-0266513.
 PR 18-AUG-1999; 99US-0149485.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLETCH-) FLETCHER CHALLENGE FORESTS LTD.
 XX PI Wood M, McGrath A, Shenk MA, Glenn M;
 XX DR WPT; 2000-579369/54.

XX New isolated polynucleotide encoding a plant transcription factor for
 PT producing a plant e.g., a woody plant, preferably eucalyptus or pine,
 PT having modified gene expression or modified activity of a polypeptide
 XX

PS Claim 8; Page 320; 747pp; English.

XX The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
 CC transcription factor. The transcription factor may be used to produce a
 plant having modified gene expression such as a woody plant e.g., a
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 CC to modify the activity of a polypeptide in a plant. The transcription
 CC factors of the present invention are members from the following families
 CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
 CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2
 CC Cys2Hs2, CCAAT box elements and MYB.

DE Antigen mc-4c.
 XX
 KW Oocysts; sporozoite.
 XX
 OS Eimeria maxima.
 XX
 PN WO9204461-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 05-SEP-1991; 91WO-US06431.
 XX
 PR 12-SEP-1990; 90US-0581694.
 XX
 PA (GENE-) GENEX CORP.
 PA (FARH) HOECHST AG.
 XX
 PI Jacobson JW, Strausberg RL, Wilson SD, Pope SH, Strausberg SL;
 PI Raether W;
 XX
 DR WPI: 1992-114366/14.
 DR N-PSDB; AAQ23077.
 XX
 PT Vaccine against avian coccidiosis - comprising recombinant
 PT Elmeria antigen mc-4c, mc-5c or mc-30c gene, etc., or
 PT microorganisms expressing them
 XX
 PS Claim 2: Page 64 + Fig 2; 94pp; English.

To identify antigens of *E. maxima*, expression libraries were prep'd.
 CC In lambda vector, lambda gt11, using cDNA prep'd from polyA mRNA
 CC isolated from *E. maxima* oocysts. The cDNA expression library was
 CC screened with rat antiserum raised against the sporozoite stage of
 CC *E. maxima*. The library to be screened was plated on a host that
 CC allows lysis and plaque formation. Following induction of the
 CC antigens encoded by the phage, the plaques were transferred to
 CC nitrocellulose filters. Positive phage were identified after
 CC screening with the rat anti-*E. maxima* sporozoite antiserum.
 CC The cDNA inserts from the positive clones were cloned into
 CC bacteriophage M13 and subjected to sequence analysis.
 CC E. maxima antigen mc-4c (21.7 kD) was identified.

SQ Sequence 210 AA;

Query Match	89.7%	Score	26	DB	13	Length	210
Best Local Similarity	83.3%	Pred.	No.	7.4e+02			
Matches	5	Mismatches	1	Indels	0	Gaps	0

Oy 1 AAAAPP 6
 Db 180 AAAAPPY 185

RESULT 29
 ID AAC91087 standard; Protein; 325 AA.
 XX
 AC AAC91087;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 C Cornefam protein fragment SEQ ID NO: 4841.
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP110870-A2.
 XX
 PD 20-JUN-2001.
 XX
 PR 18-DEC-2000; 2000PP-0127688.

RESULT 30
 ID AAB79630 standard; Protein; 325 AA.
 XX
 AC AAB79630;
 XX
 DT 30-APR-2001 (first entry)

DE Corynebacterium glutamicum SMP protein sequence SEQ ID NO:776.
 XX
 KW Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study.
 XX
 OS Corynebacterium glutamicum.
 PN WO200100844-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000WO-IB00943.
 XX
 PR 25-JUN-1999; 99US-0141031.
 PR 08-JUL-1999; 99DE-1031412.

PR 08-JUL-1999; 99DE-1031413.
 PR 08-JUL-1999; 99DE-1031419.
 PR 08-JUL-1999; 99DE-1031420.
 PR 08-JUL-1999; 99DE-1031424.
 PR 08-JUL-1999; 99DE-1031428.
 PR 08-JUL-1999; 99DE-1031431.
 PR 08-JUL-1999; 99DE-1031433.
 PR 08-JUL-1999; 99DE-1031434.
 PR 08-JUL-1999; 99DE-1031510.
 PR 08-JUL-1999; 99DE-1031562.
 PR 09-JUL-1999; 99DE-1031634.
 PR 09-JUL-1999; 99DE-1032180.
 PR 09-JUL-1999; 99DE-1032227.
 PR 09-JUL-1999; 99DS-0132230.
 PR 09-JUL-1999; 99DS-0143208.
 PR 14-JUL-1999; 99DE-1032273.
 PR 14-JUL-1999; 99DE-1033005.
 PR 27-AUG-1999; 99DE-1042095.
 PR 31-AUG-1999; 99US-0151372.
 PR 03-SEP-1999; 99DE-1042076.
 PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042086.
 PR 03-SEP-1999; 99DE-1042087.
 PR 03-SEP-1999; 99DE-1042088.
 PR 03-SEP-1999; 99DE-1042095.
 PR 03-SEP-1999; 99DE-1042123.
 PR 03-SEP-1999; 99DE-1042125.
 XX (BADI) BASF AG.
 PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
 DR WPI: 2001-061975/07.
 DR N-PSDB; RAF71747.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes
 XX
 PS Claim 20: Page 1235-1236; 1246pp; English.
 XX
 CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 CC metabolism and oxidative phosphorylation (SMP) Proteins given in carbon metabolism and
 CC AAB79243 to AAB79633 which are involved in energy production. The C. glutamicum SMP gene can be used in vectors
 CC (II) for expression in host cells and production or modulation of
 CC production of fine chemicals, such as, an organic acid, a proteinogenic
 CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty
 CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
 CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins
 CC (III) encoded by them are used for diagnosing the presence or activity of
 CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
 CC containing them are used to map genomes of organisms related to
 CC. glutamicum, identify and localise C. glutamicum sequences of interest,
 CC in evolutionary studies, in determining SMP protein regions required
 CC for function, in modulating SMP protein activity, in modulating the
 CC metabolism of sugars, and in modulating high-energy molecule production
 CC in a cell (i.e. ATP, NADPH).
 XX
 SO Sequence 325 AA:
 Query Match 89.7%; Score 26; DB 22; Length 325;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03; Mismatches 5; Conservative 1; Indels 0; Gaps 0;
 Matches 1 AAAAPF 6
 QY 1 1111: 1111: 013455.
 Db 40 AAAPPY 45

PR	18-JUN-1999;	990S-0139459.	PR	20-AUG-1999;	990S-0149929.
PR	18-JUN-1999;	990S-0139460.	PR	23-AUG-1999;	990S-0149902.
PR	18-JUN-1999;	990S-0139461.	PR	23-AUG-1999;	990S-0149930.
PR	18-JUN-1999;	990S-0139462.	PR	25-AUG-1999;	990S-0150566.
PR	18-JUN-1999;	990S-0139463.	PR	26-AUG-1999;	990S-0150884.
PR	18-JUN-1999;	990S-0139750.	PR	27-AUG-1999;	990S-0151065.
PR	18-JUN-1999;	990S-0139763.	PR	27-AUG-1999;	990S-0151066.
PR	21-JUN-1999;	990S-0139817.	PR	27-AUG-1999;	990S-0151080.
PR	22-JUN-1999;	990S-0139899.	PR	30-AUG-1999;	990S-0151303.
PR	23-JUN-1999;	990S-0140353.	PR	31-AUG-1999;	990S-0151438.
PR	23-JUN-1999;	990S-0140354.	PR	01-SEP-1999;	990S-0151930.
PR	24-JUN-1999;	990S-0140695.	PR	07-SEP-1999;	990S-0152363.
PR	06-JUL-1999;	990S-0140823.	PR	10-SEP-1999;	990S-0153070.
PR	29-JUN-1999;	990S-0140991.	PR	13-SEP-1999;	990S-0153758.
PR	30-JUN-1999;	990S-0141287.	PR	15-SEP-1999;	990S-0154018.
PR	01-JUL-1999;	990S-0141842.	PR	16-SEP-1999;	990S-0154039.
PR	02-JUL-1999;	990S-0142154.	PR	20-SEP-1999;	990S-0154779.
PR	06-JUL-1999;	990S-0142390.	PR	22-SEP-1999;	990S-0155139.
PR	08-JUL-1999;	990S-0142803.	PR	23-SEP-1999;	990S-0155486.
PR	12-JUL-1999;	990S-0142920.	PR	24-SEP-1999;	990S-0155659.
PR	13-JUL-1999;	990S-0142977.	PR	28-SEP-1999;	990S-0156458.
PR	14-JUL-1999;	990S-0143542.	PR	04-OCT-1999;	990S-0157117.
PR	15-JUL-1999;	990S-0144005.	PR	05-OCT-1999;	990S-0157753.
PR	16-JUL-1999;	990S-0144085.	PR	06-OCT-1999;	990S-0157865.
PR	19-JUL-1999;	990S-0144305.	PR	07-OCT-1999;	990S-0158029.
PR	19-JUL-1999;	990S-0144325.	PR	08-OCT-1999;	990S-0158232.
PR	19-JUL-1999;	990S-0144331.	PR	12-OCT-1999;	990S-0158369.
PR	19-JUL-1999;	990S-0144332.	PR	13-OCT-1999;	990S-0158293.
PR	19-JUL-1999;	990S-0144334.	PR	13-OCT-1999;	990S-0159294.
PR	19-JUL-1999;	990S-0144334.	PR	14-OCT-1999;	990S-0159295.
PR	20-JUL-1999;	990S-0144335.	PR	14-OCT-1999;	990S-0159329.
PR	20-JUL-1999;	990S-0144352.	PR	14-OCT-1999;	990S-0159330.
PR	20-JUL-1999;	990S-0144632.	PR	14-OCT-1999;	990S-0159331.
PR	20-JUL-1999;	990S-0144884.	PR	14-OCT-1999;	990S-0159637.
PR	21-JUL-1999;	990S-0144816.	PR	14-OCT-1999;	990S-0159638.
PR	21-JUL-1999;	990S-0145086.	PR	18-OCT-1999;	990S-0159584.
PR	21-JUL-1999;	990S-0145088.	PR	21-OCT-1999;	990S-0160741.
PR	22-JUL-1999;	990S-0145224.	PR	21-OCT-1999;	990S-0160767.
PR	22-JUL-1999;	990S-0145226.	PR	21-OCT-1999;	990S-0160768.
PR	22-JUL-1999;	990S-0145226.	PR	21-OCT-1999;	990S-0160770.
PR	22-JUL-1999;	990S-0145226.	PR	21-OCT-1999;	990S-0160814.
PR	22-JUL-1999;	990S-0145912.	PR	21-OCT-1999;	990S-0160815.
PR	23-JUL-1999;	990S-0145919.	PR	22-OCT-1999;	990S-0160980.
PR	23-JUL-1999;	990S-0145919.	PR	22-OCT-1999;	990S-0160981.
PR	23-JUL-1999;	990S-0145919.	PR	22-OCT-1999;	990S-0160989.
PR	24-JUL-1999;	990S-0146386.	PR	25-OCT-1999;	990S-0161404.
PR	25-JUL-1999;	990S-0146388.	PR	25-OCT-1999;	990S-0161405.
PR	02-AUG-1999;	990S-0146389.	PR	25-OCT-1999;	990S-0161405.
PR	03-AUG-1999;	990S-0147030.	PR	25-OCT-1999;	990S-0161406.
PR	04-AUG-1999;	990S-0147204.	PR	26-OCT-1999;	990S-0161359.
PR	05-AUG-1999;	990S-0147302.	PR	26-OCT-1999;	990S-0161360.
PR	05-AUG-1999;	990S-0147303.	PR	26-OCT-1999;	990S-0161361.
PR	06-AUG-1999;	990S-0147416.	PR	26-OCT-1999;	990S-0161920.
PR	09-AUG-1999;	990S-0147493.	PR	28-OCT-1999;	990S-0161992.
PR	10-AUG-1999;	990S-0147935.	PR	28-OCT-1999;	990S-0161993.
PR	11-AUG-1999;	990S-0148171.	PR	29-OCT-1999;	990S-0162142.
PR	12-AUG-1999;	990S-0148311.			
PR	13-AUG-1999;	990S-0148341.			
PR	13-AUG-1999;	990S-0148684.			
PR	16-AUG-1999;	990S-0149368.			
PR	17-AUG-1999;	990S-0149415.			
PR	18-AUG-1999;	990S-0149426.			
PR	20-AUG-1999;	990S-0149426.			
PR	20-AUG-1999;	990S-0149722.			
PR	20-AUG-1999;	990S-0149723.			

Query Match 89.7%; Score 26; DB 21; Length 327;

Best Local Similarity 83.3%; Pred. No. 1 1e+03; Matches 5; Conservative 1; Mismatches 0; Indexes 0; Gaps 0;

Qy	1 AAAAPF 6
Db	311 ASAAPP 316

RESULT 32

ARG3030

ID ARG3030 standard; Protein: 329 AA.

XX

AC AAG3030;

XX

DT 17-OCT-2000 (first entry)

XX			PR	21-JUN-1999;	9905-0139817.
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 36240.		PR	22-JUN-1999;	9905-0139899.
XX			PR	23-JUN-1999;	9905-0140353.
KW	protein identification; signal transduction pathway; metabolic pathway;		PR	23-JUN-1999;	9905-0140354.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		PR	24-JUN-1999;	9905-0140695.
KW	termination sequence.		PR	28-JUN-1999;	9905-0140823.
XX			PR	29-JUN-1999;	9905-0140991.
OS	Arabidopsis thaliana.		PR	30-JUN-1999;	9905-0141287.
XX			PR	01-JUL-1999;	9905-0141842.
PN	EP1033405-A2.		PR	01-JUL-1999;	9905-0142154.
XX			PR	02-JUL-1999;	9905-0142055.
PD	06-SEP-2000.		PR	02-JUL-1999;	9905-0142390.
XX			PR	08-JUL-1999;	9905-0142803.
PF	25-FEB-2000; 2000EP-0301439.		PR	09-JUL-1999;	9905-0142920.
XX			PR	12-JUL-1999;	9905-0142977.
PR	25-FEB-1999; 9905-0121825.		PR	13-JUL-1999;	9905-0143542.
PR	05-MAR-1999; 9905-0123180.		PR	14-JUL-1999;	9905-0143624.
PR	09-MAR-1999; 9905-0123548.		PR	15-JUL-1999;	9905-0144085.
PR	23-MAR-1999; 9905-0125788.		PR	16-JUL-1999;	9905-0144866.
PR	25-MAR-1999; 9905-0126264.		PR	19-JUL-1999;	9905-0144932.
PR	29-MAR-1999; 9905-0126785.		PR	19-JUL-1999;	9905-0144991.
PR	01-APR-1999; 9905-0127462.		PR	19-JUL-1999;	9905-0144332.
PR	06-APR-1999; 9905-0128234.		PR	19-JUL-1999;	9905-014433.
PR	08-APR-1999; 9905-0128714.		PR	19-JUL-1999;	9905-0144334.
PR	16-APR-1999; 9905-0129845.		PR	19-JUL-1999;	9905-0144335.
PR	19-APR-1999; 9905-0130077.		PR	20-JUL-1999;	9905-0144352.
PR	21-APR-1999; 9905-0130449.		PR	20-JUL-1999;	9905-0144632.
PR	23-APR-1999; 9905-0130510.		PR	20-JUL-1999;	9905-0144884.
PR	23-APR-1999; 9905-0130891.		PR	21-JUL-1999;	9905-0144814.
PR	28-APR-1999; 9905-0131149.		PR	21-JUL-1999;	9905-0145086.
PR	30-APR-1999; 9905-0132048.		PR	21-JUL-1999;	9905-0145088.
PR	30-APR-1999; 9905-0132407.		PR	22-JUL-1999;	9905-0145085.
PR	04-MAY-1999; 9905-0132484.		PR	22-JUL-1999;	9905-0145087.
PR	05-MAY-1999; 9905-0132485.		PR	22-JUL-1999;	9905-0145089.
PR	06-MAY-1999; 9905-0132486.		PR	22-JUL-1999;	9905-0145145.
PR	06-MAY-1999; 9905-0132487.		PR	23-JUL-1999;	9905-0145218.
PR	07-MAY-1999; 9905-0132863.		PR	23-JUL-1999;	9905-0145224.
PR	11-MAY-1999; 9905-0134256.		PR	26-JUL-1999;	9905-0145276.
PR	14-MAY-1999; 9905-0134218.		PR	27-JUL-1999;	9905-0145918.
PR	14-MAY-1999; 9905-0134219.		PR	27-JUL-1999;	9905-0145919.
PR	14-MAY-1999; 9905-0134370.		PR	28-JUL-1999;	9905-0145951.
PR	18-MAY-1999; 9905-0134768.		PR	02-AUG-1999;	9905-0146386.
PR	19-MAY-1999; 9905-0134941.		PR	02-AUG-1999;	9905-0146388.
PR	20-MAY-1999; 9905-0135124.		PR	03-AUG-1999;	9905-0147038.
PR	21-MAY-1999; 9905-0135353.		PR	04-AUG-1999;	9905-0147204.
PR	24-MAY-1999; 9905-0135629.		PR	04-AUG-1999;	9905-0147302.
PR	25-MAY-1999; 9905-0136021.		PR	05-AUG-1999;	9905-0147192.
PR	27-MAY-1999; 9905-0136392.		PR	05-AUG-1999;	9905-0147260.
PR	28-MAY-1999; 9905-0136782.		PR	06-AUG-1999;	9905-0147303.
PR	01-JUN-1999; 9905-0137222.		PR	09-AUG-1999;	9905-0147493.
PR	03-JUN-1999; 9905-0137528.		PR	09-AUG-1999;	9905-0147935.
PR	04-JUN-1999; 9905-0137502.		PR	10-AUG-1999;	9905-0148171.
PR	07-JUN-1999; 9905-0137724.		PR	11-AUG-1999;	9905-0148319.
PR	08-JUN-1999; 9905-0138094.		PR	12-AUG-1999;	9905-0148341.
PR	10-JUN-1999; 9905-0138540.		PR	13-AUG-1999;	9905-0148565.
PR	10-JUN-1999; 9905-0138847.		PR	16-AUG-1999;	9905-0148684.
PR	14-JUN-1999; 9905-0139119.		PR	17-AUG-1999;	9905-0149368.
PR	16-JUN-1999; 9905-0139452.		PR	18-AUG-1999;	9905-0149426.
PR	16-JUN-1999; 9905-0139453.		PR	20-AUG-1999;	9905-0149722.
PR	17-JUN-1999; 9905-0139459.		PR	20-AUG-1999;	9905-0149723.
PR	18-JUN-1999; 9905-0139454.		PR	23-AUG-1999;	9905-0149929.
PR	18-JUN-1999; 9905-0139455.		PR	23-AUG-1999;	9905-0149930.
PR	18-JUN-1999; 9905-0139456.		PR	25-AUG-1999;	9905-0150566.
PR	18-JUN-1999; 9905-0139457.		PR	26-AUG-1999;	9905-0150884.
PR	18-JUN-1999; 9905-0139458.		PR	27-AUG-1999;	9905-0151065.
PR	18-JUN-1999; 9905-0139459.		PR	27-AUG-1999;	9905-0151066.
PR	18-JUN-1999; 9905-0139460.				
PR	18-JUN-1999; 9905-0139461.				
PR	18-JUN-1999; 9905-0139462.				
PR	18-JUN-1999; 9905-0139463.				
PR	18-JUN-1999; 9905-0139465.				
PR	18-JUN-1999; 9905-0139467.				
PR	18-JUN-1999; 9905-0139468.				
PR	18-JUN-1999; 9905-0139469.				
PR	18-JUN-1999; 9905-0139470.				
PR	18-JUN-1999; 9905-0139471.				
PR	18-JUN-1999; 9905-0139472.				
PR	18-JUN-1999; 9905-0139473.				
PR	18-JUN-1999; 9905-0139474.				
PR	18-JUN-1999; 9905-0139475.				
PR	18-JUN-1999; 9905-0139476.				
PR	18-JUN-1999; 9905-0139477.				
PR	18-JUN-1999; 9905-0139478.				
PR	18-JUN-1999; 9905-0139479.				
PR	18-JUN-1999; 9905-0139480.				
PR	18-JUN-1999; 9905-0139481.				
PR	18-JUN-1999; 9905-0139482.				
PR	18-JUN-1999; 9905-0139483.				
PR	18-JUN-1999; 9905-0139484.				
PR	18-JUN-1999; 9905-0139485.				
PR	18-JUN-1999; 9905-0139486.				
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PR	18-JUN-1999; 9905-0139489.				
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PR	18-JUN-1999; 9905-0139491.				
PR	18-JUN-1999; 9905-0139492.				
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PR	18-JUN-1999; 9905-0139498.				
PR	18-JUN-1999; 9905-0139499.				
PR	18-JUN-1999; 9905-0139500.				
PR	18-JUN-1999; 9905-0139501.				
PR	18-JUN-1999; 9905-0139502.				
PR	18-JUN-1999; 9905-0139503.				
PR	18-JUN-1999; 9905-0139504.				
PR	18-JUN-1999; 9905-0139505.				
PR	18-JUN-1999; 9905-0139506.				
PR	18-JUN-1999; 9905-0139507.				
PR	18-JUN-1999; 9905-0139508.				
PR	18-JUN-1999; 9905-0139509.				
PR	18-JUN-1999; 9905-0139510.				
PR	18-JUN-1999; 9905-0139511.				
PR	18-JUN-1999; 9905-0139512.				
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PR	18-JUN-1999; 9905-0139515.				
PR	18-JUN-1999; 9905-0139516.				
PR	18-JUN-1999; 9905-0139517.				
PR	18-JUN-1999; 9905-0139518.				
PR	18-JUN-1999; 9905-0139519.				
PR	18-JUN-1999; 9905-0139520.				
PR	18-JUN-1999; 9905-0139521.				
PR	18-JUN-1999; 9905-0139522.				
PR	18-JUN-1999; 9905-0139523.				
PR	18-JUN-1999; 9905-0139524.				
PR	18-JUN-1999; 9905-0139525.				
PR	18-JUN-1999; 9905-0139526.				
PR	18-JUN-1999; 9905-0139527.				
PR	18-JUN-1999; 9905-0139528.				
PR	18-JUN-1999; 9905-0139529.				
PR	18-JUN-1999; 9905-0139530.				
PR	18-JUN-1999; 9905-0139531.				
PR	18-JUN-1999; 9905-0139532.				
PR	18-JUN-1999; 9905-0139533.				
PR	18-JUN-1999; 9905-0139534.				
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PR	18-JUN-1999; 9905-0139538.				
PR	18-JUN-1999; 9905-0139539.				
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PR	18-JUN-1999; 9905-0139547.				
PR	18-JUN-1999; 9905-0139548.				
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PR	18-JUN-1999; 9905-0139551.				
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PR	18-JUN-1999; 9905-0139558.				
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PR	18-JUN-1999; 9905-0139561.				
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PR	18-JUN-1999; 9905-0139564.				
PR	18-JUN-1999; 9905-0139565.				
PR	18-JUN-1999; 9905-0139566.				
PR	18-JUN-1999; 9905-0139567.				
PR	18-JUN-1999; 9905-0139568.				
PR	18-JUN-1999; 9905-0139569.				
PR	18-JUN-1999; 9905-0139570.				
PR	18-JUN-1999; 9905-0139571.				
PR	18-JUN-1999; 9905-0139572.				
PR	18-JUN-1999; 9905-0139573				

PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0152070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157111.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158253.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 14-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159657.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160771.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-016104.
 PR 25-OCT-1999; 99US-0161360.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

 Query Match 89.7%; Score 26; DB 21; Length 329;
 Best local Similarity 83.3%; Pred. No. 1.2e+03; Mismatches 0;
 Matches 5; Conservative 1; Indels 0; Gaps 0;
 OS Homo sapiens.

Qy 1 AAAAPF 6
Db 82 AASAPF 87

RESULT 33
 ABG12782 standard; Protein: 331 AA.
 ID ABG12782
 XX
 AC
 AAU10957
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #12773.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder
 XX Homo sapiens.

Qy 1 AAAAPF 6
Db 82 AASAPF 87

RESULT 34
 AAU10957
 ID AAU10957 standard; Protein: 407 AA.
 AC
 AAU10957
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Even-skipped homeo box 1 (EVX1).
 XX
 KW Ever-skipped homeo box 1; EVX1; neurological disease; drug screening; haplotyping; single nucleotide polymorphism; SNP; human.
 XX
 OS Homo sapiens.

PN WO20010175067-A2.

XX
 PN
 XX
 PD 11-OCT-2001.
 XX
 PR 30-MAR-2001; 2001WO-US08631.
 PR
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PT Drmanac RT, Liu C, Tang YT;
 DR WPI; 2001-639362/73.
 DR N-PSDB; HAT76969.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
 PS Claim 20; SEQ ID NO 43141; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pctc_sequences.
 CC Sequence 331 AA;
 XX

XX
XX 29-NOV-2001.
PD
XX
PF 21-MAY-2001; 2001WO-US16559.
XX
PR 19-MAY-2000; 2000US-205437P.
XX
PA (GENA-) GENAISANCE PHARM INC.
XX
PT Duda A, Kliem SE, Kumar AM;
XX
DR WPI; 2002-089913/12.
DR N-PSDB; AAU18559.
XX
PT Novel genetic variants of even-skipped homeo box 1, EVXL gene useful
PT for therapeutic purposes and for expressing EVXL protein useful in
PT identifying drugs to treat neurological diseases
XX
PS Claim 28; Fig 3; 69pp; English.
XX
CC The invention relates to an isolated polynucleotide (I), comprising a
CC nucleotide sequence which is a polymorphic variant of a reference
CC sequence for the even-skipped homeo box 1 (homologue of *Drosophila*)
CC (EVXL) gene or its fragment, or a polymorphic variant of a reference
CC sequence for a EVXL cDNA or its fragment. EVXL polypeptide (II) is
CC useful for screening for drugs targeting the polypeptide, by contacting
CC the EVXL polymorphic variant with a candidate agent and assaying for
CC binding activity. A method is described for identifying an association
CC between a trait such as a clinical response to a drug targeting EVXL and
CC a haplotype or haplotype pair of EVXL gene. The methods are useful
CC in developing diagnostic tests and therapeutic treatments for
CC neurological diseases. (I) is useful for studying the expression and
CC function of EVXL and expressing EVXL protein for use in screening for
CC candidate drugs to treat diseases related to EVXL activity. The
CC polymorphism and haplotype data are useful for validating whether EVXL is
CC a suitable target for drugs to treat neurological diseases, screening for
CC such drugs and reducing bias in clinical trials of such drugs. (I) is
CC useful for therapeutic purposes. (I) is useful for determining if an
CC individual has one of the haplotypes 1-4 or the haplotype pairs.
CC establishing the EVXL haplotype or haplotype pair of an individual is
CC useful for improving the efficiency and reliability of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with EVXL activity e.g. neurological diseases. The haplotyping method
CC is useful to validate EVXL as a candidate target for treating a
CC specific condition or disease predicted to be associated with EVXL
CC activity. (I) is useful for studying expression of the EVXL isogenes
CC in vivo, for in vivo screening and testing of drugs against EVXL
CC protein and for testing the efficacy of therapeutic agents and
CC compounds for neurological diseases in a biological system. Antibody
CC raised against (II) is useful for diagnostic and prognostic formats and
CC therapeutic methods, for immunoprecipitating (II) from solution, for
CC detecting EVXL protein isoforms in biological samples, frozen tissue
CC sections, cells which have been fixed or unfixed and prepared on slides,
CC for use in immunocytochemical, immunohistochemical and immunofluorescence
CC techniques. The present sequence represents the amino acid sequence of
CC human even-skipped homeo box 1 (EVXL) isomer #1.
CC Note: The present sequence is not shown in the specification but is
CC derived from the wild type human EVXL sequence given in figure 3 (see
CC AAU1957).
XX
XX 12-MAR-2002 (first entry)
DT
XX
DE Even-skipped homeo box 1 (EVXL) isoform #1.
XX
KW Even-skipped homeo box 1; EVXL; neurological disease; drug screening;
KW haplotyping; single nucleotide polymorphism; SNP; human.
XX
OS Homo sapiens.
XX
FH Key /note= "Wild type Ala substituted by Val"
FT Misc-difference 82
FT
XX
PR 19-MAY-2000; 2000US-205437P.
XX
PA (GENA-) GENAISANCE PHARM INC.
XX
PT 29-NOV-2001.
XX
DR WPI; 2002-089913/12.
DR
XX
PN WO2001190120-A2.
XX
PT
XX
PS Disclosure; Page -; 69pp; English.
XX
CC The invention relates to an isolated polynucleotide (I), comprising a
CC nucleotide sequence which is a polymorphic variant of a reference
CC sequence for the even-skipped homeo box 1 (homologue of *Drosophila*)
CC (EVXL) gene or its fragment, or a polymorphic variant of a reference
CC sequence for a EVXL cDNA or its fragment. EVXL polypeptide (II) is
CC useful for screening for drugs targeting the polypeptide, by contacting
CC the EVXL polymorphic variant with a candidate agent and assaying for
CC binding activity. A method is described for identifying an association
CC between a traits such as a clinical response to a drug targeting EVXL and
CC a haplotype or haplotype pair of EVXL gene. The methods are useful
CC in developing diagnostic tests and therapeutic treatments for
CC neurological diseases. (I) is useful for studying the expression and
CC function of EVXL and expressing EVXL protein for use in screening for
CC candidate drugs to treat diseases related to EVXL activity. The
CC polymorphism and haplotype data are useful for validating whether EVXL is
CC a suitable target for drugs to treat neurological diseases, screening for
CC such drugs and reducing bias in clinical trials of such drugs. (I) is
CC useful for therapeutic purposes. (I) is useful for determining if an
CC individual has one of the haplotypes 1-4 or the haplotype pairs.
CC establishing the EVXL haplotype or haplotype pair of an individual is
CC useful for improving the efficiency and reliability of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with EVXL activity e.g. neurological diseases. The haplotyping method
CC is useful to validate EVXL as a candidate target for treating a
CC specific condition or disease predicted to be associated with EVXL
CC activity. (I) is useful for studying expression of the EVXL isogenes
CC in vivo, for in vivo screening and testing of drugs against EVXL
CC protein and for testing the efficacy of therapeutic agents and
CC compounds for neurological diseases in a biological system. Antibody
CC raised against (II) is useful for diagnostic and prognostic formats and
CC therapeutic methods, for immunoprecipitating (II) from solution, for
CC detecting EVXL protein isoforms in biological samples, frozen tissue
CC sections, cells which have been fixed or unfixed and prepared on slides,
CC for use in immunocytochemical, immunohistochemical and immunofluorescence
CC techniques. The present sequence represents the amino acid sequence of
CC human even-skipped homeo box 1 (EVXL) isomer #1.
CC Note: The present sequence is not shown in the specification but is
CC derived from the wild type human EVXL sequence given in figure 3 (see
CC AAU1957).
XX
XX
RESULT 35
AAU10958
ID AAU10958 standard; Protein; 407 AA.
XX
AC AAU10958;

XX Sequence 407 AA;
 SQ CC
 Query Match 89.7%; Score 26; DB 23; Length 407;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 0;
 Indels 0; Gaps 0;
 QY 1 AAAAPP 6
 |||||
 Db 295 AAASPF 300

RESULT 36
 AAU10959
 AAU10959 standard; Protein; 407 AA.
 AC AAU10959;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Even-skipped homeo box 1 (EVXL) isoform #2.
 XX
 KW Even-skipped homeo box 1; EVXL; neurological disease; drug screening;
 KW haplotyping; single nucleotide polymorphism; SNP; human.
 OS Homo sapiens.
 XX
 FH Key-difference Location/Qualifiers
 FT Misc-difference 320
 /note= "Wild type Pro substituted by Ala"
 PN WO20010120-A2.
 XX
 PR 29-NOV-2001.
 XX
 PT 21-MAY-2001; 2001WO-US16559.
 XX
 PR 19-MAY-2000; 2000US-205437P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PT Duda A, Klem SE, Kumar AM;
 XX
 DR WPI; 2002-089913/12.
 XX
 PT Novel genetic variants of even-skipped homeo box 1, EVXL gene useful in
 PT identifying drugs to treat neurological diseases
 PS Disclosure; Page -; 69pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (I), comprising a
 CC nucleotide sequence which is a polymorphic variant of a reference
 CC sequence for the even-skipped homeo box 1 (homologue of *Drosophila*)
 CC sequence (EVXL) gene or its fragment, or a polymorphic variant of a reference
 CC sequence for a EVXL cDNA or its fragment. EVXL polypeptide (II) is
 CC useful for screening for drugs targeting the polypeptide by contacting
 CC the EVXL polymorphic variant with a candidate agent and assaying for
 CC binding activity. A method is described for identifying an association
 CC between a trait such as a clinical response to a drug targeting EVXL and
 CC a haplotype or haplotype pair of EVXL gene. The methods are useful
 CC in developing diagnostic tests and therapeutic treatments for
 CC neurological diseases. (I) is useful for studying the expression and
 CC function of EVXL and expressing EVXL protein for use in screening for
 CC candidate drugs to treat diseases related to EVXL activity. The
 CC polymorphism and haplotype data are useful for validating whether EVXL is
 CC a suitable target for drugs to treat neurological diseases, screening for
 CC such drugs and reducing bias in clinical trials of such drugs. (I) is
 CC useful for therapeutic purposes. (I) is useful for determining if an
 CC individual has one of the haplotypes 1-4 or the haplotype pairs.
 CC establishing the EVXL haplotype or haplotype pair of an individual is
 CC useful for improving the efficiency and reliability of several steps in
 CC the discovery and development of drugs for treating diseases associated

CC with EVXL activity e.g., neurological diseases. The haplotyping method
 CC is useful to validate EVXL as a candidate target for treating a
 CC specific condition or disease predicted to be associated with EVXL
 CC activity. (I) is useful for studying expression of the EVXL isogenes
 CC in vivo, for in vivo screening and testing of drugs against EVXL
 CC protein and for testing the efficacy of therapeutic agents and
 CC compounds for neurological diseases in a biological system. Antibody
 CC raised against (II) is useful for diagnostic and prognostic formats and
 CC therapeutic methods, for immunoprecipitating (II) from solution, for
 CC detecting EVXL protein isoforms in biological samples, frozen tissue
 CC sections, cells which have been fixed or unfixed and prepared on slides,
 CC for use in immunocytochemical, immunohistochemical and immunofluorescence
 CC techniques. The present sequence represents the amino acid sequence of
 CC human even-skipped homeo box 1 (EVXL) isoform #2.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the wild type human EVXL sequence given in figure 3 (see
 CC AAU10957).
 XX
 SQ Sequence 407 AA;
 CC
 Query Match 89.7%; Score 26; DB 23; Length 407;
 CC Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 CC Matches 5; Conservative 1; Mismatches 0;
 CC Indels 0; Gaps 0;
 QY 1 AAAAPP 6
 |||||

RESULT 37
 AAG78989
 ID AAG78989 standard; Protein; 414 AA.
 XX
 AC AAG78989;
 XX
 DT 18-JAN-2002 (first entry)
 XX
 DE Escherichia coli Lole protein, involved in lipoprotein localisation.
 XX
 KW Lole; lipoprotein localisation; Gram-negative bacterium.
 XX
 PT Escherichia coli.
 OS
 PN JP2001231570-A.
 XX
 PR 28-AUG-2001.
 XX
 PT 24-FEB-2000; 2000JP-0047702.
 PR 24-FEB-2000; 2000JP-0047702.
 XX
 PA (MTTA) MITSUI CHEM INC.
 DR WPI; 2001-650996/75.
 DR N-PSDB; AA171758.
 PT New protein for controlling localization of a lipoprotein in the cell
 PT of a Gram-negative microbe and a DNA encoding it
 XX
 PS Disclosure; Page 10-12; 17pp; Japanese.
 XX
 CC The present invention relates to novel proteins from *Escherichia coli*,
 CC which control the localisation of lipoprotein in Gram-negative microbes.
 CC The present sequence is one such protein, Lole.
 XX
 SQ Sequence 414 AA;
 CC
 Query Match 89.7%; Score 26; DB 22; Length 414;
 CC Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 CC Matches 5; Conservative 1; Mismatches 0;
 CC Indels 0; Gaps 0;

FT /note= "Encoded by TPA"
 XX
 PN WO200233050-A2.
 XX
 PD 25-APR-2002.
 XX
 PR 12-OCT-2001; 2001WO-US42673.
 XX
 PR 14-OCT-2000; 2000US-0688071.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Lassner MN, Savidge B, Weiss JD, Mitsky TA, Post-Beittnermiller MA;
 PI Valentin HE;
 XX
 DR WPI; 2002-463312/49.
 DR N-PSDB; AB062166.

XX Novel nucleic acid sequences encoding prenyltransferase derived from
 PT eukaryotic and prokaryotic sources useful for producing plants and
 PT seeds with altered tocopherol content and compositions -
 XX
 PS Example 1; Fig 2; 148pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid sequence encoding
 CC a prenyltransferase (PTS). The nucleic acid construct of the invention is
 CC useful for altering isoprenoid content and for producing an isoprenoid
 CC compound of interest in a host cell, such as *Synechocystis* sp., or a
 CC plant cell obtained from *Arabidopsis*, corn, rice, wheat, leek, canola,
 CC cotton or tomato. The construct is also useful for increasing
 CC biosynthetic flux in a host cell toward production of an isoprenoid
 CC compound such as tocopherol and tocotrienol. The polynucleotide is useful
 CC for producing plants and plant parts, such as seeds, enriched in
 CC tocopherols. The sequence shown represents *Arabidopsis* sp. API4, a
 CC polytransferase identified in the invention.
 XX

SQ Sequence 431 AA.
 Query Match 89.7%; Score 26; DB 23; Length 431;
 Best Local Similarity 83.3%; Pred No. 1.5e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAPF 6
 Db 415 ASAAPF 420

Search completed: December 6, 2002, 13:28:03
 Job time : 40 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 13:26:14 ; Search time 14 Seconds
 12.610 Million cell updates/sec

title: US 10-033-526-4
perfect-score: 29

Sequence: 1 AAAAPP 6

Scoring table: BL0SUM62
 Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

total number of hits satisfying chosen parameters: 262574
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	29	100.0	55	1	US-08-366-953A-42
2	29	100.0	55	1	US-08-366-953A-43
3	29	100.0	60	2	US-08-484-337A-35
4	29	100.0	362	4	US-09-196-520-04
5	26	89.7	4551	3	US-09-320-878-1
6	26	89.7	4513	4	US-09-105-537-31
7	25	89.7	1187	4	US-09-105-537-6
8	25	86.2	72	1	US-08-366-73-48
9	25	86.2	57	4	US-08-984-151-2
10	25	86.2	64	4	US-08-759-463-4
11	25	86.2	64	4	US-09-328-153-4
12	25	85.2	72	1	US-08-217-360-5
13	25	86.2	72	1	US-08-217-360-8
14	25	86.2	72	1	US-08-217-360-10
15	25	86.2	72	1	US-08-217-360-12
16	25	86.2	453	4	US-09-134-001C-4873
17	25	85.2	488	4	US-08-472-728-2
18	25	85.2	548	1	US-08-468-700-37
19	25	86.2	548	1	US-08-445-971-5
20	25	86.2	548	2	US-08-468-220-35
21	25	86.2	548	2	US-08-468-698-35
22	25	86.2	548	2	US-08-470-706A-37
23	25	85.2	548	3	US-08-890-383-6
24	25	86.2	548	3	US-08-914-679A-45
25	25	86.2	548	4	US-08-659-383
26	25	86.2	548	4	US-08-194-664A-35
27	25	86.2	548	4	PCT-US4-01553A-35

ALIGNMENTS

RESULT 1
 US-08-366-953A-42
 ; Sequence 42, Application US/08366953A
 Patent No. 576653
 GENERAL INFORMATION:
 APPLICANT: Lichenstein, Henri S.
 ATTORNEY/AGENT INFORMATION:
 NAME: Cook Ph.D., Robert R.
 REGISTRATION NUMBER: 31-602
 REFERENCE/DOCKET NUMBER: A-324
 INFORMATION FOR SEQ ID NO: 42:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Cook Ph.D., Robert R.
 REGISTRATION NUMBER: 31-602
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 55 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-366-953A-42

Query Match Similarity 100.0%; pred No. 15; DB 1; Length 55;
 Best Local Similarity 100.0%; pred No. 15; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAPP 6
 DB 45 AAAAPP 50

RESULT 2
 US-08-366-953A-43
 ; Sequence 43, Application US/08366953A

Patent No. 5766593
GENERAL INFORMATION:

APPLICANT: Lichtenstein, Henri S.

APPLICANT: Wright, Samuel D.

TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 PEPTIDES

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1720

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/366,953A

FILING DATE: 30-DEC-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Cook Ph.D., Robert R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-324

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 55 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-484-397A-35

RESULT 3

US-08-484-397A-35

Sequence 35, Application US/08484397A

Patent No. 5869055

GENERAL INFORMATION:

APPLICANT: Juan, Shao-Chieh

APPLICANT: Lichenstein, Henri S.

APPLICANT: Wright, Samuel D.

TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: CA

COUNTRY: US

ZIP: 91320-1780

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,397A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Curry, Daniel R.

REGISTRATION NUMBER: 32,727

REFERENCE/DOCKET NUMBER: A-324A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/447-1000
TELEFAX: 805/447-1090

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 60 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-196-520-4

RESULT 4

US-09-196-520-4

Sequence 4, Application US/09196520

Patent No. 6204039

GENERAL INFORMATION:

APPLICANT: Falco, Carl S.

APPLICANT: Allen, Stephen M.

TITLE OF INVENTION: Plant Isocitrate Dehydrogenase Homologs

FILE REFERENCE: BB-1291

CURRENT APPLICATION NUMBER: US/09/196,520

CURRENT FILING DATE: 1998-11-19

EARLIER APPLICATION NUMBER: 60/067,388

EARLIER FILING DATE: December 2, 1997

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 4

LENGTH: 362

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

NAME/KEY: UNSURE

LOCATION: (58)

US-09-196-520-4

RESULT 5

US-09-320-878-1

Query Match

Best Local Similarity

100.0%; Score 29;

DB: 4; Length 362;

Mismatches

0; Pred. No: 93;

Indels 0;

Gaps 0;

Db 19 AAAAPF 24

Query Match

Best Local Similarity

100.0%; Score 29;

DB: 4; Length 362;

Mismatches

0; Pred. No: 93;

Indels 0;

Gaps 0;

Db 19 AAAAPF 24

Query Match

Best Local Similarity

100.0%; Score 29;

DB: 4; Length 362;

Mismatches

0; Pred. No: 93;

Indels 0;

Gaps 0;

Db 19 AAAAPF 24

Query Match

Best Local Similarity

100.0%; Score 29;

DB: 4; Length 362;

Mismatches

0; Pred. No: 93;

Indels 0;

Gaps 0;

Db 19 AAAAPF 24

Query Match

Best Local Similarity

100.0%; Score 29;

DB: 4; Length 362;

Mismatches

0; Pred. No: 93;

Indels 0;

Gaps 0;

Db 19 AAAAPF 24

Query Match

Best Local Similarity

100.0%; Score 29;

DB: 4; Length 362;

Mismatches

0; Pred. No: 93;

Indels 0;

Gaps 0;

Db 19 AAAAPF 24

; ORGANISM: Streptomyces venezuelae
; US-09-105-537-6
; Query Match 89.7%; Score 26; DB 3; Length 11877;
; Best Local Similarity 83.3%; Pred. No. 1.1e+04; Indels 0; Gaps 0;
; Matches 5; Conservative 1; Mismatches 0;
; SEQ ID NO 1
; LENGTH: 4128
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-320-878-1
; Query Match 89.7%; Score 26; DB 3; Length 4551;
; Best Local Similarity 83.3%; Pred. No. 4.3e+03; Indels 0; Gaps 0;
; Matches 5; Conservative 1; Mismatches 0;
; SEQ ID NO 1
; LENGTH: 4351
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-320-878-1
; Query Match 89.7%; Score 26; DB 3; Length 4551;
; Best Local Similarity 83.3%; Pred. No. 4.3e+03; Indels 0; Gaps 0;
; Matches 5; Conservative 1; Mismatches 0;
; SEQ ID NO 1
; LENGTH: 4351
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-105-537-31
; Sequence 31, Application US/09105537A
; Patent No. 626502
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600_43801
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSBQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 4613
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-105-537-31
; Query Match 89.7%; Score 26; DB 4; Length 4613;
; Best Local Similarity 83.3%; Pred. No. 4.4e+03; Indels 0; Gaps 0;
; Matches 5; Conservative 1; Mismatches 0;
; SEQ ID NO 1
; LENGTH: 4613
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-105-537-31
; Query Match 89.7%; Score 26; DB 4; Length 4613;
; Best Local Similarity 83.3%; Pred. No. 4.4e+03; Indels 0; Gaps 0;
; Matches 5; Conservative 1; Mismatches 0;
; SEQ ID NO 1
; LENGTH: 4613
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-105-537-31
; Query Match 89.7%; Score 26; DB 4; Length 4613;
; Best Local Similarity 83.3%; Pred. No. 4.4e+03; Indels 0; Gaps 0;
; Matches 5; Conservative 1; Mismatches 0;
; SEQ ID NO 1
; LENGTH: 4613
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-105-537-6
; Sequence 48, Application US/08666473
; Patent No. 5843113
; GENERAL INFORMATION:
; APPLICANT: YOSHIDA, Aruto
; APPLICANT: TAKENICHI, Makoto
; TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORKS MUCIN SUGAR
; TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
; TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 300 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,473
; FILING DATE: 19-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP95/02238
; FILING DATE: 01-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-22101
; FILING DATE: 09-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-269111
; FILING DATE: 01-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16887/837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-666-473-48
; Query Match 86.2%; Score 25; DB 2; Length 7;
; Best Local Similarity 83.3%; Pred. No. 2e+05; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 1;
; SEQ ID NO 1
; LENGTH: 11877
; TYPE: PRT

RESULT 9
 US-08-984-151-2
 Sequence 2, Application US/08984151
 ; PATENT NO. 6130366
 ; GENERAL INFORMATION:
 ; APPLICANT: HERRERA-ESTRELLA, LUIS
 ; APPLICANT: VAN DEN BROEK, GUIDO
 ; APPLICANT: VAN MONTAGU, MARC
 ; APPLICANT: SCHREIER, PETER
 ; APPLICANT: SCHELL, JOSEF
 ; APPLICANT: BOHNERT, HANS J.
 ; APPLICANT: CASHMORE, ANTONY
 ; APPLICANT: TIMKO, MICHAEL P.
 ; APPLICANT: KAUSCH, ALBERT P.
 ; TITLE OF INVENTION: CHIMAERIC GENE CODING FOR A TRANSIT
 ; TITLE OF INVENTION: PEPTIDE AND A HETEROLOGOUS POLYPEPTIDE (AS AMENDED)
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
 ; STREET: P.O. Box 747
 ; CITY: Falls Church
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/984,151
 ; FILING DATE: 03-DEC-1997
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SVENSON, LEONARD R.
 ; REGISTRATION NUMBER: 30,330
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; TELEX: 248345
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 57 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE: Pisum sativum
 ; ORGANISM: Pisum sativum
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..57
 ; OTHER INFORMATION: /note= "transit peptide of the
 ; OTHER INFORMATION: small subunit of RubP of pea cells."
 ; US-08-984-151-2
 ; Query Match 86.2%; Score 25; DB 4; Length 57;
 ; Best Local Similarity 83.3%; Pred. No. 98; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 5; Conservative 0;
 ; QY 1 AAAAPF 6
 ; Db 22 AAVAPF 27
 ;
 ; RESULT 10
 ; US-08-159-463-4
 ; Sequence 4, Application US/08759463
 ; PATENT NO. 601198
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenton Ko
 ; APPLICANT: Zdenka W. Ko
 ;
 ; Query Match 86.2%; Score 25; DB 4; Length 64;
 ; Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;
 ; Matches 5; Conservative 0;
 ; QY 1 AAAAPF 6
 ; Db 22 AAVAPF 27
 ;
 ; RESULT 11
 ; US-09-338-153-4
 ; Sequence 4, Application US/09328153
 ; PATENT NO. 6239332
 ; GENERAL INFORMATION:
 ; APPLICANT: KO, Kenton
 ; APPLICANT: KO, Zdenka W.
 ; APPLICANT: Labate, Carlos A.
 ; APPLICANT: Granell, Antonio
 ; TITLE OF INVENTION: CONSTRUCTS AND METHODS FOR ENHANCING
 ; TITLE OF INVENTION: PROTEIN LEVELS IN PHOTOSYNTHETIC ORGANISMS
 ; CURRENT APPLICATION NUMBER: US/09/328,153
 ; CURRENT FILING DATE: 1999-06-08
 ; PRIOR APPLICATION NUMBER: US 08/759,463
 ; PRIOR FILING DATE: 1996-12-05
 ; PRIOR APPLICATION NUMBER: US 08/7568,168
 ; PRIOR FILING DATE: 1995-12-06
 ; PRIOR APPLICATION NUMBER: PCT/CA96/00807
 ; PRIOR FILING DATE: 1996-11-26
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 64
 ; TYPE: PRT
 ; ORGANISM: Pisum sativum
 ; US-09-328-153-4
 ; Query Match 86.2%; Score 25; DB 4; Length 64;
 ; Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;
 ; Matches 5; Conservative 0;
 ; QY 1 AAAAPF 6
 ; Db 22 AAVAPF 27
 ;

Qy 1 AAAAPP 6
 1111
 Db 22 AAVAPP 27

RESULT 12
 US-08-217-360-6
 ; Sequence 6, Application US/08217360
 ; Patent No. 5530191
 ; GENERAL INFORMATION:
 ; APPLICANT: MALIGA, Pal
 ; TITLE OF INVENTION: METHODS FOR PRODUCING CYTOPLASMIC
 ; TITLE OF INVENTION: MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF HYBR
 ; TITLE OF INVENTION: MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF HYBR
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
 ; ADDRESSEE: P.C.
 ; STREET: 1601 Market Street, Suite 720
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103-2307

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/217,360
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: REED, Janet E.
 REGISTRATION NUMBER: 36,252
 REFERENCE/DOCKET NUMBER: Rutgers University
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215)563-4100
 TELEFAX: (215)563-4044

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 72 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

US-08-217-360-8

Query Match 86.2% Score 25; DB 1; Length 72;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 83.3%; O; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAAPP 6
 1111
 Db 22 AAVAPP 27

RESULT 14
 US-08-217-360-10
 ; Sequence 10, Application US/08217360
 ; Patent No. 5530191
 ; GENERAL INFORMATION:
 ; APPLICANT: MALIGA, Pal
 ; TITLE OF INVENTION: METHODS FOR PRODUCING CYTOPLASMIC
 ; TITLE OF INVENTION: MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF HYBR
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
 ; ADDRESSEE: P.C.
 ; STREET: 1601 Market Street, Suite 720
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103-2307

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/217,360
 FILING DATE: 24-MAR-1994
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: REED, Janet E.
 REGISTRATION NUMBER: 36,252
 REFERENCE/DOCKET NUMBER: Rutgers University
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215)563-4100
 TELEFAX: (215)563-4044

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-217-360-10

Query Match 86.2%; Score 25; DB 1; Length 72;
Best Local Similarity 83.3%; Pred. No. 1.2e+02; Length 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AAAAPF 6
Db 22 AAVAPF 27

RESULT 15

US-08-217-360-12

Sequence 12, Application US/08217360

GENERAL INFORMATION:

APPLICANT: MALIGA, Pal

TITLE OF INVENTION: METHODS FOR PRODUCING CYTOPLASMIC

TITLE OF INVENTION: MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF HYBR

TITLE OF INVENTION: SEED

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman,

STREET: 1601 Market Street, Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,360

FILING DATE: 24-MAR-1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: REED, JENNIFER E.

REGISTRATION NUMBER: 36,252

REFERENCE/DOCKET NUMBER: Rutgers University

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215)563-4100

TELEFAX: (215)563-0444

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-217-360-12

RESULT 16

US-08-134-001C-4873

Sequence 37, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4873

LENGTH: 453

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4873

Sequence 2, Application US/09444728

Patent No. 646899

GENERAL INFORMATION:

APPLICANT: Burrell, Michael M

TITLE OF INVENTION: Genetically Modified Plants With Altered Starch

FILE REFERENCE: 9341-019

CURRENT APPLICATION NUMBER: US/09/444,728

CURRENT FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 488

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: linked to E. coli glgC16 CDS

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: COLIN MITCHINSON

APPLICANT: CAROL A. REQUADT

APPLICANT: TRACI H. ROPP

APPLICANT: LELIE P. SOLHEIM

TITLE OF INVENTION: MUTANT ALPHA-AMYLASE

NUMBER OF SEQUENCES: 40

SEQ ID NO 4873

LENGTH: 453

TYPE: PRT

ORGANISM: Pea ssu TP

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: COLIN MITCHINSON

APPLICANT: CAROL A. REQUADT

APPLICANT: TRACI H. ROPP

APPLICANT: LELIE P. SOLHEIM

TITLE OF INVENTION: MUTANT ALPHA-AMYLASE

NUMBER OF SEQUENCES: 40

SEQ ID NO 4873

LENGTH: 453

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4873

Sequence 2, Application US/09444728

Patent No. 646899

GENERAL INFORMATION:

APPLICANT: Burrell, Michael M

TITLE OF INVENTION: Genetically Modified Plants With Altered Starch

FILE REFERENCE: 9341-019

CURRENT APPLICATION NUMBER: US/09/444,728

CURRENT FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 488

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: linked to E. coli glgC16 CDS

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: COLIN MITCHINSON

APPLICANT: CAROL A. REQUADT

APPLICANT: TRACI H. ROPP

APPLICANT: LELIE P. SOLHEIM

TITLE OF INVENTION: MUTANT ALPHA-AMYLASE

NUMBER OF SEQUENCES: 40

SEQ ID NO 4873

LENGTH: 453

TYPE: PRT

ORGANISM: Pea ssu TP

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: COLIN MITCHINSON

APPLICANT: CAROL A. REQUADT

APPLICANT: TRACI H. ROPP

APPLICANT: LELIE P. SOLHEIM

TITLE OF INVENTION: MUTANT ALPHA-AMYLASE

NUMBER OF SEQUENCES: 40

SEQ ID NO 4873

LENGTH: 453

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4873

Sequence 37, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4873

LENGTH: 453

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: linked to E. coli glgC16 CDS

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: Burrell, Michael M

TITLE OF INVENTION: Genetically Modified Plants With Altered Starch

FILE REFERENCE: 9341-019

CURRENT APPLICATION NUMBER: US/09/444,728

CURRENT FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 488

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: linked to E. coli glgC16 CDS

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: Burrell, Michael M

TITLE OF INVENTION: Genetically Modified Plants With Altered Starch

FILE REFERENCE: 9341-019

CURRENT APPLICATION NUMBER: US/09/444,728

CURRENT FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 488

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: linked to E. coli glgC16 CDS

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: Burrell, Michael M

TITLE OF INVENTION: Genetically Modified Plants With Altered Starch

FILE REFERENCE: 9341-019

CURRENT APPLICATION NUMBER: US/09/444,728

CURRENT FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 488

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: linked to E. coli glgC16 CDS

US-09-444-728-2

Sequence 37, Application US/08468700

Patent No. 5736499

GENERAL INFORMATION:

APPLICANT: Burrell, Michael M

TITLE OF INVENTION: Genetically Modified Plants With Altered Starch

FILE REFERENCE: 9341-019

CURRENT APPLICATION NUMBER: US/09/444,728

CURRENT FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 488

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: linked to E. coli glgC16 CDS

US-09-444-728-2

CORRESPONDENCE ADDRESS: International
 ADDRESSEE: Genencor International
 STREET: 180 Kimball Way
 CITY: South San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/468,700
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 252

ATTORNEY/AGENT INFORMATION:
 NAME: Stone, Christopher L.
 REGISTRATION NUMBER: 35,696
 REFERENCE/DOCKET NUMBER: GC275
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 742-7217
 TELEFAX: (415) 742-7217

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:
 LENGTH: 548 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

US-08-468-700-37

Query Match 86.2%; Score 25; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAPF 6
 Db 34 AAPF 38

RESULT 19

US-08-645-971-5
 Sequence 5, Application US/08645971
 ; Patent No. 5763385
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Modified Alpha-Amylases Having Altered Calcium Binding Properties
 ; TITLE OF INVENTION: Calcium Binding Properties
 ; NUMBER OF SEQUENCES: 5
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US-08/645,971
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 548 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-645-971-5

Query Match 86.2%; Score 25; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAPF 6
 Db 34 AAPF 38

RESULT 21

US-08-468-698-35
 Sequence 35, Application US/08468698
 ; Patent No. 5824332
 ; GENERAL INFORMATION:
 ; APPLICANT: Autrim, Richard L.
 ; APPLICANT: Barnett, Christopher
 ; APPLICANT: Hutchinson, Colin
 ; APPLICANT: Power, Scott D.
 ; APPLICANT: Requard, Carol P.
 ; APPLICANT: Solheim, Leif P.

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:
 LENGTH: 548 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

ORIGINAL SOURCE: ORGANISM: Bacillus stearothermophilus

US-08-468-698-35

Query Match 86.2%; Score 25; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAPF 6
 Db 34 AAPF 38

APPLICANT: Requadt, Carol
 APPLICANT: Soheim, Leif P.
 TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International, Inc.
 STREET: 180 Kimball Way
 CITY: South San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,698
 FILING DATE: 06-JUN-95
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/194,664
 FILING DATE: 10-FEB-94
 PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Stone, Christopher L.
 REGISTRATION NUMBER: 35,696
 REFERENCE/DOCKET NUMBER: GC220D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 742-7555
 TELEFAX: (415) 742-2117
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 548 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US 08-468-698-35

Query Match Best Local Similarity 86.2%; Score 25; DB 2; Length 548; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AAPF 6
 Db 34 AAPF 38

RESULT 22
 US-08-704-706A-37
 Sequence 37, Application US/08704706A
 ; Patient No. 5958739
 GENERAL INFORMATION:
 APPLICANT: GENENCOR INTERNATIONAL, INC.
 APPLICANT: COLIN MITCHINSON
 APPLICANT: ANTHONY G. DAY
 APPLICANT: ANDREW SHAW
 TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International, Inc.
 STREET: 925 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1013
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,383
 FILING DATE: To Be Assigned
 ATTORNEY/AGENT INFORMATION:
 NAME: Stone, Christopher L.
 REGISTRATION NUMBER: 35,696
 REFERENCE/DOCKET NUMBER: GC377
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 846-7555
 TELEFAX: (650) 845-6504
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 548 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-890-383-6

Query Match Best Local Similarity 86.2%; Score 25; DB 3; Length 548; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AAPF 6
 Db 34 AAPF 38

RESULT 23
 US-08-890-383-6
 Sequence 6, Application US/08890383
 ; Patient No. 6008026
 ; GENERAL INFORMATION:
 APPLICANT: Anthony G. Day
 TITLE OF INVENTION: MUTANT ALPHA-AMYLASE HAVING INTRODUCED
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International, Inc.
 STREET: 925 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1013
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,383
 FILING DATE: To Be Assigned
 ATTORNEY/AGENT INFORMATION:
 NAME: Stone, Christopher L.
 REGISTRATION NUMBER: 35,696
 REFERENCE/DOCKET NUMBER: GC377
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 846-7555
 TELEFAX: (650) 845-6504
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 548 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-890-383-6

Query Match Best Local Similarity 86.2%; Score 25; DB 3; Length 548; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
US-08-914-679A-6
; Sequence 6, Application US/08914679A
; Patent No. 608058
; GENERAL INFORMATION:
; APPLICANT: Anthony G. Day
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASE COMPRISING MODIFICATION
; TITLE OF INVENTION: AT RESIDUES CORRESPONDING TO A210, H405 AND/OR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,679A
; FILING DATE: To Be Assigned
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 846-7555
; TELEFAX: (650) 845-6504
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 548 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-914-679A-6

Query Match 86.2%; Score 25; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 26
US-08-194-664A-35
; Sequence 35, Application US/08194664A
; Patent No. 6297037
; GENERAL INFORMATION:
; APPLICANT: Antim, Richard L.
; APPLICANT: Barnett, Christopher
; APPLICANT: Hutchinson, Colin
; APPLICANT: Power, Scott D.
; APPLICANT: Regaud, Carol
; APPLICANT: Solheim, Leif P.
; TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,664A
; FILING DATE: 10-FEB-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher L.
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC220-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7217
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 548 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-194-664A-35

Query Match 86.2%; Score 25; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 27
PCT-US94-01553A-35
; Sequence 35, Application FC/RUS9401553A
; GENERAL INFORMATION:

APPLICANT: GENENCOR INTERNATIONAL, INC.
 TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International, Inc.
 STREET: 180 Kimball Way
 CITY: South San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/01553A
 FILING DATE:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Horn, Margaret A.
 REGISTRATION NUMBER: 33,401
 REFERENCE/DOCKET NUMBER: GC220-2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 742-7536
 TELEFAX: (415) 742-7217
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 548 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

PCT-US94-01553A-35

Query Match 86.2%; Score 25; DB 5; Length 548;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 2 AAPF 6
 Db 34 AAPF 38

RESULT 28
 PCT-US95-10426-35
 Sequence 35, Application PC/TUS9510426

GENERAL INFORMATION:
 APPLICANT: GENENCOR INTERNATIONAL, INC.
 TITLE OF INVENTION: An Improved Cleaning Composition
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International
 STREET: 180 Kimball Way
 CITY: South San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/720,899
 FILING DATE: 10-OCT-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/343,804
 FILING DATE: 22-NOV-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Lowmyer Dr., Karen A.
 REFERENCE/DOCKET NUMBER: 31 274
 PCT-US95-10426-35

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 549 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-720-899-6

Query Match 86.2%; Score 25; DB 1; Length 549;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 2 AAPF 6
 Db 34 AAPF 38

RESULT 29
 US-08-720-899-6

; Sequence 6, Application US/08/720,899
 ; Patent No. 5753660
 ; GENERAL INFORMATION:
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Borchart, Torben Vedel
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Thellersen, Marianne
 ; APPLICANT: Van der Zee, Pia
 ; TITLE OF INVENTION: AMYLASE VARIANTS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5753660 No. 5753460 disk off No. 5753460th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10174-6401

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/720,899
 FILING DATE: 10-OCT-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/343,804
 FILING DATE: 22-NOV-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Lowmyer Dr., Karen A.
 REFERENCE/DOCKET NUMBER: 31 274
 PCT-US95-10426-35

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 549 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-720-899-6

Query Match 86.2%; Score 25; DB 1; Length 549;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 2 AAPF 6
 Db 34 AAPF 38

RESULT 30
US-08-459-610-6
; Sequence 6, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchart, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343, 804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/343, 804
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459, 610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowmyer Dr., Karen A.
; REGISTRATION NUMBER: 31, 274
; REFERENCE/DOCKET NUMBER: 4054. 214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-343-804-6
; Query Match 86.2%; Score 25; DB 1; Length 549;
; Best Local Similarity 100.0%; Pred. No. 8.9e+02;
; Matches 5; Conservative 100.0%; 0; Mismatches 0;
; QY 2 AAAPF 6
; Db 34 AAAPF 38
; RESULT 32
US-08-687-399-6
; Sequence 6, Application US/08687399
; Patent No. 5928381
; GENERAL INFORMATION:
; APPLICANT: Toft, Annette H.
; APPLICANT: Marcher, Dorthe H.
; APPLICANT: Pedersen, Hanne H.
; APPLICANT: Nilsson, Thomas E.
; TITLE OF INVENTION: A Combined Desizing and Bleaching
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59283810 No. 5928381disk of No. 5928381th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687, 399
; FILING DATE:
; CLASSIFICATION: 00B
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33, 728
; REFERENCE/DOCKET NUMBER: 4127. 204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-687-399-6

Query Match 86.2%; Score 25; DB 2; Length 549;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAPF 6
 Db 34 AAPF 38

RESULT 33
 US-08-600-908A-6
 ; Sequence 6, Application US/08600908A
 ; Patent No. 5989169
 GENERAL INFORMATION:
 APPLICANT: Svendsen, Allan
 APPLICANT: Blsg rd-Frantzen, Henrik
 APPLICANT: Borchart, Torben Vedel
 TITLE OF INVENTION: '-Amylase Mutants
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESS: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/683, 838A
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/600, 908
 FILING DATE: 13-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Reza
 REGISTRATION NUMBER: 38,475
 REFERENCE/DOCKET NUMBER: 4394-204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 549 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-600-908A-6

Query Match 86.2%; Score 25; DB 3; Length 549;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAPF 6
 Db 34 AAPF 38

RESULT 34
 US-08-683-838A-6
 ; Sequence 6, Application US/08683838A
 ; Patent No. 6022724
 GENERAL INFORMATION:
 APPLICANT: Svendsen, Allan
 APPLICANT: Blsg rd-Frantzen, Henrik
 APPLICANT: Borchart, Torben Vedel
 TITLE OF INVENTION: '-Amylase Mutants
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESS: No. 6022724o No. 6022724disk of No. 6022724th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/683, 838A
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/600, 908
 FILING DATE: 13-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Reza
 REGISTRATION NUMBER: 38,475
 REFERENCE/DOCKET NUMBER: 4394-204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 549 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-683-838A-6

Query Match 86.2%; Score 25; DB 2; Length 549;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAPF 6
 Db 34 AAPF 38

RESULT 35
 US-09-636-252A-6
 ; Sequence 6, Application US/09636252A
 ; Patent No. 6440116
 GENERAL INFORMATION:
 APPLICANT: Svendsen, Allan
 APPLICANT: Blsg rd-Frantzen, Henrik
 APPLICANT: Borchart, Torben Vedel
 TITLE OF INVENTION: Alpha-Amylase Mutants
 FILE REFERENCE: 07751/F216-US2
 CURRENT APPLICATION NUMBER: US/09/636, 252A
 CURRENT FILING DATE: 2000-08-10
 PRIOR APPLICATION NUMBER: 08/683, 838
 PRIOR FILING DATE: 1996-07-18
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 6
 LENGTH: 549
 TYPE: PRT
 ORGANISM: B. stearothermophilus
 US-09-636-252A-6

Query Match 86.2%; Score 25; DB 4; Length 549;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAPF 6
 Db 34 AAPF 38

RESULT 36
US-09-313-677-17
; Sequence 17, Application US/09313677
; Patent No. 6300115
; GENERAL INFORMATION:
; APPLICANT: Teague, W. Martin
; APPLICANT: Brumm, Phillip J.
; APPLICANT: Allen, Larry N.
; APPLICANT: Brikun, Igor A.
; TITLE OF INVENTION: Pullulanase Expression Constructs Containing Alpha
FILE REFERENCE: Pullulanase Promoter and Leader Sequences
; CURRENT APPLICATION NUMBER: US/09/313, 677
; CURRENT FILING DATE: 1999-01-18
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-313-677-17
Query Match 86.2%; Score 25; DB 4; Length 967;
Best Local Similarity 83.3%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AAAPF 6
Db 34 AAAPF 38

RESULT 37
US-09-171-461-14
; Sequence 14, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:
; APPLICANT: Baker, Adam
; APPLICANT: Cottrell, Matthew
; APPLICANT: Chiocca, Susanna
; APPLICANT: Kurzbauer, Robert
; APPLICANT: Schaffner, Gorthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
FILE REFERENCE: 0652.1800000
; CURRENT APPLICATION NUMBER: US/09/171, 461
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: PCT/EP97/01944
; EARLIER FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 14
; LENGTH: 984
; TYPE: PRT
; ORGANISM: CELO Virus
; FEATURE:
; OTHER INFORMATION: Position: 23680..26634 /gene: L4 /product: L4 100K
US-09-171-461-14

Query Match 86.2%; Score 25; DB 4; Length 984;
Best Local Similarity 83.3%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAAAPF 6
Db 644 AAAPF 649

RESULT 38
US-08-459-568-2
; Sequence 2, Application US/08459568

Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Phuang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399, 411
; FILING DATE: 06-MAR-1995

RESULT 39
US-08-399-411-2
; Sequence 2, Application US/08399411
; Patent No. 5831108
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399, 411
; FILING DATE: 06-MAR-1995

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.8115
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-399-411-2

Query Match, Score 25; DB 2; Length 1706;
Best Local Similarity 85.2%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1;
Matches 5; Conservative 0; Mismatches 1;
QY 1 AAAAPF 6
Db 1694 AAATPF 1699

RESULT 40
US-08-516-859A-2
Sequence 2, Application US/08516859A
Patent No. 606931
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516.859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399, 411
FILING DATE: 08-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292, 683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.8115
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-516-859A-2

Query Match, Score 25; DB 3; Length 1706;
Best Local Similarity 85.2%; Pred. No. 2.7e+03;

	Matches	Conservative	Mismatches	Indels	Gaps	O;
QY	1 AAAAPF 6					
Db	1694 AAATPF 1699					

Search completed: December 6, 2002, 13:31:54
Job time : 17 secs

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Gencore version 5.1.3

OM protein - protein search, using sw model

Run on: December 6, 2002, 13:30:14 ; Search time 7.33333 Seconds
 (without alignments)
 13.289 Million cell updates/sec

Title:	US-10-033-526-4
Sequence:	1 AAAAPF 6
Scoring table:	BLOSUM62
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Total number of hits satisfying chosen parameters:	103943
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
Maximum Match 100%	
Listing first 45 summaries	

database : Published Applications_AA:*

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13: /cgn2_6/ptodata/1/pubpea/us60_NEWPUB.pep:*

14: /cgn2_6/ptodata/1/pubpea/us60_PUBCOM.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	29	100.0	6	US-10-033-526-4
2	29	100.0	405	Sequence 4, Appli
3	29	100.0	410	Sequence 18, Appli
4	29	100.0	9	Sequence 14, Appli
5	29	100.0	482	Sequence 2, Appli
6	29	100.0	484	Sequence 12, Appli
7	26	89.7	9	Sequence 1, Appli
8	26	89.7	597	Sequence 25, Appli
9	26	89.7	4613	Sequence 146, Appli
10	26	89.7	4613	Sequence 31, Appli
11	26	89.7	11877	Sequence 6, Appli
12	25	89.7	11877	Sequence 13, Appli
13	25	89.7	51	Sequence 25, Appli
14	25	89.7	51	Sequence 146, Appli
15	25	86.2	89	Sequence 31, Appli
16	25	86.2	10	Sequence 6, Appli
17	25	85.2	129	Sequence 13, Appli
18	25	85.2	135	Sequence 25, Appli
19	25	86.2	17	Sequence 146, Appli

ALIGNMENTS

QY	1 AAAAPF 6	Db	1 AAAAPF 6
RESULT 2			
Query Match Score	100.0%	Score	29;
Best Local Similarity	100.0%	DB	12;
Matches	6;	Len	
	Conservative	Mismatches	0;
		In	
QY	1 AAAAPF 6	Db	1 AAAAPF 6
RESULT 2			
US-09-40-288A-18			
; Sequence 18, Application US/09740288A			
Patent No. US2001003902A1			
GENERAL INFORMATION:			
; APPLICANT: Allien, Stephen			
; APPLICANT: Kinney, Anthony			
; APPLICANT: Miao, Guo-Hua			
APPLICANT: Orozco, Emil			

SUMMARIES

TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/09/740,288A
PRIORITY FILING DATE: 2000-12-19
PRIORITY APPLICATION NUMBER: US 60/172929
PRIORITY FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 18
SOFTWARE: Microsoft Office 97
ORGANISM: Hordeum vulgare
US-09-740-288A-18

Query Match Similarity 100.0%; Score 29; DB 10; Length 405;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPP 6
Db 11 AAAAPP 16

RESULT 3
US-10-078-650-14
Sequence 14, Application US/10078650
Patent No. US20020169301A1
GENERAL INFORMATION:
APPLICANT: Fujimoto, Katsumi
APPLICANT: Shin, Mei
APPLICANT: Kato, Yukio
TITLE OF INVENTION: NOVEL BHLH TYPE TRANSCRIPTION FACTOR
FILE REFERENCE: 06501-101001
CURRENT APPLICATION NUMBER: US/10/078,650
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/JP00/03991
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: JP 11-233286
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 410
TYPE: PRT
ORGANISM: Mus musculus
US-10-078-650-14

Query Match Similarity 100.0%; Score 29; DB 9; Length 410;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPP 6
Db 321 AAAAPP 326

RESULT 4
US-10-078-650-2
Sequence 2, Application US/10078650
GENERAL INFORMATION:
Patent No. US20020169301A1
APPLICANT: Fujimoto, Katsumi
APPLICANT: Shin, Mei
APPLICANT: Kato, Yukio
TITLE OF INVENTION: NOVEL BHLH TYPE TRANSCRIPTION FACTOR
FILE REFERENCE: 06501-101001
CURRENT APPLICATION NUMBER: US/10/078,650
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/JP00/03991
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: JP 11-233286
PRIOR APPLICATION NUMBER: JP 11-233286

Query Match Similarity 100.0%; Score 29; DB 9; Length 482;
Best Local Similarity 100.0%; Pred. No. 48; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPP 6
Db 380 AAAAPP 385

RESULT 5
US-10-078-650-12
Sequence 12, Application US/10078650
Patent No. US20020169301A1
GENERAL INFORMATION:
APPLICANT: Fujimoto, Katsumi
APPLICANT: Shin, Mei
APPLICANT: Kato, Yukio
TITLE OF INVENTION: NOVEL bHLH TYPE TRANSCRIPTION FACTOR
FILE REFERENCE: 06501-101001
CURRENT APPLICATION NUMBER: US/10/078,650
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/JP00/03991
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: JP 11-233286
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 484
TYPE: PRT
ORGANISM: Homo sapiens
US-10-078-650-12

Query Match Similarity 100.0%; Score 29; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 48; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPP 6
Db 382 AAAAPP 387

RESULT 6
US-08-821-739A-13
Sequence 13, Application US/08821739A
Patent No. US20020168374A1
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 2060-005000A
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT FILING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: 60/013,833
PRIOR FILING DATE: 1996-03-21
PRIOR APPLICATION NUMBER: 08/589,107
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 08/4451,913
PRIOR FILING DATE: 1995-05-26
PRIOR APPLICATION NUMBER: 08/347,610
PRIOR FILING DATE: 1994-12-01

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PRIORITY APPLICATION NUMBER: 08/186,266
PRIORITY FILING DATE: 1994-01-25
PRIORITY APPLICATION NUMBER: 08/159,339
PRIORITY FILING DATE: 1993-11-29
PRIORITY APPLICATION NUMBER: 08/103,396
PRIORITY FILING DATE: 1993-08-06
PRIORITY APPLICATION NUMBER: 08/027,746
PRIORITY FILING DATE: 1993-03-05
PRIORITY APPLICATION NUMBER: 07/926,666
PRIORITY FILING DATE: 1992-08-07
NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin version 3.1
SEQ ID NO: 13
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-08-821-739A-13

Query Match          Score 26: DB 1; Length 9;
Best Local Similarity 89.7%; Pred. No. 8.6e+04; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OQ      1 AAAAPP 6
Dy      4 AAAPPY 9

RESULT 7
Sequence 25, Application US/08821739A
Patent No. US20020108374A1
GENERAL INFORMATION:
APPLICANT: Campos Neto, Antonio
APPLICANT: Sheiky, Yesir
APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: Of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 146
LENGTH: 597
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:mRTC#3-His
US-09-793-306-146

Query Match          Score 26: DB 10; Length 597;
Best Local Similarity 83.3%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OQ      1 AAAAPP 6
Dy      4 AAAPPY 79

RESULT 9
Sequence 31, Application US/09860846
Patent No. US20020164742A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xie, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 6004300US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1999-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 31
LENGTH: 4613
TYPE: PRT
ORGANISM: Streptomyces venezuelae
US-09-860-846-31

Query Match          Score 26: DB 9; Length 4613;
Best Local Similarity 89.7%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OQ      1 AAAAPP 6
Dy      4 AAAPPY 3792

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RESULT 10
US-09-861-289-31
; Sequence 31, Application US/09861289
; Patent No. US2002110887A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D. H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; CURRENT APPLICATION NUMBER: US/09/861, 289
; CURRENT FILING DATE: 2001-05-18
; PRIORITY APPLICATION NUMBER: 09/105, 537
; PRIORITY FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 31
; LENGTH: 4613
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-861-289-31

Query Match 89.7%; Score 26; DB 10; Length 4613;
Best Local Similarity 83.3%; Pred. No. 2.1e+03; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 3787 AAAAPY 3792

RESULT 11
US-09-860-846-6
; Sequence 6, Application US/09860846
; Patent No. US20020164742A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600_438051
; CURRENT APPLICATION NUMBER: US/09/860, 846
; CURRENT FILING DATE: 2001-05-18
; PRIORITY FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO: 6
; LENGTH: 11877
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-860-846-6

Query Match 89.7%; Score 26; DB 10; Length 4613;
Best Local Similarity 83.3%; Pred. No. 2.1e+03; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 3787 AAAAPY 3792

RESULT 12
US-09-861-289-6
; Sequence 6, Application US/09861289
; Patent No. US2002010897A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; CURRENT APPLICATION NUMBER: US/09/861, 289
; CURRENT FILING DATE: 2001-05-18
; PRIORITY APPLICATION NUMBER: 09/105, 537
; PRIORITY FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 4613
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-861-289-6

Query Match 89.7%; Score 26; DB 9; Length 11877;
Best Local Similarity 83.3%; Pred. No. 5.5e+03; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 4123 AAAAPY 4128

RESULT 13
US-09-925-291-566
; Sequence 566, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925, 297
; CURRENT FILING DATE: 2001-08-10
; PRIORITY FILING DATE: 2000-07-08
; PRIORITY APPLICATION NUMBER: 60/124, 270
; PRIORITY FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 566
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; US-09-925-291-566

Query Match 85.2%; Score 25; DB 10; Length 51;
Best Local Similarity 83.3%; Pred. No. 31; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 19 AVAAPF 24

RESULT 14
US-09-925-301-1206
; Sequence 1206, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925, 301

CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05882
; PRIORITY FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60/124,270
; PRIORITY FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1664
; SEQ ID NO: 1206
; SOFTWARE: Patentin Ver. 2.0
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-725-301-1206

Query Match 86.2%; Score 25; DB 10; Length 89;
; Best Local Similarity 100.0%; Pred. No. 56; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 2 AAAPE 6
; Db 77 AACAPF 81

RESULT 15
; US-09-764-864-1090
; Sequence 1090; Application US/09764864
; Patent No. US200132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ23
; CURRENT APPLICATION NUMBER: US/09/764 864
; CURRENT FILING DATE: 2001-01-17
; PRIORITY APPLICATION DATA REMOVED - CONSULT PALM OR FILE WRAPPER
; NUMBER OF SEQ ID NOS: 1792
; SEQ ID NO: 1090
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; US-09-764-1090

Query Match 86.2%; Score 25; DB 10; Length 129;
; Best Local Similarity 83.3%; Pred. No. 82; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; QY 1 AAAAPF 6
; Db 6 AACAPF 11

RESULT 16
; US-09-764-864-1511
; Sequence 1511; Application US/09764864
; Patent No. US200132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1511
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; US-09-764-864-1511

Query Match 86.2%; Score 25; DB 10; Length 129;
; Best Local Similarity 83.3%; Pred. No. 82; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; QY 1 AAAAPF 6
; Db 6 AACAPF 11

RESULT 17
; US-09-764-847-844
; Sequence 824; Application US/09764847
; Patent No. US200132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; PRIORITY APPLICATION DATA REMOVED - CONSULT PALM OR FILE WRAPPER
; NUMBER OF SEQ ID NOS: 2003
; SEQ ID NO: 824
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (106)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (135)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; US-09-764-847-824

Query Match 86.2%; Score 25; DB 10; Length 136;
; Best Local Similarity 83.3%; Pred. No. 86; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; QY 1 AAAAPF 6
; Db 26 AXAPF 31

RESULT 18
 US-09-923-779-154
 Sequence 154, Application US/09923779
 ; Patent No. US20020076721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
 FILE REFERENCE: 210121.553
 CURRENT APPLICATION NUMBER: US/09/923, 779
 CURRENT FILING DATE: 2001-08-06
 NUMBER OF SEQ ID NOS: 155
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 154
 LENGTH: 247
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-09-923-779-154

Query Match 86.2%; Score 25; DB 10; Length 247;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAPPF 6
 Db 13 AVAAPF 18

RESULT 19
 US-09-741-669-411
 Sequence 411, Application US/09741669
 ; Patent No. US2002002218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Forsyth, R. Allyn
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; TITLE OF INVENTION: Genes identified as required for
 ; TITLE OF INVENTION: Proliferation of E. coli
 FILE REFERENCE: ELTRRA.009A
 CURRENT APPLICATION NUMBER: US/09/741,669
 CURRENT FILING DATE: 2000-12-19
 PRIOR APPLICATION NUMBER: US 60/173005
 PRIOR FILING DATE: 1999-12-23
 NUMBER OF SEQ ID NOS: 481
 SEQ ID NO 411
 LENGTH: 254
 TYPE: PRT
 ORGANISM: Escherichia coli
 ; US-09-741-669-411

Query Match 86.2%; Score 25; DB 10; Length 254;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAPPF 6
 Db 60 AVAAPF 65

RESULT 20
 US-10-062-254-244
 Sequence 244, Application US/10062254
 ; Patent No. US20020138882A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Edgar B
 ; APPLICANT: Cahoon, Rebecca E
 ; APPLICANT: Falco, Saverio Carl
 ; APPLICANT: Fang, Yilwen
 ; APPLICANT: Hantke, Sabine S.
 ; APPLICANT: Lee, Jian-Ming
 ; APPLICANT: Li, Zhongsen
 ; APPLICANT: Miao, Guo-Hua
 ; APPLICANT: Morganate, Michele
 ; APPLICANT: Niu, Xiping
 ; APPLICANT: Odell, Joan
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Zheng, Peizhong
 ; APPLICANT: Zhu, Qun
 ; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism

APPLICANT: Hantke, Sabine S.
 APPLICANT: Lee, Jian-Ming
 APPLICANT: Li, Zhongsen
 APPLICANT: Miao, Guo-Hua
 APPLICANT: Morganate, Michele
 APPLICANT: Niu, Xiping
 APPLICANT: Odell, Joan
 APPLICANT: Rafalski, Antoni
 APPLICANT: Sakai, Hajime
 APPLICANT: Zheng, Peizhong
 APPLICANT: Zhu, Qun

FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIORITY APPLICATION NUMBER: 09/630,346
; PRIORITY FILING DATE: 2000-07-28
; PRIORITY APPLICATION NUMBER: 60/146311
; PRIORITY FILING DATE: 1999-07-30
; PRIORITY APPLICATION NUMBER: 60/156006
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: 60/156899
; PRIORITY FILING DATE: 1999-09-30
; PRIORITY APPLICATION NUMBER: 60/157287
; PRIORITY FILING DATE: 1999-10-01
; PRIORITY APPLICATION NUMBER: 60/169767
; PRIORITY FILING DATE: 1999-11-09
; PRIORITY APPLICATION NUMBER: 60/17054
; PRIORITY FILING DATE: 1999-12-16
; PRIORITY APPLICATION NUMBER: 60/172958
; PRIORITY FILING DATE: 1999-12-21
; PRIORITY APPLICATION NUMBER: 60/171515
; PRIORITY FILING DATE: 1999-12-22
; PRIORITY APPLICATION NUMBER: 60/173535
; PRIORITY FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 248
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Zea mays
; US-10-062-254-248

Query Match 86.2%; Score 25; DB 12; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAPP 6
Db 408 AAAPP 412

RESULT 22
US-09-989-920-175
; Sequence 175, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins
; CURRENT APPLICATION NUMBER: DEX-0291
; CURRENT FILING DATE: 2001-11-21
; PRIORITY APPLICATION NUMBER: US/09/989,920
; PRIORITY FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 175
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-989-920-175

Query Match 86.2%; Score 25; DB 9; Length 456;
Best Local Similarity 83.3%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAPP 6
Db 181 AAAGPF 186

RESULT 23
US-09-93-811-2
; Sequence 2, Application US/09993811
; Patent No. US20020119476A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia AB
; TITLE OF INVENTION: Nucleotide Sequences
; FILE REFERENCE: 00248
; CURRENT APPLICATION NUMBER: US/09/993,811
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-993-811-2

Query Match 86.2%; Score 25; DB 10; Length 456;
Best Local Similarity 83.3%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAPP 6
Db 181 AAAGPF 186

RESULT 24
US-09-974-712-2
; Sequence 2, Application US/09974712
; Patent No. US20020119540A1
; GENERAL INFORMATION:
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020119540A1 Human Ion Channel Protein and Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/974,712
; CURRENT FILING DATE: 2001-10-10
; PRIORITY APPLICATION NUMBER: US 60/239,623
; PRIORITY FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-974-712-2

Query Match 86.2%; Score 25; DB 10; Length 456;
Best Local Similarity 83.3%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAPP 6
Db 181 AAAGPF 186

RESULT 25
US-10-058-020-4
; Sequence 4, Application US/10058820
; Patent No. US20020155479A1
; GENERAL INFORMATION:
; APPLICANT: Bogan, Jonathan S.
; APPLICANT: Lodalish, Harvey F.
; TITLE OF INVENTION: Expression Cloning Method
; FILE REFERENCE: 0399-2025-002
; CURRENT APPLICATION NUMBER: US/10/058,820
; CURRENT FILING DATE: 2002-08-17
; PRIORITY APPLICATION NUMBER: US 60/325,651
; PRIORITY FILING DATE: 2001-09-28
; PRIORITY APPLICATION NUMBER: US 60/298,963

PRIOR FILING DATE: 2001-06-18
 PRIORITY APPLICATION NUMBER: US 60/264,816
 PRIORITY FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 476
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-058-820-4

Query Match Similarity 86.2%; Score 25; DB 9; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAPP 6
 Db 161 AAAPP 165

RESULT 26
 US-10-058-820-3
 Sequence 3, Application US/10058820
 ; GENERAL INFORMATION:
 ; APPLICANT: Bogan, Jonathan S.
 ; PATENT NO. US2002015479A1
 ; TITLE OF INVENTION: Expression Cloning Method
 FILE REFERENCE: 0399_2025-002
 CURRENT APPLICATION NUMBER: US/10/058,820
 CURRENT FILING DATE: 2002-06-17
 PRIOR APPLICATION NUMBER: US 60/325,651
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: US 60/298,963
 PRIOR FILING DATE: 2001-06-18
 PRIOR APPLICATION NUMBER: US 60/264,816
 PRIOR FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 553
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-058-820-3

Query Match Similarity 86.2%; Score 25; DB 9; Length 580;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAPP 6
 Db 439 AAAPP 443

RESULT 28
 US-09-741-669-401
 Sequence 401, Application US/09741669
 ; PATENT NO. US20020022718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Forsyth, R. Allyn
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; TITLE OF INVENTION: Genes identified as required for
 ; TITLE OF INVENTION: proliferation of E. coli
 FILE REFERENCE: ELITRA.009A
 CURRENT APPLICATION NUMBER: US/09/741,669
 CURRENT FILING DATE: 2000-12-19
 PRIOR APPLICATION NUMBER: US 60/173005
 PRIOR FILING DATE: 1999-12-23
 NUMBER OF SEQ ID NOS: 401
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 401
 LENGTH: 770
 TYPE: PRT
 ORGANISM: Escherichia coli
 US-09-741-669-401

Query Match Similarity 86.2%; Score 25; DB 10; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAPP 6
 Db 15 AAAPP 19

RESULT 27
 US-09-928-457-37
 Sequence 37, Application US/09928457
 ; PATENT NO. US20020164603A1
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: DNA, specific proteins and peptides
 ; TITLE OF INVENTION: of the Neisseria meningitidis species bacteria, method
 ; NUMBER OF SEQUENCES: 99
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/928,457
 FILING DATE: 2001-08-14
 PRIOR APPLICATION DATA:

Query Match Similarity 86.2%; Score 25; DB 9; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAPP 6
 Db 161 AAAPP 165

RESULT 29
 US-09-970-711-14
 Sequence 14, Application US/09970711
 ; PATENT NO. US20020081279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Adam
 ; APPLICANT: Cottrell, Matthew
 ; APPLICANT: Chicca, Susanna
 ; APPLICANT: Kurzbauer, Robert
 ; APPLICANT: Schaffner, Gottbold
 ; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) VIRUS
 FILE REFERENCE: 0652.180001
 CURRENT APPLICATION NUMBER: US/09/970,711
 CURRENT FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 09/171,461
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: PCT/EP97/01944
 PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 984
; TYPE: PRT
; ORGANISM: CELO VIRUS
; OTHER INFORMATION: Position: 23680..26634 /gene: L4 /product: L4 100K
; US-09-970-711-14

Query Match 86.2%; Score 25; DB 10; Length 984;
; Best Local Similarity 83.3%; Pred. No. 6.8e+02; Mismatches 1; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 30
US-09-858-081-2
; Sequence 2, Application US/09858081
; Patent No. US20020072490A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: Cook, William James
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: A NOVEL HUMAN METALLOPROTEASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-049001
; CURRENT APPLICATION NUMBER: US/09/858, 081
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/204, 159
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: 60/204, 160
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1068
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-858-081-2

Query Match 86.2%; Score 25; DB 10; Length 1068;
; Best Local Similarity 100.0%; Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31
US-09-858-068-2
; Sequence 2, Application US/09858068
; Patent No. US20020076778A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: Cook, William James
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: A NOVEL HUMAN METALLOPROTEASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 10448-057001
; FILE REFERENCE: 10448-057001
; CURRENT APPLICATION NUMBER: US/09/858, 068
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: 60/204, 160
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2

Query Match 86.2%; Score 25; DB 10; Length 1133;
; Best Local Similarity 100.0%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32
US-09-908-322-44
; Sequence 44, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Aravanis-Trakonas, Spyridon
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10035-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058, 322
; FILING DATE: 17-JUL-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981, 392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9864
; TELEX: 6614 PENNIE
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
; US-09-908-322-44

Query Match 82.8%; Score 24; DB 10; Length 93;
; Best Local Similarity 83.3%; Pred. No. 94; Mismatches 1; Indels 0; Gaps 0;
; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAPP 6
Db 644 AVAAPP 649

Query Match 86.2%; Score 25; DB 10; Length 1133;
; Best Local Similarity 100.0%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAPP 6
Db 883 AAAPP 887

RESULT 33
 US-09-867-550-508
 ; Sequence 508, Application us/09867550
 ; Patent No. US20020082206A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Mehraban, Fuad,
 ; APPLICANT: Conley, Pamela
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Topper, James
 ; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
 ; FILE REFERENCE: 21402-013 (Cura-313)
 ; CURRENT APPLICATION NUMBER: US/09/867, 550
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: USSN 60/208, 427
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 2125
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 508
 ; LENGTH: 144
 ; OTHER INFORMATION: wherein Xaa may be any one of Leu or Phe
 ; LOCATION: (137)
 ; OTHER INFORMATION: NAME/KEY: VARIANT
 ; OTHER INFORMATION: TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; Query Match 82.8%; Score 24; DB 10; Length 144;
 ; Best Local Similarity 83.3%; Pred. No. 1.7e+02; Mismatches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAPPF 6
 Db 51 AAAPPF 56

RESULT 34
 US-09-864-761-49050
 ; Sequence 49050, Application US/09864761
 ; Patent No. US20020041763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aeonica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864, 761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180, 312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207, 456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632, 366
 ; PRIOR APPLICATION NUMBER: GB 24263, 6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236, 359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668

RESULT 35
 US-09-867-550-668
 ; Sequence 668, Application US/09867550
 ; Patent No. US20020082206A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Mehraban, Fuad,
 ; APPLICANT: Conley, Pamela
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Topper, James
 ; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
 ; FILE REFERENCE: 21402-013 (Cura-313)
 ; CURRENT APPLICATION NUMBER: US/09/867, 550
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: USSN 60/208, 427
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 2125
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 668
 ; LENGTH: 190
 ; OTHER INFORMATION: TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; Query Match 82.8%; Score 24; DB 10; Length 190;
 ; Best Local Similarity 83.3%; Pred. No. 2e+02; Mismatches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AAAPPF 6
 Db 87 AAAPPF 92

RESULT 36
 US-09-764-853-620
 ; Sequence 620, Application US/09764853

; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJJ26
; CURRENT APPLICATION NUMBER: US/09/7764 853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 620
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-853-620
; Query Match 82.8%; Score 24; DB 10; Length 248;
; Best Local Similarity 83.3%; Pred. No. 2.6e-02; Mismatches 1; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO: 9
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Curr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELTRA-011A
; CURRENT APPLICATION NUMBER: US/09/815, 242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191, 078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 12216
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12716
; Query Match 82.8%; Score 24; DB 10; Length 290;
; Best Local Similarity 83.3%; Pred. No. 3.1e-02; Mismatches 1; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO: 9
; Patent No. US10041400A
; Sequence 9, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
; US-10-041-006A-9
; Query Match 82.8%; Score 24; DB 9; Length 315;
; Best Local Similarity 83.3%; Pred. No. 3.3e-02; Mismatches 1; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO: 9
; Patent No. US10040655
; GENERAL INFORMATION:
; APPLICANT: QI, Jian Shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040, 655
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
; US-10-040-655-9
; Query Match 82.8%; Score 24; DB 12; Length 315;
; Best Local Similarity 83.3%; Pred. No. 3.3e-02; Mismatches 1; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO: 9
; Patent No. US10041400A
; Sequence 9, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew

APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Oi, Jensen
TITLE OF INVENTION: DNA Encoding the Human Serine
Protease Eos
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US10/041,400A
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 9
LENGTH: 316
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
sequence of EOS zymogen fusion gene

OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-400A-9

Query Match_h 82.8%; Score 24; DB 12; Length 316;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AAAPP 6
| ||||
Db 41 ALAAPF 46

Search completed: December 6, 2002, 13:42:09
Job time : 10.333 secs

Copyright (c) 1993 - 2002 CompuGen Ltd.	GenCore version 5.1.3				
Run on:	December 6, 2002, 13:25:59 ; Search time 15.3333 Seconds (without alignments) 37.618 Million cell updates/sec				
Title:	US-10-033-526-4				
Perfect score:	29				
Sequence:	1 AAAAPF 6				
Scoring table:	BLOSUM62				
Gapop 10.0 , Gapext 0.5					
Searched:	283224 seqs, 96134422 residues				
Total number of hits satisfying chosen parameters:	283224				
Minimum DB seq length: 0					
Maximum DB seq length: 200000000					
Post-processing:	Minimum Match 100% Listing first 45 summaries				
Database :	1: PIR:73;* 2: PIRI:*3: PIR3:*4: pir4:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query % Match	Length	DB ID	Description
1	29	100.0	102	2 H70898	probable PE protein - <i>Mycobacterium tuberculosis</i> (strain H37RV)
2	29	100.0	130	2 T29498	C;Species: <i>Mycobacterium tuberculosis</i> C;Accession: H70898 C;Date: 17-Jul-1998 #sequence_revision R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.N.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
3	29	100.0	389	2 E99422	A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Reference number: A70500; MUID:98295987; PMID:9634230
4	29	100.0	410	2 JC2584	A;Accession: H70898
5	29	100.0	446	2 A42029	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
6	29	100.0	482	2 JC7583	A;Residues: 1-102 <COL>
7	29	100.0	554	2 A75596	A;Experimental source: Strain H37RV
8	29	100.0	554	2 A75596	C;Genetics:
9	29	100.0	1044	2 S019666	A;Gene: PE
10	26	89.7	134	2 A72489	Query Match Similarity 100.0%; Score 29; DB 2; Length 102;
11	26	89.7	161	2 AF2262	Best Local Similarity 100.0%; Pred. No. 28; Mismatches 0; Indels 0; Gaps 0;
12	26	89.7	192	2 T13106	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13	26	89.7	206	2 H83887	Db 29 AAAAPF 34
14	26	89.7	206	2 T36633	QY 1 AAAAPF 6
15	26	89.7	301	2 C87796	RESULT 2
16	26	89.7	301	2 C87402	T29498
17	26	89.7	329	2 T0833	hypothetical protein K06B9.. - <i>Caenorhabditis elegans</i>
18	26	89.7	333	2 D70792	C;Species: <i>Caenorhabditis elegans</i> C;Accession: T29498 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
19	26	89.7	334	2 T35939	R;Miller, N.; Bradshaw, H. Submitted to the EMBL Data Library, February 1995
20	26	89.7	400	2 T29121	A;Description: The sequence of <i>C. elegans</i> cosmid K06B9.
21	26	89.7	403	2 H70931	A;Reference number: Z2028
22	26	89.7	407	2 S22596	A;Accession: I22498
23	26	89.7	409	2 A70617	A;Status: preliminary; translated from GB/EMBL/DDJB
24	26	89.7	414	2 R90815	A;Molecule type: DNA
25	26	89.7	414	2 AD0645	A;residues: 1-130 <ML>
26	26	89.7	414	2 C64856	A;Cross-references: EMBL:U50072; PIDN:AAA93448.1; CESP:K06B9.3
27	26	89.7	414	2 S12541	C;Genetics:
28	26	89.7	416	2 F84379	A;Gene: CESP:K06B9.3
29	26	89.7	418		A;Introns: 32/3; 64/1
					Query Match Similarity 100.0%; Score 29; DB 2; Length 130;
					Best Local Similarity 100.0%; Pred. No. 35;
ALIGNMENTS					
30	26	89.7	434	2 B54843	nemo, form II - fr
31	26	89.7	434	2 E84879	probable heme A fa
32	26	89.7	443	2 C70760	probable PPE prote
33	26	89.7	460	2 I48137	copper amine oxida
34	26	89.7	463	2 C70931	probable PPE prote
35	26	89.7	463	2 T13425	regulatory protein
36	26	89.7	468	2 B70932	probable PPE prote
37	26	89.7	469	2 T01529	heme A farnesyltra
38	26	89.7	471	1 S08325	flavonol 3-O-gluco
39	26	89.7	477	2 A54843	nemo, form I - fru
40	26	89.7	499	2 AH2761	penicillin-binding
41	26	89.7	506	2 G97542	iron (III)-transpo
42	26	89.7	512	2 E83050	NADH dehydrogenas
43	26	89.7	515	1 DNETU2	probable amino aci
44	26	89.7	521	2 T11710	Probable PPE prote
45	26	89.7	552	2 D70604	

Matches 6; conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPPF 6
Db 321 AAAAPP 326

RESULT 3

E9522 probable transmembrane transport protein Sha2377 [imported] - Sinorhizobium meliloti (strain E9522) #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Species: Sinorhizobium meliloti¹
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: E95422
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.; Bows, J.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti genome. A;Reference number: A95262; MUID:21396509; PMID:11484432

A;Accession: E95422
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <KUR>
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hubler, L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauze, H.; Lebault, P.; Vandebol, M.; Vorholter, F.J.; Wiedner, S.; Weiss, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A95039; MUID:21368234; PMID:11474104

A;Contents: annotation
C;Genetics:
A;Gene: SMA2377
C;Genome: plasmid

Query Match 100.0%; Score 29; DB 2; Length 389; Best Local Similarity 100.0%; Pred. No. 1.e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPPF 6
Db 354 AAAAPP 359

RESULT 4

JC7584 basic helix-loop-helix protein, DBC2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7584
R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, Biocem. Biophys. Res. Commun. 280, 164-171, 2001

A;Title: Molecular cloning and characterization of DBC2, a new member of basic helix-loop-helix proteins. A;Reference number: JC7583; MUID:21092582; PMID:11162494

A;Accession: JC7583
A;Molecule type: mRNA
A;Residues: 1-482 <FUJ>
A;Cross-references: DDBJ:AB044088
C;Comment: This protein, a novel member of the DBC subfamily of basic helix-loop-helix proteins, is highly conserved at the amino acid level. It contains a basic helix-loop-helix domain and a leucine zipper domain. It is predicted to bind DNA and regulate gene expression.

C;Genetics:
A;Gene: dec2
A;Map position: 12p11.23-p12.1.
C;Keywords: transcription factor
F;1-173/Region: highly conserved #status predicted
F;1-173/Region: highly conserved #status predicted <ORA>
F;130-173/Region: Orange #status predicted <ORA>
F;286-411/Region: alanine and glycine-rich #status predicted

Query Match 100.0%; Score 29; DB 2; Length 482; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPPF 6
Db 380 AAAAPP 385

RESULT 5

A42029 transcription factor E3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A42029
R;Roman, C.; Matera, A.G.; Cooper, C.; Artandi, S.; Blain, S.; Ward, D.C.; Calame, K. Mol. Cell. Biol. 12, 817-827, 1992

A;Title: mTFE3, an X-linked transcriptional activator containing basic helix-loop-helix motif. A;Reference number: A42029; MUID:92123207; PMID:1732746

A;Accession: A42029
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-446 <ROM>
A;Cross-references: GB:S76673; NID:9243439; PID:9243440
A;Note: sequence extracted from NCBI backbone (NCBIN:76673; NCBIPI:76674)

Query Match 100.0%; Score 29; DB 2; Length 446; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPPF 6
Db 10 AAAAPP 15

RESULT 6

JC7583 basic helix-loop-helix protein, DBC2 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7583
R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, Biocem. Biophys. Res. Commun. 280, 164-171, 2001

A;Title: Molecular cloning and characterization of DBC2, a new member of basic helix-loop-helix proteins. A;Reference number: JC7583; MUID:21092582; PMID:11162494

A;Accession: JC7583
A;Molecule type: mRNA
A;Residues: 1-482 <FUJ>
A;Cross-references: DDBJ:AB044088
C;Comment: This protein, a novel member of the DBC subfamily of basic helix-loop-helix proteins, is highly conserved at the amino acid level. It contains a basic helix-loop-helix domain and a leucine zipper domain. It is predicted to bind DNA and regulate gene expression.

C;Genetics:
A;Gene: dec2
A;Map position: 12p11.23-p12.1.
C;Keywords: transcription factor
F;1-173/Region: highly conserved #status predicted
F;1-173/Region: Orange #status predicted <ORA>
F;130-173/Region: alanine and glycine-rich #status predicted

Query Match 100.0%; Score 29; DB 2; Length 482; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPPF 6
Db 380 AAAAPP 385

RESULT 7

A75296 probable erythromycin esterase - Deinococcus radiodurans (strain R1)
C;Species: deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C;Accession: A75296
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J. Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75296
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1554 <RHI>
A;Experimental source: strain R1
A;Gen: DR257
A;Map position: 1

RESULT 8

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity 100.0%; Score 29; DB 2; Length 554; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	29	2	554	100.0%	1.4e+02	0	0	0	0
QY 1 AAAAPF 6									
Db 324 AAAAPF 329									

A71267

hypothetical protein tp0900 - syphilis spirochete

C;Species: *Treponema pallidum* subsp. *pallidum* (*syphilis spirochete*)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Nov-1999
C;Accession: A71267
C;Residues: 1-1797 <COL>
C;Gene: AP0900
C;Superfamily: Aeropyrum pernix

A;Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A;Reference number: A71267
A;Accession: A71267
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1797 <COL>
A;Cross-references: GB:AE001259; GB:AE000520; NID:9323209; PIDN: AAC65868.1; PID:932322
A;Experimental source: strain Nichols
A;Gen: TP0900
C;Species: *Treponema pallidum* subsp. *pallidum* (*syphilis spirochete*)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Nov-1999
C;Accession: A71267
C;Residues: 1-1797 <COL>
C;Gene: AP0900
C;Superfamily: Aeropyrum pernix

Query Match 100.0%; Score 29; DB 2; Length 797; Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAPF 6

Db 512 AAAAPF 517

RESULT 9

GTPase-activating protein - bovine

C;Species: *Bos primigenius taurus* (cattle)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 05-Nov-1999
C;Accession: S01966
C;Residues: 1-1044 <VOG>
C;Gene: apcb
C;Superfamily: phycocyanin

A;Title: Cloning of bovine GAP and its interaction with oncogenic ras p21.
A;Reference number: S01966; MUID:80318957; PMID:2842690
A;Accession: S01966
A;Molecule type: mRNA
A;Residues: 1-1044 <VOG>
A;Cross-references: EMBL:X12602; NID:93B4; PIDN:CAA31122.1; PID:9385
A;Note: part of this sequence was confirmed by protein sequencing
C;Superfamily: Pleckstrin repeat homology; ras-specific GAP catalytic domain homology; s

Query Match 100.0%; Score 29; DB 2; Length 161; Best Local Similarity 89.7%; Pred. No. 1.8e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAPF 6

Db 147 AAAAPY 152

RESULT 10

hypothetical protein APE2552 - *Aeropyrum pernix* (strain K1)

C;Species: *Aeropyrum pernix*
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: A72489
C;Residues: 1-134 <RAW>
C;Gene: APE2552
C;Superfamily: Aeropyrum pernix

Query Match 89.7%; Score 26; DB 2; Length 134; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAPF 6

Db 121 ASAAPF 126

RESULT 11

allophycocyanin B alpha chain [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AF22622
C;Residues: 1-161 <KOR>
C;Gene: apcb
C;Superfamily: phycocyanin

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriugita, Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Azotobacter vinelandii*.
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF22622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <KOR>
A;Cross-references: GB:BA00019; PIDN: BAB75352.1; PID:917132786; GSPDB:GN00179
A;Experimental source: strain PCC 7120
A;Gen: apcb
C;Species: *Nostoc* sp. strain PCC 7120

Query Match 89.7%; Score 26; DB 2; Length 161; Best Local Similarity 83.3%; Pred. No. 1.8e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAPF 6

Db 147 AAAAPY 152

RESULT 12

T13106

minor tail protein gp20 - phage N15
 C;Species: phage N15
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Nov-2000
 C;Accession: T13106
 R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.
 submitted to the EMBL Data Library, May 1998
 A;Reference number: Z17603
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-192 <HEN>
 A;Cross-references: EMBL:AF064539; NID:93192683; PIDN:93192703; PIDN:AAC19056.1
 C;Genetics:
 C;Note: gene 20
 C;Superfamily: phage lambda tail assembly protein I
 Query Match 89.7%; Score 26; DB 2; Length 192;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPP 6
 Db 112 AAASPF 117

RESULT 13
 HB3887
 conserved hypothetical protein PA0467 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: H83587
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradmin, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Harbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 939-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: H83587
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-206 <STO>
 A;Experimental source: strain PA01
 A;Cross-references: GB:AE004484; GB:AE004091; NID:9946320; PIDN:AAG03856.1; GSPDB:GN001
 C;Genetics:
 A;Gene: PA0467

RESULT 14
 T36643
 probable integral membrane protein - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Accession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A;Reference number: Z21610
 A;Accession: T36643
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-206 <OLI>
 A;Cross-references: EML:AL078610; PIDN:CA04411.1; GSPDB:GN00070; SCOEDB:SCH35.16
 C;Genetics:
 A;Gene: SCOEDB:SCH35.16

RESULT 15
 C87296
 beta-glucanase [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C;Accession: C87296
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klein, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, D.; Ventre, J.C.; Fraser, C; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: C87296
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-301 <STO>
 A;Cross-references: GB:AE005673; NID:913421537; PIDN:AAK22367.1; GSPDB:GN00148
 C;Genetics:
 A;Gene: CC0380

RESULT 16
 C87402
 conserved hypothetical protein CC1233 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Accession: C87402
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klein, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, D.; Ventre, J.C.; Fraser, C; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: C87402
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-317 <STO>
 A;Cross-references: GB:AE005673; NID:913422561; PIDN:AAK223215.1; GSPDB:GN00148
 A;Gene: CC1233

RESULT 17
 T00873
 hypothetical protein At2g45600 [imported] - Arabidopsis thaliana
 N;Alternative names: hypothetical protein Fl17k2.13
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001

C;Accession: T00873; E94892
 R;Rounseley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.; Submitted to the EMBL Data Library, March 1998
 A;Description: Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence.
 A;Reference number: Z14207
 A;Accession: T00873
 A;Status: translated from GB/EMBL/DBBJ
 A;Molecule type: DNA
 A;Residues: 1-329 <ROU>
 A;Cross-references: EMBL:AC003680; NID:92979540; PID:92979555
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Morfat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talon, I.; euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: E94892
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-329 <STO>
 A;Cross-references: GB:AE002093; NID:92979555; PIDN: AAC06164.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: F17K2.13; At2g45600
 A;Map position: 2
 Query Match 89.7%; Score 26; DB 2; Length 329;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAPF 6
 1:1:1
 Db 82 AAASPF 87
 RESULT 18
 D70792
 hypothetical protein Ry3691 - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Accession: D70792
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: D70792
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-333 <COL>
 A;Cross-references: GB:AL022121; GB:ALL23456; NID:93261559; PIDN:CAA18013.1; PID:e126455
 A;Experimental source: strain H37RV
 C;Genetics:
 Query Match 89.7%; Score 26; DB 2; Length 333;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAPF 6
 1:1:1
 Db 88 AAASPF 93
 RESULT 19
 T35939
 probable transport permease protein - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C;Accession: T35939
 R;Seeger, R.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-403 <COL>
 A;Cross-references: GB:AL022021; GB:ALL23456; NID:93250699; PIDN:CAA17728.1; PID:e126455
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: PPE
 A;PPE
 Query Match 89.7%; Score 26; DB 2; Length 403;
 Best Local Similarity 83.3%; Pred. No. 4.5e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 71 AAAAPY 76

RESULT 22
S22585 homeotic protein EVXL - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
R;Falella, A.; d'Esposito, M.; Rambaldi, M.; Acampora, D.; BalsiFiore, S.; Stornaiuolo, Nucleic Acids Res. 19, 6541-6545, 1991
A;Title: Isolation and mapping of EVXL, a human homeobox gene homologous to even-skipped
A;Reference number: S22586; MUID:92093615; PMID:1684419
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-407 <RAI>
A;Cross-references: EMBL:X60555; NID:g31278; PIDN:CAA43062.1; PID:g773576
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;184 240/Domain: homeobox homology <HOX>

Query Match 89.7%; Score 26; DB 2; Length 407;
Best Local Similarity 83.3%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 295 AAAAPF 300

RESULT 23
A70647 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis (strain H37RV)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70647
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98255987; PMID:9634230
A;Accession: A70647
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-409 <COL>
A;Cross-references: GB:Z83867; GB:AL123456; NID:g3261695; PIDN:CAB06293.1; PID:e1299813;
C;Genetics:
A;Gene: PPE

Query Match 89.7%; Score 26; DB 2; Length 409;
Best Local Similarity 83.3%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 67 AAAAPY 72

RESULT 24
H90815 probable kinase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: H90815
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001.

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and 9
A;Reference number: A99629; MUID:2115621; PMID:1125796
A;Accession: H90815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-414 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA834919.1; PID:91330960; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC1496
C;Superfamily: hypothetical protein HI1555
Query Match 89.7%; Score 26; DB 2; Length 414;
Best Local Similarity 83.3%; Pred. No. 4.6e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 92 AAAAPY 97

RESULT 25
D85675 probable kinase ycfW [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D85675
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-414 <STO>
A;Cross-references: GB:BA005174; NID:g1251668; PIDN:AAG55864.1; GSPDB:GN00145; UMGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ycfW
C;Superfamily: hypothetical protein HI1555
Query Match 89.7%; Score 26; DB 2; Length 414;
Best Local Similarity 83.3%; Pred. No. 4.6e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 92 AAAAPY 97

RESULT 26
A0045 ABC transporter integral membrane chain STY1259 [imported] - Salmonella enterica subspecies enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Note: this species has also been called *Salmonella typhi*
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: A0045
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church Th., T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr S.; Moulle, S.; O'Gara, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi
A;Reference number: AB0502; PMID:11677608
A;Accession: A0045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-414 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08343.1; PID:g16502388; GSPDB:GN00176
C;Genetics:
A;Gene: STY1259
C;Superfamily: hypothetical protein HI1555

Query Match 89.7%; Score 26; DB 2; Length 414;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

Oy 1 AAAAPF 6
 Db 92 AAAAPY 97

RESULT 27

C64856 probable permease YcfW - Escherichia coli (strain K-12)
 C; Species: Escherichia coli
 C; Date: 12-Sep-1997 #sequence_revision 17-sep-1997 #text_change 01-Mar-2002
 C; Accession: C64856
 R; Blattner, F.R.; Plunkett, III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vega, L.A.; Rosz, D.J.; Maur, B.; Shao, Y.
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-414 <BLAT>
 A; Cross-references: GB:AE000212; GB:U00096; NID:91787358; PIDN:AAC74202.1; PID:91787362;
 A; Experimental source: strain K-12, substrain MG1655
 A; Gene: ycfW
 C; Genetics:
 C; Superfamily: hypothetical protein
 F; 28-44/Domain: transmembrane #status predicted <TM1>
 F; 325-341/Domain: transmembrane #status predicted <TM2>
 F; 378-394/Domain: transmembrane #status predicted <TM3>
 F; 378-394/Domain: transmembrane #status predicted <TM4>

Query Match 89.7%; Score 26; DB 2; Length 414;
 Best Local Similarity 83.3%; Pred. No. 4.5e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

Oy 1 AAAAPF 6
 Db 92 AAAAPY 97

RESULT 28

S12541 evx1 protein - murine sarcoma virus
 C; Species: murine sarcoma virus
 C; Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999
 C; Accession: S12541
 R; Bastian, H.; Gross, P.
 EMBO J. 9, 1839-1852, 1990
 A; Title: A murine even-skipped homologue, Evx 1, is expressed during early embryogenesis
 A; Reference number: S12541; MUID:90269218; PMID:1971786
 A; Accession: S12541
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-416 <BAS>
 A; Cross-references: GB:X51239; NID:950875; PIDN:CAA38145.1; PID:950876
 C; Superfamily: unassigned homeobox proteins; homeobox homology
 C; Keywords: DNA binding; homeobox; nucleic; transcription regulation
 F; 184-240/Domain: homeobox homology <Hox>

Query Match 89.7%; Score 26; DB 2; Length 416;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

Oy 1 AAAAPF 6
 Db 295 AAAAPF 300

RESULT 29

R84379 probable heme A farnesyltransferase [imported] - Halobacterium sp. NRC-1
 C; Species: Halobacterium sp. NRC-1
 C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
 C; Accession: R84379
 R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leithauser, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A; Authors: Hou, S.; Daniels, C.J.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventre, J.
 A; Title: Genome sequence of Halobacterium species NRC-1
 A; Reference number: AB4160; MUID:20504483; PMID:11016950
 A; Accession: R84379
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-418 <STO>
 A; Cross-references: GB:AE004437; NID:910581701; PIDN:AAC74202.1; GSDB:GN00138
 C; Genetics:
 A; Gene: mal
 C; Superfamily: Citrobacter amalonaticus methylaspartate ammonia-lyase
 Query Match 89.7%; Score 26; DB 2; Length 418;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

Oy 1 AAAAPF 6
 Db 262 AAAAPY 267

RESULT 30

B54843 nemo, form II - fruit fly (Drosophila melanogaster)
 C; Species: Drosophila melanogaster
 C; Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 19-Dec-1997
 C; Accession: B54843
 R; Choi, K.W.; Benzer, S.
 Cell 78, 125-136, 1994
 A; Title: Rotation or photoreceptor clusters in the developing Drosophila eye requires Rho GTPase activity
 A; Reference number: A54843; MUID:94306509; PMID:8033204
 A; Accession: B54843
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-434 <CHO>
 A; Cross-references: GB:U12009
 C; Genetics:
 A; Gene: nmo
 A; Cross-references: FlyBase:FBgn0011817
 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologs
 F; 38-301/Domain: protein kinase homology <KIN>
 F; 46-541/Region: protein kinase ATP-binding motif

Query Match 89.7%; Score 26; DB 2; Length 434;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

Oy 1 AAAAPF 6
 Db 25 AAAAPY 30

RESULT 31

R84879 probable heme A farnesyltransferase [imported] - Arabidopsis thaliana
 C; Species: Arabidopsis thaliana (mouse-eared cress)
 C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C; Accession: R84879
 R; Lin, X.; Kaul, S.; Rounsey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffet, K.S.; Crokin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tally, J.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventre, J.
 Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: AB4420; MUID:20083487; PMID:10617197
A;Accession: E84879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-434 <STO>
A;Cross-references: GB:AE002093; NID:96598392; PIDN:ACC27454.2; GSPDB:GN00139
A;Gene: At2g44520
A;Map position: 2

RESULT 32

Query Match	89.7%	Score	26	DB	2	Length	434
Best Local Similarity	83.3%	Pred. No.	4.8e+02				
Matches	5	Conservative	1	Mismatches	0	Indels	0
QY	1 AAAAPF 6			Gaps	0		
Db	418 ASAAPPF 423						

C70780

probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)

C;Species: *Mycobacterium tuberculosis*
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70931

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: C70780

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-443 <COL>

A;Cross-references: GB:Z73101; GB:AL123456; NID:93261565; PIDN:CAA97385.1; PID:91314016

A;Experimental source: strain H37RV

A;Gene: PPE

C;Species: Phaseolus glycine-rich cell wall protein 1.8

RESULT 33

Query Match	89.7%	Score	26	DB	2	Length	433
Best Local Similarity	83.3%	Pred. No.	5.1e+02				
Matches	5	Conservative	1	Mismatches	0	Indels	0
QY	1 AAAAPF 6			Gaps	0		
Db	70 AAAPPY 75						

T13425

regulatory protein K10, oocyte-specific - fruit fly (*Drosophila melanogaster*)

N;Alternate names: protein T4C9.110 EG:30BB.5
C;Species: *Drosophila melanogaster*
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C;Accession: T13425; A28826

R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
A;Reference number: Z17668

A;Accession: T13425

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-460 <BEV>
A;Reference number: 224485

A;Accession: T48137

A;Cross-references: EMBL:AL080318
A;Experimental source: cultivar Columbia; BAC clone T4C9
A;Genetics:
A;Map position: 4

A;Note: TAC9.110; 459/3

RESULT 34

Query Match	89.7%	Score	26	DB	2	Length	460
Best Local Similarity	83.3%	Pred. No.	5.1e+02				
Matches	5	Conservative	1	Mismatches	0	Indels	0
QY	1 AAAAPE 6			Gaps	0		
Db	187 AASAPP 192						

C70931

probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)

C;Species: *Mycobacterium tuberculosis*
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70931

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: C70931

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-463 <COL>

A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17723.1; PID:e1221

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: PPE

RESULT 35

Query Match	89.7%	Score	26	DB	2	Length	463
Best Local Similarity	83.3%	Pred. No.	5.1e+02				
Matches	5	Conservative	1	Mismatches	0	Indels	0
QY	1 AAAAPF 6			Gaps	0		
Db	66 AAAPPY 71						

T13425

regulatory protein K10, oocyte-specific - fruit fly (*Drosophila melanogaster*)

N;Alternate names: protein EG:30BB.5
C;Species: *Drosophila melanogaster*
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C;Accession: T13425; A28826

R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
A;Reference number: Z17668

A;Accession: T13425

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-463 <HUR>

A;Cross-references: EMBL:AL09195; NID:e1355203; PID:e1202207; PIDN:CAA157022.1

R;Prost, E.; Derryckere, F.; Roos, C.; Heulin, M.; Pantesco, V.; Mohier, E.
Genes Dev. 2, 891-900, 1988

A;Title: Role of the oocyte nucleus in determination of the dorsoventral polarity of

A;Reference number: A28826

A;Accession: A28826

A;Molecule type: mRNA
A;Residues: 1-276, 'HH', 279-281, 'VDHHR', 287-453 <PRO>

A;Cross-references: GB:X12836; NID:98148; PID:9295771

A;Genetics:

A;Gene: FlyBase:fs(1)K10

A;Cross-references: FlyBase:FBgn0000810

A;Map position: X

A;Introns: 432/3

A;KeyWords: DNA binding

Matches 5; conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAAAPP 6 Db 53 AAAPPY 58 RESULT 36

B70932
probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)
Species: *Mycobacterium tuberculosis*
C; Date: 11-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: B70932

R; Cole, S.T.; Brosh, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.N.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998

A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A; Reference number: A05050; MUID:9295987; PMID:9631230

A; Accession: B70932
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-468 <COL>
A; Cross-references: GB:AL022021; PID:CAA123456; NTID:93250699; PIDN:CAA17730.1; PID:e125462
A; Experimental source: strain H37RV
C; Genetics:
A; Gene: PPE

Query Match 89.7%; Score 26; DB 2; Length 468;
Best Local Similarity 83.3%; Pred. No. 5.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAAAPP 6 Db 67 AAAPPY 72

RESULT 37

T01579
heme A farnesylyltransferase homolog F16B22.1 - *Arabidopsis thaliana* (fragment)
C; Species: *Arabidopsis thaliana* (mouse-ear cress)
C; Date: 16-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 14-May-1999
C; Accession: T01579; T02407
R; Rounseley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998
A; Description: *Arabidopsis thaliana* chromosome II BAC F16B22 genomic sequence.
A; Reference number: Z14284
A; Accession number: T01579
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-469 <ROU>
A; Cross-references: EMBL:AC003672; NID:93341571; PID:93341572
A; Experimental source: cultivar Columbia
R; Rounseley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, submitted to the EMBL Data Library, May 1998
A; Description: *Arabidopsis thaliana* chromosome II BAC F411 genomic sequence.
A; Reference number: Z14667
A; Accession: T02407
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 36-469 <ROW>
A; Cross-references: EMBL:AC004521; NID:93128166; PID:93128194
A; Map Position: 2
A; Note: 1422; 1863; 2323; 2772; 3192; 3571
A; Note: F16B22.1; F411.33

Query Match 89.7%; Score 26; DB 2; Length 477;
Best Local Similarity 83.3%; Pred. No. 5.2e+02; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAAAPP 6 Db 25 AAAPPY 30

RESULT 38

S08325
flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele BzMcC2) - maize
N; Alternate names: UDP-glucose flavonoid glucosyl-transferase
C; Species: *Zea mays* (maize)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: S08325

R; Furukawa, D.; Schleiflein, J.W.; Johnston, F.; Nelson Jr., O.E.; Plant Mol. Biol. 11, 473-481, 1988
A; Title: Sequence comparisons of three wild-type Bronze-1 alleles from *Zea mays*.
A; Reference number: S08324

A; Accession: S08325

A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-471 <FUR>
A; Cross-references: EMBL:X13501; NTID:922361; PIDN:CAA31856.1; PID:g295854
C; Genetics:
A; Gene: Bz1
A; Introns: 175/1
A; Superfamily: flavonol 3-O-glucosyltransferase
C; Keywords: glycosyltransferase, hexosyltransferase

Query Match 89.7%; Score 26; DB 1; Length 471;
Best Local Similarity 83.3%; Pred. No. 5.2e+02; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAAAPP 6 Db 315 ASAAPP 320

RESULT 39

A54843
A; memo: Form I - fruit fly (*Drosophila melanogaster*)
C; Species: *Drosophila melanogaster*
C; Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
C; Accession: A54843

R; Choi, K.W.; Benzer, S.; Cell 78, 125-136, 1994
A; Title: Rotation of photoreceptor clusters in the developing *Drosophila* eye requires A; Reference number: A54843; MUID:94306509; PMID:8033204
A; Accession: A54843
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-477 <CHO>
A; Cross-references: GB:U12009; NTID:9515669; PIDN:AAA21124.1; PID:9532558
C; Genetics:
A; Gene: nmo
A; Cross-references: FlyBase:FBgn0011817
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C; Keywords: alternative splicing; ATP
F; 38-31/Domain: protein kinase homology <KIN>
F; 46-54/Region: protein kinase ATP-binding motif

Query Match 89.7%; Score 26; DB 2; Length 477;
Best Local Similarity 83.3%; Pred. No. 5.2e+02; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAAAPP 6 Db 25 AAAPPY 30

RESULT 40

AH2761
Penicillin-binding protein dac [imported] - *Agrobacterium tumefaciens* (strain C58, Du
C; Species: *Agrobacterium tumefaciens*
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C;Accession: AH2761
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erger, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutjavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AH2761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-499 <KUR>
A;Cross-references: GB:AE003688; PIDN:AAL42510.1; PDB:q17739929; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dac
A;Map position: circular chromosome

Query Match 89.7%; Score 26; DB 2; Length 499;
Best Local Similarity 83.3%; Pred No 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAAAPF 6
Db |||||:
314 AAAAPY 319

Search completed: December 6, 2002, 13:31:03
Job time : 16.3333 secs

Copyright	GenCore version 5.1.3						
(c) 1993 - 2002	CompuGen Ltd.						
OM protein - protein search, using sw model							
Run on:	December 6, 2002, 13:20:29 ; Search time 8:33:33 Seconds						
	(without alignments)						
	29.863 Million cell updates/sec						
Title:	us-10-033_526_4						
Perfect score:	29						
Sequence:	1 AAAAPPF 6						
Scoring table:	BUSUM62						
Gapop 10.0 , Gapext 0.5							
Searched:	112892 seqs, 41476328 residues						
Total number of hits satisfying chosen parameters:	112892						
Minimum DB seq length:	0						
Maximum DB seq length:	200000000						
Post-processing:	Maximum Match 0% Maximum Match 100% Listing First 45 summaries						
Database:	swissprot_40:*						
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Score	Query	Length	DB	ID	Description	
1	29	100.0	102	1	YD86_MYCTU	P71656 mycobacteri	RESULT 1
2	29	100.0	410	1	BHB3_MOUSE	Q99PVS mus musculu	YD86_MYCTU
3	29	100.0	410	1	BHB3 RAT	Q95779 ratius norv	STANDARD:
4	29	100.0	446	1	TFE3_MOUSE	P04092 mus musculu	PRT: 102 AA.
5	29	100.0	482	1	BHB3_HUMAN	Q9C019 homo sapien	
6	29	100.0	743	1	TFE3_HUMAN	P79532 homo sapien	
7	29	100.0	797	1	Y900_TREPA	Q93870 treponema p	
8	29	100.0	1044	1	RSG1_BOVIN	Q91851 bos taurus	
9	26	89.7	160	1	PIAC_ANASP	P05056 anabaena sp	
10	26	89.7	272	1	TNFS5_CHICK	Q918db gallus gallu	
11	26	89.7	407	1	EYX1_HUMAN	P95960 homo sapien	
12	26	89.7	413	1	LOLE_ECOLI	P75958 escherichia	
13	26	89.7	416	1	EYX1_MOUSE	P23683 mus musculus	
14	26	89.7	443	1	Y878_MYCTU	Q10540 mycobacteri	
15	26	89.7	463	1	K102_MYCTU	P13468 drosophila	
16	26	89.7	463	1	UF02_MALZE	Q53955 mycobacteri	
17	26	89.7	471	1	NUTB_BETVU	P46165 zea mays (m	
18	26	89.7	515	1	YCV4_SCHPO	P05688 betta vulgar	
19	26	89.7	521	1	YCV4_SCHPO	P074543 schizosacch	
20	26	89.7	602	1	GAP1_YEAST	P79145 saccharomy	
21	26	89.7	608	1	DIP5_YEAST	P053388 saccharomy	
22	26	89.7	647	1	CNL6_ECOLI	Q98331 escherichia	
23	26	89.7	647	1	CNL6_SALTY	P026265 salmonella	
24	26	89.7	652	1	CNL6_VERNEN	P23052 yersinia en	
25	26	89.7	689	1	PPCE_AERHY	Q06903 aeromonas h	
26	26	89.7	930	1	PRGR_RABIT	P06186 oryctolagus	
27	26	89.7	1171	1	DPROL_HSV1	Q9yus helminthiviru	
28	26	89.7	1171	1	DPOL_HSV2	Q9yus2 herpesviru	
29	26	89.7	1783	1	RAA3_CHLRE	Q9fec4 chlamydomon	
30	25	86.2	652	1	CNL6_ACCHO	P19991 acheta domo	
31	25	86.2	127	1	Y355_TREPA	P03374 treponema p	
32	25	86.2	141	1	YEF2616	P23616 sacccharomy	
33	25	86.2	168	1	RRS_SACHY	Q01373 sacccharomy	

DE TFE3_MOUSE
ID TFE3_MOUSE STANDARD; PRT; 446 AA.
AC 064092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TFE3 OR TCFE3.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9212207; PubMed=1732746;
RA Roman C., Matera A.G., Cooper C., Artandi S., Blain S., Ward D.C.,
Carame K.;
CC *mTFE3, an X-linked transcriptional activator protein containing basic helix-loop-helix and zipper domains, utilizes the zipper to stabilize DNA binding and multimerization.;
RL Cell Biol. 12:817-827(1992).
CC -!- FUNCTION: POSITIVE-ACTING TRANSCRIPTION FACTOR THAT BINDS TO THE IMMUNOGLOBULIN ENHANCER MOE3 MOTIF. IT BINDS ALSO VERY WELL TO A USF/MITF SITE. BINDING OF TFE3 TO DNA INDUCES DNA BENDING.
CC -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER CC BHLH PROTEIN.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
CC ---
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CC ---
DR EMBL: S74673; AAB21130; 1; .
DR HSSP: P36956; IAW9;
DR MGII: MGI:198511; Tcfte3;
DR Interpro: IPR001052; HUH_basic.
DR SMART: SM00353; HUH; 1;
DR PROSITE: PS00038; HUH; 1;
DR PROSITE: PS00888; HUH; 2; 1.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
FT DOMAIN 133 144 STRONG TRANSCRIPTION ACTIVATION DOMAIN (POTENTIAL).
FT DOMAIN 217 232 BASIC DOMAIN.
FT DOMAIN 233 273 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 282 303 LEUCINE-ZIPPER (POTENTIAL).
SQ SEQUENCE 446 AA; 47891 MW; 7911537AD7F131E CRC64;

Query Match Best Local Similarity 100.0%; Score 29; DB 1; Length 446; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 10 AAAAPF 15

RESULT 5
BH3_HUMAN STANDARD; PRT; 482 AA.

ID BH3_HUMAN STANDARD; PRT; 482 AA.
AC 09C039;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Class B basic helix-loop-helix protein 3 (BH3_HB3) (Differentially expressed in chondrocytes protein 2) (HBEC2) (Enhancer-of-split and

DE hairy-related protein 1) (SHARP-1).
GN BH3_HB3 OR DEC2 OR SHARP1.
OS Homo sapiens (Human).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2109582; PubMed=11162494;
RA Fujimoto K., Shio M., Matsubara K., Shingu S., Honda K., Yoshida E., Sillarda K., Matsuda Y., Keto Y.;
RT Molecular cloning and characterization of DEC2, a new member of basic helix-loop-helix proteins.;
RL Biochem. Biophys. Res. Commun. 280:164-171(2001).
RN [2]
RP FUNCTION.
RX MEDLINE=21226716; PubMed=11278948;
RA Garriga-canut M., Roopa A., Buckley N.J.;
RT By a histone deacetylase-dependent and histone deacetylase-independent mechanism.;
RL J. Biol. Chem. 276:14821-14828(2001).
CC -!- FUNCTION: May be a transcriptional repressor that represses both basal and activated transcription.
CC -!- SUBUNIT: Homodimerize.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Highly expressed in skeletal muscle and brain, moderately expressed in pancreas and heart, weakly expressed in placenta, lung, liver and kidney.
CC ---
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CC ---
DR EMBL: AB044088; BAB21502; 1; .
DR Genew: HGENC:15617; BH3_HB3.
DR MM: 60200;
DR Interpro: IPR001052; HUH basic.
DR Interpro: IPR003650; Orange.
DR Pfam: PF00010; HUH; 1;
DR SMART: SM0033; HUH; 1;
DR PROSITE: PS00038; HUH; 1;
DR PROSITE: PS50088; HUH; 2; 1.
KW Transcription regulation; Repressor; DNA-binding; Nuclear protein.
FT DOMAIN 45 57 BASIC DOMAIN.
FT DOMAIN 58 100 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 129 175 ORANGE.
FT DOMAIN 297 431 ALA/GLY-RICH.
SQ SEQUENCE 482 AA; 50497 MW; 2BECD2FDB7CE14 CRC64;

Query Match Best Local Similarity 100.0%; Score 29; DB 1; Length 482; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
Db 380 AAAAPF 385

RESULT 6
TFC3_HUMAN STANDARD; PRT; 743 AA.

ID TFE3_HUMAN STANDARD; PRT; 743 AA.
AC P19532; Q99964; Q27575; Q27578;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Transcription factor E3.
 DR GN TFE3.
 OS Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 SEQUENCE OF 1-219 FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
 RX MEDLINE=97140324; PubMed=896805;
 RA Weterman M.A.J., Wilbrink M., Geurts van Kessel A.;
 "Fusion of the transcription factor TFE3 gene to a novel gene, PRCC,
 in t(X;1)(p11;q21-positive papillary renal cell carcinomas.);
 Proc. Natl. Acad. Sci. U.S.A. 93:15294-15298(1996).
 RN [2]
 SEQUENCE OF 149-743 FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
 RT TISSUE=Monocytes;
 MEDLINE=97026295; PubMed=882474;
 RA Sidiar S.K., Clark J., Gill S., Hamoudi R., Crew A.J.,
 Gwilliam R., Ross M., Linehan W.M., Birdsall S., Shipley J.,
 Cooper C.S.;
 "The t(X;1)(p11.2;q21.2) translocation in papillary renal cell
 carcinoma fuses a novel gene PRCC to the TFE3 transcription factor
 gene.,"
 Hum. Mol. Genet. 5:1333-1338(1996).
 RN [3]
 REVISIONS.
 RA Clark J.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 SEQUENCE OF 208-743 FROM N.A.
 MEDLINE=90249724; PubMed=2338243;
 RA Beckmann H., Su L.-K., Kadesch T.;
 RT "TFE3: a helix-loop-helix protein that activates transcription
 through the immunoglobulin enhancer muE3 motif.,"
 Genes Dev. 4:167-179(1990).
 RN [5]
 SEQUENCE OF 266-353 FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
 RX MEDLINE=98054131; PubMed=9393982;
 RA Clark J., Lu Y.-J., Sidiar S.K., Parker C., Gill S., Smedley D.,
 Hamoudi R., Linehan W.M., Shipley J., Cooper C.S.;
 "Fusion of splicing factor genes PSF and Nono (P54nrb) to the TFE3
 gene in papillary renal cell carcinoma.,"
 RT Oncogene 15:2233-2239(1997).
 RT -1- FUNCTION: POSITIVE-ACTING TRANSCRIPTION FACTOR THAT BINDS TO THE
 CC IMMUNOGLOBULIN ENHANCER MUE3 MOTIF. IT BINDS ALSO VERY WELL TO A
 CC USE/FMLT SITE. BINDING OF TFE3 TO DNA INDUCES DNA BINDING.
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHHL PROTEIN.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: Ubiquitous IN FETAL AND ADULT TISSUES.
 CC -1- DISEASE: INVOLVED IN PAPILLARY RENAL CELL CARCINOMA (PRCC), BY
 CC CHROMOSOMAL TRANSLOCATIONS T(X;1)(p11.2;q21.2) WHICH INVOLVES TFE3
 AND PRCC; T(X;1)(p11.2;p34) WHICH INVOLVES TFE3 AND PSF, AND
 CC INV(X)(p11.2;q12) THAT INVOLVES TFE3 AND NONO.
 CC -1- SIMILARITY: 21.0% THAT BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHHL) FAMILY OF
 CC TRANSCRIPTION FACTORS. BHHL-ZIP SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X99721; CA68061.1; -.
 DR EMBL: X97160; CA65800.1; -.
 DR EMBL: X97161; CA65800.1; JOINED.
 DR EMBL: X97162; CA65800.1; JOINED.
 DR EMBL: X96717; CA65478.1; -.
 DR EMBL: X51330; CA35714.1; -.
 DR EMBL: X34596; A34596.

DR PIR: S10379; S10379.
 DR HSSP: P22415; LAN4.
 DR TRANSFAC: T00311; -.
 DR GeneW: HGNC:1752; TFE3.
 DR MIM: 314310; -.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00010; HLH; 1.
 DR SMART: SM00355; HLH; 1.
 DR PROSITE: PS00038; HLH 1; 1.
 DR DOMAIN: 360 400 430 470
 KW Chromosomal translocation; DNA-binding; Activator; Nuclear protein;
 DOMAIN 409 430 470 510
 DOMAIN 475 517 557 593
 DOMAIN 575 743 775 810
 DOMAIN 260 271 290 320
 DOMAIN 295 296 310 330
 DOMAIN 310 330 340 360
 DOMAIN 344 359 360 380
 DOMAIN 360 400 430 470
 DOMAIN 409 430 470 510
 DOMAIN 475 517 557 593
 DOMAIN 575 743 775 810
 SITE 178 179 190 210
 SITE 295 296 310 330
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 EMBL; AEG01259; AAC65568.1; -;
 TIGR; TPF900; -;
 KW HYPOTHETICAL protein; Complete proteome.
 SEQUENCE 797 AA; 89503 MW; DEBB344OCB6D799 CRC64;
 Query Match 100%; Score 29; DB 1; Length 797;
 Best Local Similarity 100%; Pred. No. 78; Mismatches 0;
 Matches 6; Conservative 0; Misnmatches 0;
 QY 1 AAAAPF 6
 Db 512 AAAAPF 517
RESULT 8
 RSG1_BOVIN STANDARD; PRT; 1044 AA.
 ID RSG1_BOVIN
 AC P09831;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Ras GTPase-activating protein 1 (GTPase-activating protein) (GAP) (Ras p21 protein activator) (p21GAP) (RasGAP).
 GN RASA1 OR RASA.
 OS Bos taurus (bovine).
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxId=9913;
 RN 11
 RR SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE:6831957; Pubmed=3842690;
 RA Vogelmann U.S., Dixon R.A.F., Schaberg M.D., Diehl R.E., Marshall M.S.,
 RA Scollnick E.M., Sigal I.S., Gibbs J.B.;
 RA "cloning of bovine GAP and its interaction with oncogenic ras p21.";
 RL Nature 335:90-93(1988).
 CC -i- FUNCTION: REGULATOR OF THE RAS-CYCCLIC AMP PATHWAY.
 CC -i- SUBCELLULAR LOCATION: CYTOSOLIC
 CC -i- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -i- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -i- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -i- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
 CC
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 EMBL; XJ12602; CA3A1122.1; -;
 PIR; S01966; S01966.
 HSSP; P20936; IWER; C2.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001949; PH.
 DR InterPro; IPR001936; RASGAP.
 DR InterPro; IPR001452; SH2.
 DR InterPro; IPR00080; SH2.
 DR InterPro; IPR0001; SH2; 2.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00515; RASGAP; 1.
 DR PRINS; PRO0401; SH2DOMAIN.
RESULT 9
 PHAC_ANASP STANDARD; PRT; 160 AA.
 ID PHAC_ANASP
 AC P80556;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Allopyocyanin alpha-B chain.
 GN APCD; OR ALI3653
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteriota; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxId=103690;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE:21595285; Pubmed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kimura T., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Matsuno A., Muraki A., Kishida Y., Kohara M., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Nakazaki N., Tabata S., Yasuda M.,
 RA "Complete genomic sequence of the filamentous cyanobacterium Anabaena sp. strain PCC 7120.";
 RT (2)
 RP SEQUENCE OF 1-28;
 RX MEDLINE:9627075; Pubmed=8665889;
 RT Durret A., Sideri W., Wehrli E., Frank G., Zuber H.;
 RT "Isolation, characterization and electron microscopy analysis of a hemidiscoidal phycobilisome type from the cyanobacterium Anabaena sp. PCC 7120.";
 RL Eur. J. Biochem. 236:1010-1024 (1995).
 CC -i- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN COMPLEX; LIQUORICYLICOPROTEIN COMPLEX; ALLOPHYCOCYANIN HAS A MAXIMUM

CC ABSORPTION AT APPROXIMATELY 654 NANOMETERS.
 CC HETEROCHEXAMER OF TWO ALPHA CHAINS, ONE ALPHA-B CHAIN AND
 CC THREE BETA CHAINS.
 CC -!- PBM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.

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CC EMBL: AP003593; BABY5352; 1;
 DR InterPro; IPR001659; Phycobilisome.
 DR Pfam; PF00502; Phycobilisome; 1.
 DR PRODom; P00040; Phycobilisome; 1.
 KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment; Methylation; Complete proteome.

FT INIT_MET 0 0
 FT MOD_RES 70 70
 FT BINDING 80 80

METHYLATION (BY SIMILARITY).
 PHYCOCYANOBILIN CHROMOPHORE (BY SIMILARITY).

SEQUENCE 160 AA; 17680 MW; 6E814C32c2857BD6 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 160;
 Best Local Similarity 83.3%; Pred. No. 77; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
 Db 146 AAAAPY 151

RESULT 10

TNF5_CHICK STANDARD; PRT; 272 AA.

ID TNF5_CHICK
 AC 091808;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 Protein).
 DE TNFSF5 OR CD40LG OR CD40L.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 OX NCBI_TAXID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

STRAIN=White Leghorn; TISSUE=Spleen;
 RA Treadskes C.A., Young J.R., Burnside J.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).
 -!- SUBUNIT: Homotrimer (By similarity).
 -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
 -!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
 -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL: AJ243435; CAB05748; 1; -.
 DR HSSP; P2965; 1ALI.
 DR InterPro; IPR003263; TNF_5.
 DR InterPro; IPR003636; TNF_abc.
 DR Pfam; PF00229; TNF; 1.
 DR PRODom; P002012; TNF_abc; 1.
 DR PRODom; P008600; TNF_5; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 272
 FT DOMAIN 45 272
 FT SITE 110 111
 FT DISULFID 190 229
 FT CARBOHYD 124 124
 FT CARBOHYD 145 145
 FT CARBOHYD 251 251
 FT CARBOHYD 272 251
 FT SEQUENCE 30862 MW; 5409F24A8E5CCD7 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 272;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPP 6
 Db 194 AASAPP 199

RESULT 11

EVXL_HUMAN STANDARD; PRT; 407 AA.

ID EVXL_HUMAN
 AC P49540;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Homeobox even-skipped homolog protein 1 (EVX-1).
 GN EVXL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo. OX NCBI_TAXID=9606;

RN [1]
 RP SEQUENCE FROM N.A.

RC MEDLINE=92093115; PubMed=1684419;
 RA Faiella A., D'Esposito M., Rambaldi M., Acampora D.,
 RA Ballofiore S., Stornaiuolo A., Maliamaci M., Migliaccio E.,
 RA Giusiano M.;
 RT "Isolation and mapping of EVXL, a human homeobox gene homologous to even-skipped, localized at the 5' end of HOX1 locus on chromosome 7.";
 RT Nucleic Acids Res. 19:6541-6545(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96070599; PubMed=7499236;
 RA Briata P., van de Werken R., Airoldi I., Ilengo C., di Blas E.,
 RA Boncinelli E., Corte G.;
 RT "Transcriptional repression by the human homeobox protein EVXL in transfected mammalian cells." J. Biol. Chem. 270:27695-27701(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Bradshaw H., Hinds K., Keppler D.;
 RA Subramanian (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: MAY PLAY A ROLE IN THE SPECIFICATION OF NEURONAL CELL TYPES.

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=92249649; PubMed=1349539;
 RA Dush M.K., Martin G.R.;
 RT "Analysis of mouse *Evx* genes: *Evx-1* displays graded expression in the primitive streak.";
 RL *Dev. Biol.* 151:273-287(1992).
 CC -!- FUNCTION: MAY PLAY A ROLE IN THE SPECIFICATION OF NEURONAL CELL TYPES. MAY PLAY A ROLE IN THE DORSOVENTRAL SPECIFICATION OF MESODERMAL CELL FATE.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DEVELOPMENTAL STAGE: SHOWS A GRADED DISTRIBUTION IN THE PRIMITIVE STREAK AND IN CELLS LATERAL TO IT. IT IS NOT DETECTED IN CELLS ALONG THE A-P AXIS OF THE EMBRYO ANTERIOR TO THE PRIMITIVE STREAK, EXCEPT AT E7.5 WHEN THERE IS TRANSIENT EXPRESSION IN THE HEAD PROCESS. THE HIGHEST LEVELS OF EXPRESSION ARE FOUND WITHIN THE PROXIMAL (POSTERIOR) PORTION OF THE PRIMITIVE STREAK AND CELLS NEAR IT, WITH EXPRESSION LEVELS DECREASING MORE DISTALLY (ANTERIORLY).
 CC -!- SIMILARITY: BELONGS TO THE EVEN-SKIPPED HOMEOBOX FAMILY.
 CC
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 CC
 DR EMBL: X54239; CAA8145_1; -.
 DR PIR: S12541; S12541.
 DR HSSP: P14653; 1B72.
 DR TRANSFAC: T02023; -.
 DR MGD: 95461; Ensembl.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF0046; homeobox; 1.
 DR PRINTS: PR0024; HOMEOROX.
 DR Prodom: PD000010; Homeobox; 1.
 DR SMART: SM0039; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 DR DNA-BINDING; Developmental protein; Homeobox; Nuclear protein.
 FT DOMAIN 114 124 ASP/GLU-RICH (ACIDIC).
 FT DNA_BIND 183 242 HOMEOBOX.
 FT DOMAIN 289 297 ALA-RICH.
 FT DOMAIN 341 349 ALA-RICH.
 FT DOMAIN 369 375 ALA-RICH.
 SQ SEQUENCE 416 AA: 43198 MW: 970E4F3677CD3EE CRC64:
 Query Match 89.7%; Score 26; DB 1; Length 416;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAAAPF 6
 Db 295 AAASPF 300
 RESULT 14
 Y878_MYCTU STANDARD; PRT: 443 AA.
 ID Y878_MYCTU
 AC 010540;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical PPE family protein Rv0878C.
 GN Rv0878C OR MNP0901 OR MYCY31_06C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TAXID=1773;
 [1] RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295087; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Teklaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Shelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence";
 RT Nature 393:537-544 (1998).
 [2] RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R.R., Gwinn M.L., Haft D., Hickie E., Kolonay J.F., Nelson W.C., Umayam L.A., Ernolajcica M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bisht W.;
 RA "Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains";
 RT Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
 CC
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 CC
 DR EMBL: Z73101; CAA97385_1; -.
 DR EMBL: AE006977; AAC45143_1; ALT_INIT.
 DR TIGR: MT0901; -.
 DR Tuberculist: Rv0878C; -.
 DR InterPro: IPR002989; Microbac_PPE.
 DR InterPro: IPR002989; Mycobac_pentapep.
 DR Pfam: PF00823; PPE; 1.
 DR Pfam: PF01469; Pentapeptide_2; 4.
 KW Hypothetical protein; Transmembrane; Repeat; Complete proteome.
 FT TRANSMEM 15 35 POTENTIAL.
 FT TRANSMEM 38 58 POTENTIAL.
 FT TRANSMEM 59 79 POTENTIAL.
 FT TRANSMEM 181 201 POTENTIAL.
 FT DOMAIN 64 73 POLY-ALA.
 FT DOMAIN 81 115 ALA-RICH.
 FT DOMAIN 231 270 4 X 10 AA APPROXIMATE REPEATS.
 SQ SEQUENCE 443 AA: 43592 MW: C58BEC607F0675E2 CRC24;
 Query Match 89.7%; Score 26; DB 1; Length 443;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAAAPF 6
 Db 70 AAAPAPY 75
 RESULT 15
 K10_DROME STANDARD; PRT: 463 AA.
 ID K10_DROME
 AC P13468; Q9W505; Created
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-binding protein K10 (Female sterile protein K10).
 FN FS11_K10 OR EG:3088.5 OR CG3218
 OS *Drosophila melanogaster* (fruit fly).

OC	Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
OC	Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.	CC	the European Bioinformatics Institute. There are no restrictions on its
OX	[1]NCBL-TAXID=7227;	CC	use by non-profit institutions as long as its content is in no way
RN	SEQUENCE FROM N.A.	CC	modified and thus statement is not removed. Usage by and for commercial
RP	"Role of the oocyte nucleus in determination of the dorsoventral	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)
RA	axis in Drosophila melanogaster.",	CC	or send an email to license@isb-sib.ch .
RT	"Role of the oocyte nucleus in determination of the dorsoventral	--	--
RT	polarity of Drosophila as revealed by molecular analysis of the k10	--	--
RT	gene.",	--	--
RL	Genes Dev. 2:891-900(1988).	--	--
RN	[2]	--	--
RP	SEQUENCE FROM N.A.	--	--
RC	STRAIN=Oregon-R;	--	--
RX	MEDLINE=2019011; PubMed=10731137;	--	--
RA	Benes P., V., Gatt M.K., Ashburner M., Murphy L., Harris D., cadieu E.,	FT	REPEAT 87 142 7 X APPROXIMATE TANDEM REPEATS.
RA	Barrelli B.G., Ferraz C., Vidal S., Brun C., Denailles J., Galibert F., Borkova S.,	FT	REPEAT 95 102 1.
RA	Dreano S., Gloux S., Leilaire V., Mottier S.,	FT	REPEAT 103 110 3.
RA	Minana S., Kafatos F.C., Louis C., Stiden-Klamio T., Bolshakov S.,	FT	REPEAT 111 118 4.
RA	Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,	FT	REPEAT 119 126 5.
RA	Modjell J., Peter A., Schoettler P., Werner M., Mourkoti F.,	FT	REPEAT 127 134 6.
RA	Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,	FT	REPEAT 135 142 7.
RA	Callister D.M., Campbell L.A., Darlamtou A., Henderson N.S.,	FT	DOMAIN 284 290 POLY-PRO.
RA	McMillan P.J., Sallies C., Tait E.A., Valenti P., Saunders R.D.C.,	FT	DNA-BIND 397 416 H-T-H MOTIF (POTENTIAL).
RA	Glover D.M.,	FT	CONFlict 277 278 PM -> HH (IN REF. 1).
RT	"From sequence to chromosome: the tip of the X chromosome of D.	FT	CONFLICT 282 286 GGRP -> VDHRR (IN REF. 1). ~
RT	melanogaster",	FT	CONFLICT 463 AA; 51267 MW; D03C097192D1FDD0 CRC64; ~
RL	RL [3]	FT	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.	FT	SEQUENCE 89.7%; Score 26; DB 1; Length 463;
RP	STRAIN=Berkeley;	FT	Best Local Similarity 83.3%; Pred No. 2e+02; ~
RC	MDLINE=2019006; PubMed=10731132;	FT	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
RX	Adams M.D., Gehrke S.E., Holt R.A., Evans C.A., Gocayne J.D.,	QY	1 AAAPPF 6
RA	Aumanitides P.G., Scheier S.E., Li P.W., Hoskins R.A., Galle R.F.,	ID	Y102-MYCTU
RA	Beezon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	AC	053951;
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotman P.,	DT	30-MAY-2000 (Rel. 39, created)
RA	Burts K.C., Busam D.A., Butler H., Cadieu E., Chandra I.,	DT	30-MAY-2000 (Rel. 39, Last sequence update)
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	DT	16-OCT-2001 (Rel. 40, Last annotation update)
RA	de Pablo B., Delcher A., Deng Z., Mayes C.R., Nelson C.R., Miklos G.L.G.,	DE	Hypothetical PPE family protein R1802.
RA	Dodson K.J., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	GN	RV1802 OR MT-851 OR MTW042.24.
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferricchio S., Fleischmann W.,	OS	Mycobacterium tuberculosis.
RA	Fosler C., Gabrielian A.E., Gaoq J., Gelbart W.M., Glasser K.,	OC	Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RA	Gildek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	OX	NCBI-TAXID=1773;
RA	Harris N.L., Harvey J., Heiman T.J., Hernandez J. R., Houck J.,	RN	[1]
RA	Houston K.A., Howland T.J., Wei M.-H., Ikegami C.,	RP	SEQUENCE FROM N.A.
RA	Jahali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	RC	STRAIN=H77RV;
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	RX	MDLINE=98295987; PubMed=9634230;
RA	Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,	RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,	RA	Gordon S.V., Elsgaard M., Gas S., Barry C.E. III, Tekla F.,
RA	Merkulov G., Mil'shina N.V., Mobarry C., Morris J., Moskrafi A.,	RA	Badcock K., Basham D., Brown J., Chillingworth T., Connor R.,
RA	Moyer S.M., Moy M., Murphy B., Murphy L., Moony D.M., Nelson D.L.,	RA	Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA	Nelson D.R., Nelson K.N., Nixon K., Nusskern D.R., Pacleb J.M.,	RA	Hornsey T., Jaelkel K., Krogh A., McInean S., Moule S., Murphy L.,
RA	Palazzolo D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	RA	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA	Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,	RA	Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
RA	Spter E., Spredling A.C., Stapleton M., Strong R., Sun E.,	RT	"Deciphering the biology of Mycobacterium tuberculosis from the
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	RT	complete genome sequence.",
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,	RL	Nature 393:537-544(1998).
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	RN	[2]
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,	RP	SEQUENCE FROM N.A.
RA	Zheng X.H., Zhong N., Zhou X., Zhu S., Zhu X., Smith H.O.,	RC	STRAT=CDC 1551 / Oshkosh;
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	RA	STRAT=CDC 1551 / Allard D., Eisen J.A., Carpenter L., White O.,
RT	"The genome sequence of Drosophila melanogaster.",	RA	Fleischmann R., Gordon D., Gwinn M.L., Haff D., Hickey E.,
RL	Science 287:2185-2195(2000).	RA	Peterson J.J., Debay R., Dodson R., Gwinn M.L., Ermolaeva M.D., Salzberg S.L.,
CC	-1- FUNCTION: MAY HAVE A REGULATORY FUNCTION.	RA	Kolonay J.F., Nelson W.C., Unayama L.A., Ermolaeva M.D., Weidman J., Khouri H., Gill J., Mikula A.,
CC	-1- SUBCELLULAR LOCATION: Nuclear.	RA	Delcher A., Utterback T., Weidman J., Weidman J., Khouri H., Gill J., Mikula A.,

RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.

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DR EMBL; AL022021; CAI1773; 1; -.
 DR EMBL; AE007044; AAK46123; 1; -.
 DR TIGR; MT1851; -.
 DR Tuberculist; Rv1802; -.
 DR InterPro; IPR000030; Microbac_PPE.
 DR Pfam; PF00823; PPE; 1.
 KW Hypothetical protein; Complete proteome.

FT CONFLICT 401 401 MW: EB6482BF09FA51 CRC64;
 SEQUENCE 463 AA: 46021 MW: EB6482BF09FA51 CRC64;

QY 1 AAAAPP 6
 |||||:
 Db 66 AAAAPP 71

RESULT 17

UFO2_MAIZE STANDARD; PRT; 471 AA.

ID UFO2_MAIZE
 AC P16165;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (UDP-glucose flavonoid 3-O-glucosyltransferase) (Bronze-1) (BZ-MC2 allele).

GN BZ1 OR UGT71M1.

OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;
 RN [1]
 SEQUENCE FROM N.A.

RP MEDLINE-90318317; PubMed=2115110;
 RA Xue Y., Davies D.R., Thomas C.M.;
 RT "Sugarbeet mitochondria contain an open reading frame showing extensive sequence homology to the subunit 2 gene of the NADH:ubiquinone reductase complex.";
 RT RL Mol. Genet. 221:195-198(1990);
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-52 IS THE INITIATOR.

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CC -!- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN PIGMENTS.

-!- CATALYTIC ACTIVITY: UDP-glucose + a flavonol = UDP + flavonol

-!- 3-O-D-glucoside.
 -!- PATHWAY: Anthocyanin biosynthesis.

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CC EMBL; X133501; CAI31855; 1; -.
 DR PIR; S08325; S08325.
 DR MaizeDB; 13885; -.
 DR InterPro; IPR002213; UDPGT.

DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00315; UDPGT; 1.
 DR Transferase; Glycosyltransferase.

KW SEQUENCE 471 AA: 48621 MW: 818897410A361299 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 471; Best Local Similarity 83.3%; Pred. No. 2.1e-02; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Sequence 515 AA: 56274 MW: 3D60F45FB2820AF CRC64;

QY 1 AAAAPP 6
 |||||:
 Db 315 ASAAPP 320

RESULT 18

NU2M_BETVU STANDARD; PRT; 515 AA.

ID NU2M_BETVU
 AC P15688;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE NADH-ubiquinone (NADH) oxidoreductase chain 2 (EC 1.6.5.3).

GN ND2 OR NAD2.

OS Beta vulgaris (Sugar beet).
 OG Mitochondrion.
 OC Buccaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

OX NCBI_TaxID=3555;
 RN [1]
 SEQUENCE FROM N.A.

RP MEDLINE-90318317; PubMed=2115110;
 RA Xue Y., Davies D.R., Thomas C.M.;
 RT "Sugarbeet mitochondria contain an open reading frame showing extensive sequence homology to the subunit 2 gene of the NADH:ubiquinone reductase complex.";
 RT RL Mol. Genet. 221:195-198(1990);
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-52 IS THE INITIATOR.

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CC -!- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN PIGMENTS.

-!- CATALYTIC ACTIVITY: UDP-glucose + a flavonol = UDP + flavonol

-!- 3-O-D-glucoside.
 -!- PATHWAY: Anthocyanin biosynthesis.

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CC EMBL; X16828; CAI34728; 1; -.
 DR EMBL; X16828; CAI34729; 1; ALT_INIT.
 DR PIR; S12804; DNET02.
 DR InterPro; IPR001750; Oxidored_Q1.
 DR Pfam; PF00361; oxidored_Q1; 1.
 DR InterPro; IPR001750; Oxidored_Q1.
 DR Pfam; PF00361; oxidored_Q1; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.

SEQUENCE 515 AA: 56274 MW: 3D60F45FB2820AF CRC64;

Query Match 89.7%; Score 26; DB 1; Length 515; Best Local Similarity 83.3%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Sequence 515 AA: 56274 MW: 3D60F45FB2820AF CRC64;

QY 1 AAAAPP 6
 |||||:
 Db 100 ASAAPP 105

RESULT 19

YCV4_SCHPO STANDARD; PRT; 521 AA.

ID YCV4_SCHPO
 AC Q74543;
 DT 16-OCT-2001 (Rel. 40, Created)

	Query Match	89 %;	Score 26;	DB 1;	Length 602;	
Matches	Best Local Similarity	83.3 %;	Pred. No.	2.6e+02;		
Matches	5;	Conservative	1;	Mismatches	0;	Indels
Qy	1	AAAAPP	6	0;	Gaps	0;
Db	357	AAASPF	362			
RESULT 21						
DIP5_YEAST	ID	DIP5 YEAST	STANDARD;	PRT;	608 AA.	
AC	P53388;					
DT	01-OCT-1996	(Rel.	34,	Created)		
DT	01-OCT-1996	(Rel.	34,	Last sequence update)		
DT	15-JUN-2002	(Rel.	41,	Last annotation update)		
DE	Dicarboxylic amino acid permease.					
GN	DIP5 OR YPL265w.					
OS	Saccharomyces cerevisiae (Baker's yeast).					
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes;					
OX	Saccharomycetales; Saccharomycetaceae; Saccharomyces.					
NCBI_TaxID	4932;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Sigma 1278B;					
RA	Vissers S., Grosjean S., Andrie B.;					
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=S288C / AB972;					
RX	MEDLINE=97313271; PubMed=9169875;					
RA	Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Duncan M., Floeth M., Portin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebbel U., Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Komar C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messeguer F., Mewes H.-W., Mirrissi S., Moesl D., Mueller-Auer S., Namath A., Nentwich N., Oefner P., Pearson D., Petrel X., Pohl T.M., Purnell D., Schafer M., Schatz M., Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh V., Wambutt S., Wang Y., Wedler H., Winnert E., Zhong W.W., Zolnier A., Vo D.H., Hani J.;					
RT	"The nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome XVI.";					
RL	Nature 387:103-105(1997).					
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein.					
CC	-- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.					
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CC	EMBL: X55802; CA65074.1; -;					
DR	SGD: S0006186; DBP5.					
DR	InterPro: IPR002293; AA_REL_PERMEASE.					
DR	InterPro: IPR004840; AAC_PERMEASE.					
DR	InterPro: IPR004762; YEAST_AA_PERM.					
DR	Pfam: PF00324; AA_PERMEASE; 1.					
DR	TIGRFAMS: TIGR00913; 2A0310; 1.					
DR	PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.					
KW	Transport; Amino-acid transport; Transmembrane.					
FT	TRANSMEM . 91 111 POTENTIAL.					
FT	TRANSMEM . 112 132 POTENTIAL.					
RP	SEQUENCE OF 20-31.					
RC	STRAIN=K12 / EMG2;					
RX	MEDLINE=97433975; PubMed=92988646;					
RA	"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12;"					
RT	Electrophoresis 18:1259-1313(1997).					
CC	-1 FUNCTION: THIS BI-FUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE REACTIONS CONVERTING 2',3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE AND THEN 3'-NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.					
CC	-1 CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2)O = nucleoside 3'-phosphate.					

CC REACTIONS CONVERTING 2', 3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE
 CC AND THEN 3'-NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.
 CC -!- CATALYTIC ACTIVITY: Nucleoside 2', 3'-cyclic phosphate + H(2)O =
 CC nucleoside 3'-phosphate
 CC -!- SUBCELLULAR LOCATION: Periplasmic
 CC -!- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.

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CC -----
 DR EMBL; D14005; BAA03105_1; -.
 DR PIR; JN0585; JN0585.
 DR HSSP; P2367; IQFM.
 DR MEROPS; S09_001; -.
 DR InterPro; IPRO01375; Peptidase_S9.
 DR InterPro; IPRO04106; Peptidase_S9_N.
 DR InterPro; IPRO02471; Prok_endopep_ser.
 DR InterPro; IPRO02470; Prolico_Prase.
 DR InterPro; IPRO0326; Peptidase_S9; 1.
 DR Pfam; PF02872; 5_nucleotidase; 1.
 DR PROSITE; PS00785; 5_NUCLEOTIDASE_2; 1.
 KW Hydrolase; Multifunctional enzyme; Periplasmic; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 652 2', 3'-CYCLIC-NUCLEOTIDE 2'-.
 FT SEQUENCE 652 AA: 71491 MW: 8781369575794E17 CRC64:
 Query Match 89.7%; Score 26; DB 1; Length 652;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPF 6
 Db 409 SAMPF 414

RESULT 25
 PPE_AERY STANDARD; PRT; 689 AA.
 ID PPE_AERY
 AC Q05903; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Prolyl endopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme)
 DE (PE).
 OS Aeromonas hydrophila.
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
 OC Aeromonas.
 OX NCBI_TaxID:644;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAINAK-9;
 RX MEDLINE:93360910; PubMed=8370677;
 RA Kanatani A., Yoshimoto T., Kitazono A., Kokubo T., Tsuru D.;
 RT "Prolyl endopeptidase from *Aeromonas hydrophila*: cloning, sequencing,
 and expression of the enzyme gene, and characterization of the
 expressed enzyme";
 RL J. Biolog. 113:790-796(1993).
 CC -!- FUNCTION: CLEAVES PEPTIDE BONDS ON THE C-TERMINAL SIDE OF PROLYL
 CC RESIDUES WITHIN PEPTIDES THAT ARE UP TO APPROXIMATELY 30 AMINO
 CC ACIDS LONG. HAS AN ABSOLUTE REQUIREMENT FOR AN X-PRO BOND IN THE
 CC TRANS CONFIGURATION IMMEDIATELY PRECEDING THE PRO-Y SCISSILE
 CC BOND.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of Pro-*Xaa* >> Ala-*Xaa* in
 CC Oligopeptides.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 59.
 CC -----
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CC -----
 DR EMBL; M14547; AMA31443_1; -.
 DR PIR; A25923; A25923.

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 CC or send an email to license@isb-sib.ch).

CC -----
 DR HSSP; P2367; IQFM.
 DR MEROPS; S09_001; -.
 DR InterPro; IPRO01375; Peptidase_S9.
 DR InterPro; IPRO04106; Peptidase_S9_N.
 DR InterPro; IPRO02471; Prok_endopep_ser.
 DR InterPro; IPRO02470; Prolico_Prase.
 DR InterPro; IPRO0326; Peptidase_S9; 1.
 DR Pfam; PF02872; 5_nucleotidase; 1.
 DR PRINTS; PR0862; PROLCOPTASE.
 DR PROSITE; PS00708; PRO_ENDOPER_SER; 1.
 KW Hydrolase; Serine protease.
 FT INIT_MET 0
 FT ACT_SITE 537 537 CHARGE RELAY SYSTEM (BY SIMILARITY);
 FT ACT_SITE 656 656 CHARGE RELAY SYSTEM (BY SIMILARITY);
 SQ SEQUENCE 689 AA: 76384 MW: 84DAF66E60B840EA CRC64:
 Query Match 89.7%; Score 26; DB 1; Length 689;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
 Db 409 ASAAPP 414

RESULT 26
 PRGR_RABT STANDARD; PRT; 930 AA.
 ID PRGR_RABT
 AC P05186; 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Progesterone receptor (PR).
 GN PGR OR NR3C3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Chondrocyte; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Oryctolagus.
 OX NCBI_TaxID:9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:87067449; PubMed=3538016;
 RA Losoff H., Atger M., Misrahi M., Guichon-Mantel A., Meriel C.,
 RA Ligeat F., Benarous R., Milgrom E.;
 RT Cloning and sequence analysis of rabbit progesterone-receptor
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9045-9049(1986).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NR3 SUBFAMILY.
 CC -----
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RESULT 29
 RAA3_CHRE STANDARD; PRT; 1783 AA.
 AC 09FEC4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Trans-splicing factor Raa3, chloroplast precursor.
 GN RAA3.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaeae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1] SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RP STRAIN=>37C / CC-125;
 RX MEDLINE=>21181833; PubMed=>1285239;
 RA Rivier C., Goldschmidt-Clermont M., Rochaix J.-D.;
 RT "Identification of an RNA-protein complex involved in chloroplast
 RL group II intron trans-splicing in Chlamydomonas reinhardtii.";
 EMBO J. 20;1765-1773(2001).
 -!- FUNCTION: Required for trans-splicing of exons 1 and 2 of the
 chloroplast encoded psaA mRNA (a group II intron). May be required
 for stability of the chloroplast RNA-protein complex in which it
 is found.
 -!- SUBUNIT: Part of a 1700 kDa complex that includes the
 precursor RNA to exon 1 and the tscA RNA.
 -!- SUBCELLULAR LOCATION: Chloroplast stroma.
 -!- DOMAIN: The N-terminal 453 amino acids are dispensable, while the
 C-terminal 630 amino acids are required for function.

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CC DR EMBL; AF310675; AAC40000.1; -.
 KW CHLOROPAST; TRANSIT PEPTIDE; RNA PROCESSING; mRNA SPlicing.
 FT CHAIN 1 40 CHLOROPAST (POTENTIAL),
 FT TRANS-SPLICING FACTOR RAA3.
 FT DOMAIN 112 311 ALA-RICH.
 FT DOMAIN 343 436 SER-RICH.
 FT DOMAIN 478 1078 ALA-RICH.
 FT DOMAIN 1310 1415 ALA-RICH.
 FT DOMAIN 1416 1430 GLN-RICH.
 FT DOMAIN 1496 1505 ARG-RICH.
 FT DOMAIN 1678 1722 ALA-RICH.
 FT DOMAIN 771 778 POLY-ALA.
 FT DOMAIN 920 925 POLY-PRO.
 FT DOMAIN 927 932 POLY-ALA.
 FT DOMAIN 1047 1055 POLY-GLY.
 FT DOMAIN 1318 1325 POLY-ALA.
 FT DOMAIN 1405 1415 POLY-ALA.
 FT DOMAIN 1669 1675 POLY-PRO.
 SQ SEQUENCE 1783 AA; 180399 MW; 4056206BA6EBDCDB CRC64;

Query Match Score 89.7%; Score 26; DB 1; Length 1783;
 Best Local Similarity 83.3%; Pred. No. 7e+02; Mismatches 5; Conservative
 Matches 5; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
 DR ||||| 638 AAASAPP 643

RESULT 30
 SUGA_ACHDO STANDARD; PRT; 5 AA.
 ID SUGA_ACHDO

Query Match Score 86.2%; Score 25; DB 1; Length 127;
 Best Local Similarity 83.3%; Pred. No. 1e+02; Mismatches 5; Conservative
 Matches 5; Indels 0; Gaps 0;

RSA3_CHRE STANDARD; PRT; 1783 AA.
 AC 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Suboesophageal ganglion pentapeptide.
 OS Acheta domesticus (House cricket).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
 OC Grylloidae; Gryllinae; Acheta.
 OX NCBI_TaxID=6997;
 RN [1] SEQUENCE.
 RA Wicker C., Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 suboesophageal ganglion of Acheta domesticus (orthoptera).";
 RL Comp. Biochem. Physiol. 88C:185-187(1987).
 CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
 CC GANGLIA.
 DR PTR; JS0319; JS0319; CRC64;
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match	Best Local Similarity	Score	DB	Length
Qy	100.0%	25	1	5
Db	100.0%	5	1	5

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR PTR; JS0319; JS0319; CRC64;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=Nichols; STANDARD; PRT; 127 AA.
 RX MEDLINE=>9832770; PubMed=>9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwynn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Soederberg H., Richardson D., Howell J.R., Chidambaram M., Utterback T., McDonald L., Aitkach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
 RL Science 281:375-388(1998).
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 CC DR EMBL; AE001215; AAC6533.1; -.
 DR TIGR; TP0355; -.
 KW Hypothetical protein; Complete Proteome.
 SQ SEQUENCE 127 AA; 14526 MW; 1B84BBFD0DC44DC4 CRC64;

QY 1 AAAAPF 6 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 QY | ||||| Spermatophytina; Magnoliophyta; Lilliopsida; Poales; Poaceae; PACC clade;
 Db 83 AGAAPF 88 OC Panicoideae; Andropogoneae; Saccharum.
 OC NCBI_TaxID=15819;
 RN [1]
 RP STRAIN=CV; R32-8360;
 RC MEDLINE=93222494; PubMed=8467089;
 RX Tang, W.; Sun, S.S.;
 RA RT "Sequence of a sugarcane ribulose-1,5-bisphosphate
 AC P3216; carboxylase/oxygenase small subunit gene.";
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1995 (Rel. 31, Last annotation update)
 DE Hypothetical 16.5 kDa protein in GLY1-GDA1 intergenic region.
 GN YE045 OR SGD-ORF33;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1] Sequence from N.A.
 RP STRAIN=CV; R32-8360;
 RC MULLIGAN, J.T., DIETRICH, F.S., HENNESSY, K.M., SEHL, P., KOMP, C.,
 RA WEI, Y., TAYLOR, P., NAKAHARA, K., ROBERTS, D., DAVIS, R.W.;
 RL Submitted (PRB-1993) to the EMBL/GenBank/DDBJ databases.
 RN [2] Sequence from N.A.
 RP STRAIN=CV; R32-8360;
 RC DIETRICH, F.S., MULLIGAN, J.T., HENNESSY, K.M., ALLEN, E., ARAUJO, R.,
 AVILES, E., BERNO, A., BRENNAN, T., CARPENTER, J., CHEN, E., CHEERY, J.M.,
 CHUNG, E., DUNCAN, M., GUZMAN, E., HARTZELL, G., HUNICKE-SMITH, S.,
 HYMAN, R., KAYSER, A., KOMP, C., LASKAI, D., LEW, H., LIN, D.,
 MOSKAL, D., NAKAHARA, K., NAMATH, A., NORRIS, R., OEFNER, P., OH, C.,
 PETER, F.X., ROBERTS, D., SENII, P., SCHRAMM, S., SHOGRON, P., SMITH, V.,
 RA TAYLOR, P., WEI, Y., YELTON, D., BOTSTEIN, D., DAVIS, R.W.;
 RL Submitted (PRC-1994) to the EMBL/GenBank/DDBJ databases.
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 or send an email to license@ebi.ac.uk).
 CC
 DR MB8717; AA333922; 1; --
 DR InterPro; IP000594; Rubisco_small.
 DR PFAM; PF00101; RUBISCO_SMALL; 1.
 DR PRINTS; PRO052; RUBISCO_SMALL; 1.
 DR PRODom; PD000290; RUBISCO_SMALL; 1.
 DR KW Photosynthesis; Carbon dioxide fixation; photorespiration;
 KW Lyase; Oxidoreductase; Monoxygenase; chloroplast; transit peptide.
 FT TRANSIT 1 46 CHLOROPLAST (BY SIMILARITY);
 FT CHAIN 47 168 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
 FT CHAIN 12 168 AA; DEBD5D100B1C314FA CRC64;
 SO SEQUENCE 168 AA; DEBD5D100B1C314FA CRC64;
 DR EMBL; U18779; AAC64997; 1; --
 DR PIR; S30832; S30332.
 DR SGD; S0000771; YE045C.
 DR KW Hypothetical protein; ATP-binding; transmembrane.
 FT NP_838722; RIB(POTENTIAL);
 FT TRANSMEM 38 58 POTENTIAL.
 SO SEQUENCE 141 AA; 16468 MW; F6604AC5343A5D5C CRC64;
 DR Query Match 86.2%; Score 25; DB 1; Length 141;
 DR Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 DR Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 AAAPF 6 Db 12 AAAPF 16
 DR 38 AAAPF 42
 RESULT 33
 RBS_SACHY STANDARD; PRT; 168 AA.
 ID RBS_SACHY STANDARD; PRT; 168 AA.
 AC 041373;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribulose bisphosphate carboxylase small chain, chloroplast precursor
 DE (EC 4.1.1.39) (RUBISCO small subunit).
 GN RBCS
 OS Saccharum hybrida (Sugarcane).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliophyta; Lilliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Saccharum.
 OC NCBI_TaxID=15819;
 RN [1]
 RP STRAIN=CV; Progress No. 9;

RX MEDLINE=85003579; PubMed=6477146;
 RA Coruzzi G., Broglie R., Edwards C., Chua N.-H.;
 RT "Tissue-specific and light-regulated expression of a pea nuclear gene
 encoding the small subunit of ribulose-1,5-bisphosphate
 carboxylase.";
 RL EMBO J. 3:1671-1679(1984).
 RN [2]
 SEQUENCE FROM N.A. (RBCS-3C).
 RX Flurb R., Moses P., Morelli G., Coruzzi G., Chua N.-H.;
 RT "Expression dynamics of the pea rbcS multigene family and organ
 distribution of the transcripts.";
 RL EMBO J. 5:2063-2071(1986).
 RN [3]
 SEQUENCE OF 25-180 FROM N.A.
 RX MEDLINE=33108917; PubMed=6296093;
 RA Coruzzi G., Broglie R., Casimiro A., Chua N.-H.;
 RT "Nucleotide sequences of two pea cDNA clones encoding the small
 subunit of ribulose 1,5-bisphosphate carboxylase and the major
 chlorophyll a/b-binding thylakoid polypeptide.";
 RL J. Biol. Chem. 258:1399-1402(1983).
 CC -!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
 D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 THE PENTOSE SUBSTRATE IN THE PHOTORESPARATION PROCESS. BOTH
 REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 ACTIVE SITE.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 -
 CC phospho-D-glycerate.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) =
 CC 3-phospho-D-glycerate + 2-phosphoglycolate.
 CC -!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.

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CC DR EMBL: J01257; AAA33686_1; -;
 CC DR EMBL: X00806; CAAX5390_1; -;
 CC DR EMBL: X04334; CAA27865_1; -;
 CC DR PIR: A01088; RKPM55;
 CC DR InterPro: IPR000834; RUBISCO_small.
 CC DR Pfam: PF00101; RUBISCO_small_1.
 CC DR PRINTS: PRO0152; RUBISCO_SMALL;
 CC DR PRODOM: PD00290; RUBISCO_small_1.
 CC KW Photosynthesis; Carbon dioxide fixation; Photorepiration;
 CC KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide;
 CC KW Multigene family.
 CC FT CHAIN 1 57 CHLOROPLAST (BY SIMILARITY). TRANSIT PEPTIDE
 CC FT CHAIN 58 180 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
 CC FT CHAIN 3C 180 AA: 212653E76E55205C CRC64;

Query Match 86.2%; Score 25; DB 1; Length 180;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAPPF 6
 Db 22 AAAPPF 27

RESULT 35
 RSS3_PEA
 ID RSS3_PEA STANDARD; PRN; 180 AA.

AC P07889; P12467;
 DR 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribulose bisphosphate carboxylase small chain 3A, chloroplast
 precursor (EC 4.1.1.39) (RUBISCO small subunit 3A).
 GN RBCS-3A.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
 OX NCBI_TaxID=3868;

[1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Progress No. 9;
 RA Flurb R., Moses P., Morelli G., Coruzzi G., Chua N.-H.;
 RT "Expression dynamics of the pea rbcS multigene family and organ
 distribution of the transcripts.";
 RL EMBO J. 5:2063-2071(1986).
 RN [2]
 SEQUENCE FROM N.A.
 RP SEQUENCE OF 154-180 FROM N.A.
 CC MEDLINE=8715615; PubMed=3827863;
 RA Anderson S., Smith S.M.;
 RT "Synthesis of the small subunit of ribulose-bisphosphate carboxylase
 from genes cloned into Plasmids containing the SP6 promoter.";
 RL Biochem. J. 240:709-715(1986).
 RN [3]
 SEQUENCE OF 154-180 FROM N.A.
 CC MEDLINE=88296081; PubMed=3042319;
 RX Hunt A.G.;
 RA "Identification and characterization of cryptic polyadenylation sites
 in the 3' region of a pea ribulose-1,5-bisphosphate carboxylase small
 subunit gene.";
 RL DNA 7:329-336(1988).
 CC -!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
 D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 THE PENTOSE SUBSTRATE IN THE PHOTORESPARATION PROCESS. BOTH
 REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 ACTIVE SITE.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 2 -
 CC phospho-D-glycerate.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 -
 CC 3-phospho-D-glycerate + 2-phosphoglycolate.
 CC -!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.

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CC DR EMBL: X04333; CAAX27864_1; -;
 CC DR EMBL: M21375; AAA33683_2; -;
 CC DR PIR: A27874; RKPM33;
 CC DR InterPro: IPR000894; RUBISCO_small.
 CC DR PRINTS: PRO0152; RUBISCO_small_1.
 CC DR PRODOM: PD00290; RUBISCO_small_1.
 CC KW Photosynthesis; Carbon dioxide fixation; Photorepiration;
 CC KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide;
 CC KW Multigene family.
 CC FT CHAIN 1 57 CHLOROPLAST (BY SIMILARITY). TRANSIT PEPTIDE
 CC FT CHAIN 58 180 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
 CC FT CHAIN 3A 180 AA: 33DADS3A45C0CFE7 CRC64;

Query Match 86.2%; Score 25; DB 1; Length 180;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches	5;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;	Db
QY	1	AAAPF	6							Db
										22 AAAPF 27
RESULT	36	US19_HCMVA	STANDARD;	PRT;	240 AA.					QY
ID	US19_HCMVA									2 AAAPF 6
AC	P09725;									
DT	01-MAR-1989 (Rel. 10, Created)									
DT	01-MAR-1989 (Rel. 10, last sequence update)									
DT	01-JUN-1994 (Rel. 29, Last annotation update)									
DE	transmembrane protein HWT24.									
GN	US19									
OS	Human cytomegalovirus (strain AD169), and									
OC	viruses; dsDNA viruses; no RNA stage; Herpesviridae;									
OC	Betaherpesvirinae; Cytomegalovirus.									
OX	NCBI_TAXID=10360, 10363;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=AD169;									
RX	MEDLINE=7169717; PubMed=3031311;									
RA	Weston K., Barrell B.G.;									
RT	"Sequence of the short unique region, short repeats, and part of the long repeats of human Cytomegalovirus.";									
RL	J. Mol. Biol. 192:177-208(1986).									
RN	[2]									
RP	COMPLETE GENOME.									
RC	STRAIN=AD169;									
RX	MEDLINE=90269039; PubMed=2161319;									
RA	Chee M.S., Bankoff A.T., Beck S., Bohni R., Brown C.M., Cerny R.,									
RA	Horschell T., Hutchinson C.A., Ilti, Konzoides T., Martignetti J.A.,									
RA	Predelli E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;									
RT	"Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169."									
RL	Curr. Top. Microbiol. Immunol. 154:125-169(1990).									
RN	[3]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=Towne;									
RX	MEDLINE=93188154; PubMed=8383226;									
RA	Guo Y.-W., Huang E.S.;									
RA	Characterization of a structurally tricistrionic gene of human cytomegalovirus composed of U(s)18, U(s)19, and U(s)20."									
RL	J. Virol. 67:2043-2054(1993).									
CC	- - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS UP TO 7 POTENTIAL TRANSMEMBRANE DOMAINS (PROBABLE).									
CC	- - DEVELOPMENTAL STAGE: EXPRESSED 34 HOURS POST-INFECTION.									
CC	- - SIMILARITY: BELONGS TO THE US12 FAMILY.									
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).									
CC	-----									
DR	EMBL: M07602; AAA61232.1. - .									
DR	PIR: B28852; B28852.									
DR	HSSP: P00763; IDPO.									
DR	MERPS: S01_258; - .									
DR	Genew: HGNC:9483; PRSS2.									
DR	MM: 601564; - .									
DR	InferPro: IER0_01314; Chymotrypsin.									
DR	InterPro: IPR0_0254; Serine-protease TRY.									
DR	InterPro: IPR0_0254; Serine-protease TRY.									
DR	Pfam: PF00089; trypsin; 1.									
DR	PRINTS: PR0722; CHYMOTRYPSIN.									
DR	SMARTP: SM00020; TRY_SPC; 1.									
DR	PROSITE: PS0020; TRYPN_DOM; 1.									
DR	PROSITE: PS00134; TRYPN_HIS; 1.									
DR	PROSITE: PS00135; TRYPN_SER; 1.									
KW	HYDROLASE; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family.									
FT	SIGNAL	1	15							
FT	PROTEIN	16	23							
FT	CHAIN	24	247							
FT	ACT_SITE	63	63							
FT	ACT_SITE	107	107							
FT	ACT_SITE	200	200							
FT	ACT_SITE	30	160							
FT	DISELFID	48	64							
FT	DISULFID	171	185							
FT	DISULFID	196	220							
SQ	SEQUENCE	247	AA;	2648	MM;	825041EBBED5DB	CRC64;			
Query Match	86.2%	Score 25;	DB 1;	Length 240;						
Best Local Similarity	100.0%	Pred. No.	1.8e+02;							
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	

Query Match		Score 86.2%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Best Local Similarity	83.3%;	Pred. No. 1.9e+02;	Mismatches 1; Indels 0; Gaps 0;
Matches	5;	Conservative	0;
2Y	1 AAAAPF 6		
Db	13 AVAAPF 18		
RESULT 38			
ID	IDNO_ECOLI	STANDARD;	PRT; 254 AA.
AC	P39345;		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Glucosidase 5-dehydrogenase (EC 1.1.1.69) (5-keto-D-gluconate 5-reductase)		
ID	IDNO_B4266.		
OC	Escherichia coli.		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
NCBI_TaxID	562;		
RN	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	STRAIN=K12 / MG1655;		
RA	MEDLINE=95334362; PubMed=610040;		
RA	Burland V.D., Punkett G. III, Sofia H.J., Daniels D.L., Blattner F.R.; "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes"; Nucleic Acids Res. 23:2105-2119(1995).		
RA	[1]		
RA	FUNCTION.		
RA	MLBLINE=98324983; PubMed=9658018;		
RA	Bausch C., Peekhaus N., Ulz C., Blais T., Murray E., Lowary T., Conway T.; "Sequence analysis of the GntII (subsidiary) system for gluconate metabolism reveals a novel pathway for L-idonic acid catabolism in Escherichia coli"; J. Bacteriol. 180:3704-3710(1998).		
RA	[2]		
RA	-I- FUNCTION: CATALYZES A REVERSIBLE REDUCTION OF 5-KETOGLUTAMATE TO FORM D-GLUCONATE, DEPENDENT ON NADP, ALMOST INACTIVE WITH NAD.		
CC	-I- CATALYTIC ACTIVITY: D-gluconate + NAD(P) ⁽⁺⁾ = 5-dehydro-D-gluconate + NAD(P)H.		
CC	-I- PATHWAY: PART OF THE GLUCONATE UTILIZATION SYSTEM GNT-II.		
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).		
CC	-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	-----		
CC	DR: AE000903; AAB85885; 1; -.		
CC	DR: IPRO004485; CbIB.		
CC	DR: PF03186; Cobb,CbIB; 1.		
CC	DR: TIGRFAMS; TIGR00380; cbIB; 1.		
CC	KW: Cobalamin biosynthesis; Transmembrane; Complete proteome.		
CC	FT: TRANSMEM_46 66 POTENTIAL.		
CC	FT: TRANSMEM_72 92 POTENTIAL.		
CC	FT: TRANSMEM_141 161 POTENTIAL.		
CC	FT: TRANSMEM_193 213 POTENTIAL.		
CC	FT: TRANSMEM_277 297 POTENTIAL.		
CC	SEQUENCE 297 AA; 32175 MW; A37DA300FBAA4CAB CRC64;		
RESULT 39			
QY	1 AAAAPF 6		
Db	60 AVAAPF 65		
RESULT 40			
PEPL_GADMO	STANDARD:	PRT: 324 AA.	
ID	PEPL_GADMO		
PRINTER	InterPro; IPR002198; ADH_short.		
PRINTER	pfam; PF00106; adh_short; 1.		
PRINTER	PRINTS; PR00080; SDRFAMILY.		
PRINTER	PRO0061; ADH_SHORT; 1.		
PRINTER	Oxidoreductase; Gluconate utilization; NADP; Complete proteome.		
ACT_SITE	NP_BIND 13 37 NADP (BY SIMILARITY).		
SEQUENCE	ACT_SITE 158 158 BY SIMILARITY.		
WT	ACT_SITE 254 AA; 27563 MW; C5AA4A044CEC1E6E CRC64;		
WT	Query Match 86.2%; Score 25; DB 1; Length 297; Best Local Similarity 83.3%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;		
WT	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 AAAAPF 6		
Db	54 AVAPP 59		

AC P56272;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DB Pepsin LIB (EC 3.4.23.-)
 OS *Gadus morhua* (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; *Gadus*.
 OX NCBL_TaxID=8049;
 RN [1]
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY.
 RC TISSUE=Stomach;
 RA Karlsen S., Rough E., Olsen R.L.;
 RP "Structure and proposed amino-acid sequence of a pepsin from Atlantic
 cod (*Gadus morhua*).";
 RL Acta Crystallogr. D 54:32-46(1998).
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY AL.
 DR PDB: 1AMS; 2A-DEC-97.
 DR InterPro: IPR001461; AsproteaseAL.
 DR InterPro: IPR001969; Asprotease_site.
 DR Pfam: PF0025; asp; 1.
 DR PRINTS: PR00792; PEPSIN.
 DR PROSITE: PS00141; PEPSIN.
 KW Hydrolase; Aspartyl protease; Digestion; 3D-structure.
 FT ACT_SITE 32 32 BY SIMILARITY.
 FT ACT_SITE 214 214 BY SIMILARITY.
 FT DISULFID 45 50 BY SIMILARITY.
 FT DISULFID 206 209 BY SIMILARITY.
 FT DISULFID 247 280 BY SIMILARITY.
 SQ SEQUENCE 324 AA; 34014 MW; EEA6097B6941DD7 CRC64;
 Query Match 86.2%; Score 25; DB 1; Length 324;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AAPF 6
 |||||
 Db 113 AAPF 117

Search completed: December 6, 2002, 13:28:35
 Job time : 9.3333 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 13:25:09 ; Search time 29.3333 Seconds
(without alignments)
42.146 Million cell updates/sec

title: US-10-033-526-4
perfect-score: 29

Sequence: 1 AAAAPP 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1 SPREMBL 21:::
1: sp-a-cheta:::
2: sp-bacteria:::
3: sp-fungi:::
4: sp-human:::
5: sp-invertebrate:::
6: sp-mammal:::
7: sp-mhc:::
8: sp-organelle:::
9: sp-phage:::
10: sp-plant:::
11: sp-rodent:::
12: sp-virus:::
13: sp-vertebrate:::
14: sp-unclassified:::
15: sp-rvirus:::
16: sp-bacteriap:::
17: sp-archaea:::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	128	4 Q96MZ3	homo sapien
2	29	100.0	130	5 Q21259	caenorhabditis elegans
3	29	100.0	235	2 Q936W6	streptomyces
4	29	100.0	271	16 Q9RCZ9	streptomyces
5	29	100.0	318	10 Q9LHUB	oryza sativa
6	29	100.0	348	10 Q9PD31	rice
7	29	100.0	362	10 Q9SSG5	oryza sativa
8	29	100.0	369	16 Q92XG9	rhizobium m
9	29	100.0	425	3 Q87GV7	tolyphocladiaceae
10	29	100.0	482	4 Q8TAI1	homo sapien
11	29	100.0	554	16 Q9RS70	deniooccus
12	29	100.0	588	10 Q9SDCO	osdc
13	29	100.0	606	10 Q94DZ6	oryza sativa
14	29	100.0	722	12 Q8Q1N0	manestra co
15	29	100.0	723	5 Q96436	drosophila
16	29	100.0	723	5 Q9W5F0	drosophila

RESULT	1	SEQUENCE FROM N.A.
ID	Q96MZ3	PRELIMINARY; PRT; 128 AA.
AC	Q96MZ3;	
DT	01-DEC-2001	(TREMBUREL, 19, Created)
DT	01-DEC-2001	(TREMBUREL, 19, Last sequence update)
DE	CDDA FLJ31668	file, clone NT2R12004916.
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Ninomuya K., Wagasuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Onura Y., Abe K., Kamihira K., Katsuta N., Saito H., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Higashimura T., Saito K., Mishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Seiine M., Kikuchi H., Murakawa K., Kaneko K., Takashashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Kaneko K., Takashashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahiro Y., Nagai K., Isogai T., RT "NEPD human cDNA sequencing Project"; Submitted Oct 2001 to the EMBL/Genbank/DBJ databases.	
RL	DR EMBL: AK056230; BAB71124.1; -;	
SQ	SEQUENCE 128 AA; 14386 MW; 7C9945A417FF0044 CRC64;	
	Query Match Similarity 100.0%; Score 29; DB 4; Length 128; Best Local Similarity 100.0%; Pkt. No. 98;保守性 6; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AAAAPP 6	
	Db 14 AAAAPP 19	
RESULT	2	
ID	Q21259	PRELIMINARY; PRT; 130 AA.

AC Q21259; DR EMBL: U13043; AAL04403.1; ~.
DT 01-NOV-1996 (TREMBLrel. 01, Created) DR InterPro; IPR002751; CbIM.
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) DR Pfam; PF01891; CbIM; 1.
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DR Prodrom; P00533; CbIM; 1.
DE Hypothetical 14.4 kDa protein. DR TIGRFAMS; TIGR00123; CbIM; 1.
GN K06B9_3 DR SEQUENCE FROM N.A. DR SEQUENCE 235 AA; 24534 MW;
OS Caenorhabditis elegans. OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderrinae; Caenorhabditis. NCBI_TAXID=6239;
RN [1] RT SEQUENCE FROM N.A.
RN STRAIN=BRISTOL N2; RT
RN None; RT
RT "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.", Science 282:2012-2018(1998).
RN [2] RL
RN SEQUENCE FROM N.A. RP
RN STRAIN=BRISTOL N2; RC
RN Bradshaw H., Miller N.; AC 09RC29
RN The sequence of *C. elegans* cosmid K06B9.". DR 09RC29;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases. DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
RN [3] DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE Hypothetical protein SC00912.
RN GN SC00912 OR SCLM_45.
RN OS Streptomyces coelicolor. OC
RN Bacteria; Firmicutes; Actinobacteridae; Streptomyctaceae; Streptomyces. OC
RN NCBI_TAXID=1902; OC
RN RN
RN SEQUENCE FROM N.A. RP
RN STRAIN=A3(2) / M145; RC
RN Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., RA Cronin A., Fraser A., Goble A., Hidalgo J., Horrisby T., Howarth S., RA Huang C.H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., RA Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., RA Warren T., Wetzorrek A., Woodward J., Barrell B.G., Parkhill J., RA Hopwood D.A., RT
RN "Complete genome sequence of the model actinomycete Streptomyces RT
RN coelicolor A3(2)". DR
RN Nature 417:141-147(2002). DR
RN EMBL; ALI33422; CAB62703.1; -. DR
RN HYPOTHETICAL PROTEIN. KW
RN SEQUENCE 271 AA; 28419 MW; 068FB213A955F84D CRC64; SQ
RN Query Match 100.0%; Score 29; DB 16; Length 271; DR
RN Best Local Similarity 100.0%; Pred. No. 2e-02; 0; Mismatches 0; DR
RN Matches 6; Conservative 0; Indels 0; Gaps 0; DR
RN Qy 1 AAAAPF 6 DR
RN Db 2 AAAAPF 7 DR
RN
RN RESULT 3 DR
RN 935BW6 ID PRELIMINARY; PRT; 235 AA.
RN AC 935BW6; DR
RN DT 01-DEC-2001 (TREMBLrel. 19, Created) DR
RN 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DR
RN 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DR
RN DE Cobalt transport protein CbtM. DR
RN CBTM; DR
RN OS Propionibacterium freudenreichii shermanii. DR
RN Bacteria; Firmicutes; Actinobacteria; Propionibacteriidae; DR
RN OC Actinomycetales; Propionibacterineae; Propionibacteriaceae; DR
RN OC Propionibacterium. DR
RN NCBI_TAXID=1752; DR
RN [1] RT
RN SEQUENCE FROM N.A. RP
RN MEDLINE=95109734; Published=7883713; DR
RN Sattler I., Roessner C.A., Stolowich N.J., Hardin S.H., DR
RN Harris-Halier L.W., Yokubaitis N.T., Murooka Y., Hashimoto Y., DR
RN Scott A.I.; DR
RN "Cloning, sequencing, and expression of the uroporphyrinogen III methyltransferase coba gene of *Propionibacterium freudenreichii* (shermanii)". DR
RN J. Bacteriol. 177:1564-1569(1995). DR
RN [2] DR
RN SEQUENCE FROM N.A. RP
RN Roessner C.A., Huang K., Scott A.I.; DR
RN "Cobalamin biosynthesis in *Propionibacterium freudenreichii* (shermanii): Isolation and characterization of 16 B12 genes.", DR
RN Submitted (APR-2001) to the EMBL/GenBank/DBJ databases. DR
RN
RN RESULT 5 DR
RN 09LH08 ID PRELIMINARY; PRT; 318 AA.
RN AC 09LH08; DR
RN DT 01-OCT-2000 (TREMBLrel. 15, Created) DR
RN 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DR
RN 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DR
RN HYPOTHETICAL PROTEIN. DR
RN OS Oryza sativa (Rice). OC
RN Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC
RN Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; OC
RN Ehrhartoideae; Oryzeae; Oryza. NCBI_TAXID=4530;
RN [1] RT
RN SEQUENCE FROM N.A. RP
RN STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.; genomic DNA, chromosome 1, PAC
 RT "Oryza sativa nipponbare(GA3)"
 RT clone:PO43E05; "
 RT Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AP00180; BAAG9537.1;
 DR Hypothetical protein; DR
 SQ SEQUENCE 318 AA; 34343 MW; ADIBF79B08225B41 CRC64;
 Query Match 100.0%; Score 29; DB 10; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPP 6
 Db 221 AAAAPP 226

RESULT 6
 O9TD31
 ID O9TD31 PRELIMINARY; PRT; 348 AA.
 AC O9TD31; 01-MAY-2000 (TREMBREL, 13, Created)
 DT 01-MAY-2000 (TREMBREL, 13, Last sequence update)
 DE NADH dehydrogenase subunit II.
 OS Rivulus punctatus.
 OC Mitochondrion.
 OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthopterygii; Percormorpha; Atheriomorpha;
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Rivulus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hrbek T., Larson A.
 RT "The evolution of diapause in the killifish family Rivulidae
 (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
 biogeographic perspective";
 RL Evolution 53(1):200-221(1999).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 DR EMBL: AF002389; RAF022976.1; -.
 DR InterPro: IPR011750; Oxidored_Q1_91.
 DR Pfam: PF00361; oxidored_Q1_1.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 SQ SEQUENCE 348 AA; 38539 MW; 7B6A086DC81A2F16 CRC64;
 Query Match 100.0%; Score 29; DB 8; Length 348;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPP 6
 Db 278 AAAAPP 283

RESULT 7
 O9SDG5
 ID O9SDG5 PRELIMINARY; PRT; 362 AA.
 AC O9SDG5; 01-MAY-2000 (TREMBREL, 13, Created)
 DT 01-MAY-2000 (TREMBREL, 13, Last sequence update)
 DE ESTs C19133 (EL0008).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cv. NIPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.; genomic DNA, chromosome 1, PAC
 RT "Oryza sativa nipponbare(GA3)" genomic DNA, chromosome 1, PAC

RESULT 8
 O92XG9
 ID O92XG9 PRELIMINARY; PRT; 389 AA.
 AC O92XG9; 01-DEC-2001 (TREMBREL, 19, Created)
 DT 01-DEC-2001 (TREMBREL, 19, Last sequence update)
 DR 01-MAR-2002 (TREMBREL, 20, Last annotation update)
 DE Putative transmembrane transport protein.
 RN RA1285 OR SMA377.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid PSYMA (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OC NCBI_TaxID=362;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21395059; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barlow-Hubler F., Bowler L., Capela D., Gaibert F., Gonzy J.,
 RA Gurjal M., Hong A., Hulzar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti PSYMA megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL: AE007314; AAC6543.1; -.
 DR Hypothetical protein; complete proteome.
 DR B4E899BaF465BF3 CRC64;
 SQ SEQUENCE 389 AA; 40252 MW; B4E899BaF465BF3 CRC64;
 Query Match 100.0%; Score 29; DB 16; Length 389;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPP 6
 Db 354 AAAAPP 359

RESULT 9
 O9PGV7
 ID O9PGV7 PRELIMINARY; PRT; 425 AA.
 AC O9PGV7; 01-JUN-2002 (TREMBREL, 21, Created)
 DT 01-JUN-2002 (TREMBREL, 21, Last sequence update)
 DE O1-JUN-2002 (TREMBREL, 21, Last annotation update)
 DR Serine protease protein.
 OS Tolypocladium inflatum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
 OC Tolypocladiaceae.
 OX NCBI_TaxID=29910;

RP SEQUENCE FROM N.A.
 RA Pluczenyczak G., Marciniaek-Rusek A., Pass-Bzegielewska L.;
 RT "the serine protease gene of cyclosporin-producing fungi Beauveria
 nivea.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF467982; AU175578.1; -.
 KW Protease.
 SQ Query Match 100.0%; Score 29; DB 3; Length 425;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPF 6
 Db 315 AAAAPF 320

RESULT 10
 Q8TAT1 PRELIMINARY; PRT; 482 AA.
 ID Q8TAT1
 AC Q8TAT1; 2002 (TREMBUREL. 21, Created)
 DT 01-JUN-2002 (TREMBUREL. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBUREL. 21, Last annotation update)
 DE Basic helix-loop-helix domain containing, class B, 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC025988; AAC025988.1; -.
 SEQUENCE 482 AA; 50525 MW; 23EBDA20C6BACE03 CRC64;

Query Match 100.0%; Score 29; DB 4; Length 482;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPF 6
 Db 380 AAAAPF 385

RESULT 11
 Q9RS70 PRELIMINARY; PRT; 554 AA.
 ID Q9RS70;
 AC Q9RS70; 2000 (TREMBUREL. 13, Created)
 DT 01-MAY-2000 (TREMBUREL. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBUREL. 16, Last annotation update)
 DE Erythromycin esterase, putative.
 GN DR2257.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OX NCBI_TaxID=1299;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=RL;
 DR MEDLINE=20036895; PubMed=10567266;
 RA White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
 RA Noffat M., Olin H., Jiang L., Pamphilis W., Crosby M., Shen M.,
 RA Yamatewan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Fraser C.M., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 radiodurans RL.",

RESULT 12
 Q9SDC0 PRELIMINARY; PRT; 588 AA.
 ID Q9SDC0
 AC Q9SDC0;
 DT 01-MAY-2000 (TREMBUREL. 13, Created)
 DT 01-MAY-2000 (TREMBUREL. 13, Last sequence update)
 DE Similar to ARABIDOPSIS THALIANA chromosome II BAC F7D8 genomic
 DE sequence.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=CV_NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0567A10.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP000969; BAB88547.1; -.
 DR EMBL: AF001073; BAB89568.1; -.
 DR InterPro: IPR002965; P_RICH_EXTENSIN.
 DR PRINTS: PRO1217; PRICHEXTEN.
 SEQUENCE 588 AA; 62565 MW; 0B023FAC2ABDE0F CRC64;

Query Match 100.0%; Score 29; DB 10; Length 588;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPF 6
 Db 244 AAAAPF 249

RESULT 13
 Q9ADZ6 PRELIMINARY; PRT; 696 AA.
 ID Q9ADZ6
 AC Q9ADZ6;
 DT 01-DEC-2001 (TREMBUREL. 19, Created)
 DT 01-DEC-2001 (TREMBUREL. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBUREL. 21, Last annotation update)
 DE Putative receptor protein kinase-like protein.
 OX P0010B10.11.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]

RP	SEQUENCE FROM N.A.	QY	1	AAAPF	6	
RC	STRAIN=Cv; NIPPONBARE;		11111			
RA	Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1. PAC	Db	563	AAAPF	568	
RT	clone:Ps010B10;"					
RL	Submitted (Feb-2001) to the EMBL/GenBank/DDBJ databases.					
DR	EMBL: AP003224; BAB63567_1; -;					
DR	InterPro: IPR000719; Euk_pk kinase.					
DR	InterPro: IPR000985; Lectin_legB.					
DR	InterPro: IPR002290; Ser-thr_pk kinase.					
DR	Pfam: PF00138; Lectin_legB_1.					
DR	Pfam: PF00139; Lectin_legB_1.					
DR	PRINTS: PRO0559; DUF24ANTIGEN.					
DR	PROSITE: PS00001; Euk_pk kinase.					
DR	ProDom: PD00711; Lectin_legB_1.					
DR	PROSITE: PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.					
DR	PROSITE: PS00307; PROTEIN_KINASE_ATP; UNKNOWN_1.					
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; UNKNOWN_1.					
KW	ATP-binding; Kinase; Receptor; Transferase.					
SQ	SEQUENCE - 696 AA; /4562 MW; 95BAE0C16B5FCCC CRC64;					
Query Match	Best local similarity 100.0%; Score 29; DB 10; Length 696;					
Matches	6; conservative 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;					
QY	1 AAAAPF 6					
Db	7 AAAAPF 12					
RESULT	14					
QBOLNO	QBOLNO PRELIMINARY; PRT; 722 AA.					
ID	QBOLNO					
AC	QBOLNO; 08QBOLNO;					
DT	01-JUN-2002 ('TREMBREL_21, Created)					
DT	01-JUN-2002 ('TREMBREL_21, Last sequence update)					
DT	01-JUN-2002 ('TREMBREL_21, Last annotation update)					
DE	Hoar.					
OS	Mamestrina configurata nucleopolyhedrovirus.					
OC	Viruses; dsDNA viruses, no RNA stage; Baculoviridae;					
OC	Nucleopolyhedrovirus.					
OX	NCBI_TaxID=191492;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RA	MEDLINE=97163493; PubMed=9010313;					
RA	Li S., Erlandson M., Moody D., Gillett C.;"A physical map of the Mamestra configurata nucleopolyhedrovirus genome and sequence analysis of the polyhedrin gene.";					
RT	"A physical map of the Mamestra configurata nucleopolyhedrovirus genome and sequence analysis of the polyhedrin gene.";					
RL	J. Gen. Virol. 78:265-271(1997).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11884635; Pubmed=11884635;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[5]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[6]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[7]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[8]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[9]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[10]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[11]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[12]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[13]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[14]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[15]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[16]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[17]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[18]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[19]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[20]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[21]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[22]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[23]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[24]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[25]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[26]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					
RT	"Sequence and organization of the Mamestra configurata nucleopolyhedrovirus genome";					
RL	Virology 294:106-121(2002).					
RN	[27]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=90/2;					
RX	MEDLINE=11886270; Pubmed=11886270;					
RA	Li O., Doni C., Li L., Willis L.G., Theilmann D.A., Erlandson M. ;					

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfnanck C., Baldwin D., Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burlis K.C., Busam D.A., Bouck J., Brokstein P., Brottier P., Buttler H., Cadieu A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dosden K., Douc L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Flischmann W., Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.J., Houck J., Hostin D., Houston K.A., Howland T.J., Ibeagwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasikro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy L., Muzy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J.H., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Tang J., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of *Drosophila melanogaster*," Science 287:2185-2195(2000). -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC DR PRINTS: PR00024; HOMEBOX.

DR PROSITE: PS00071; HOMEBOX_1; PS00071; HOMEBOX_2; PROSITE; PS50027; HOMEBOX_2; DR HSSP: P22808; IYND DR PROSITE; PS00027; HOMEBOX_1; DR PROSITE; PS50071; HOMEBOX_2; DR PFBn003986; vnd. DR InterPro; IPR001336; Homeobox. DR Pfam; PF00045; homeobox; 1. DR PRINTS: PR00024; HOMEBOX.

DR PRODOM: PD000010; Homeobox; 1. DR SMART: SM00349; HOX; 1. DR EMBL: AE045521; 1. DR HSSP: P22808; IYND DR PROSITE; PS00027; HOMEBOX_1; 1. DR PROSITE; PS50071; HOMEBOX_2; 1. DR DNA-binding; Homeobox; Nuclear protein. KW SEQUENCE 723 AA; 811F20B03A93C95E CRC64;

Query Match 100.0%; Score 29; DB 5; Length 723; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAAAPF 6 Db 150 AAAAPF 155

RESULT 17

Q9B43 ID Q9B43 PRELIMINARY; PRT; 723 AA.

AC Q9B43; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update) DE EG-118B3.1 protein. GN VND OR EG:118B3.1 OR CG6172. OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; OC Ephydriidae; Drosophilidae; Drosophila. NCBI_TaxID=7227; DR FIBase; FBgn003986; vnd.

RESULT 18

Q95F2 ID Q95F2 PRELIMINARY; PRT; 735 AA.

AC Q95F2; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update) DE LDI5404P. RN CGI2527.

OS Drosophila melanogaster (Fruit fly).

RC SEQUENCE FROM N.A.

RA STRAIN=BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., RA Chame M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., RA "Nunoo J.", Paclef J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celiker S., RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases. DR EMBL; AV059450; AAU13366; 1. DR FIBase; FBgn003977; CG12527. DR SEQUENCE 735 AA; 74871 MW; 8BBB8919360B7556 CRC64;

Query Match 100.0%; Score 29; DB 5; Length 735; Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAAAPF 6 Db 294 AAAAPF 299

RESULT 19

Q9VWNL ID Q9VWNL PRELIMINARY; PRT; 747 AA.

AC Q9VWNL; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update) DE CG12527 protein.

RA de Pablos B., Madueno E., Modolell J.;

GN CG1257.	OX OS
OS Drosophila melanogaster (Fruit fly).	
OC Euryptera; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC Drosophilidae; Drosophila.	
OX NCBI_TAXID=7227;	
RP [1]	
RN SEQUENCE FROM N.A.	
RN STRAIN=BERKELEY;	
RX MEDLINE=2016606; PubMed=10731132;	
RA Adams M.D., Gelnicker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA Amantadines P.G., Schaefer S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,	
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,	
RA Abrial J.-F., Agbayani A., An H.-J., Andrews P., Franko C., Baldwin D.,	
RA Balliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	
RA Borikova D., Botchan M.R., Bouck J., Broksstein P., Brotrier P.,	
RA Burttis K.C., Busam D.A., Butler R., Cadieu E., Center A., Chandra I.,	
RA Cherry J.M., Cawley S., Danilek P., Davenport T.B., Davies P.,	
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Ferreria S., Fleischmann W.,	
RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreria S., Gelbart K.,	
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart K., Glasser K.,	
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchuk K.A.,	
RA Kimmel B.E., Kodira C.D., Kraft Z., Kravitz S., Kulp D., Lai Z.,	
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang J., Lin X.,	
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskaleff A.,	
RA Mount S.M., Moy M., Murphy L., Murphy D.M., Nelson D.L.,	
RA Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,	
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA Shue B.C., Sinden-Klamo T., Simpson M., Skupsik M.P., Smith T.,	
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,	
RA Svistak R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,	
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA Ye J., Yeh J.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,	
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	
RT "The genome sequence of Drosophila melanogaster.";	
RL Science 207:2185-2195(2000).	
DR EMBL: AE003510; AAC489071..	
DR FBgn0030977; CG1227.	
SQ SPQUENCE 747 AA; 76047 MW;	
Query Match 100.0%; Score 29; DB 5; Length 747;	
Best Local Similarity 100.0%; Pred. No. 5.1e-02;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 AAAFP 6	
DB 294 AAAFP 299	
RESULT 20	
Q9WL0 PRELIMINARY; PRN: 815 AA.	
ID Q9WL0	
AC Q9WL0;	
DT 01-OCT-2000 (TREMBLrel. 15, Created)	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Similar to Arabidopsis thaliana chromosome 1 BAC F19G10.	
OS Oryza sativa (Rice).	
OC Eukaryota; Viriciliophyta; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatozoa; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC Ehrhartioidae; Oryzae; Oryza.	
OX NCBI_TAXID=4530;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=CV; NIPPONBARE;	
RA Saeki T., Matsunoto T., Yamamoto K.;	
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC	
RT clone:PO485D09";	
RT Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	
RL EMBL: AP001859; BAA9477; 1; -	
DR InterPro: IPR001613; Znf_modRING.	
DR SMART: SM00504; Ubox; 1;	
SQ SEQUENCE 815 AA; 85892 MW; E6F2ADBC8E869BE CRC64;	
Query Match 100.0%; Score 29; DB 10; Length 815;	
Best Local Similarity 100.0%; Pred. No. 5.5e+02;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 AAAFP 6	
DB 517 AAAFP 522	
RESULT 21	
Q86643 PRELIMINARY; PRN: 821 AA.	
ID Q86643	
AC 086643;	
DT 01-NOV-1996 (TREMBLrel. 01, Created)	
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)	
DE Glycoprotein H homolog.	
OS Feline herpesvirus (Felid herpesvirus 1).	
OC Viruses; dsDNA viruses; no RNA stage; Herpesviridae;	
OC Alphaherpesvirinae; Varicellovirus.	
OX NCBI_TAXID=10334;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=9335636; PubMed=8394688;	
RA Mikan T.; Kamaguchi Y., Kamiya N., Ono M., Tohya Y., Kai C.,	
RA Mada K.; Kamaguchi Y., Kamiya N., Ono M., Tohya Y., Kai C.,	
RT Identification and nucleotide sequence of a gene in feline	
RT herpesvirus type 1 homologous to the herpes simplex virus gene	
RT encoding the glycoprotein H.;	
RT Arch. Virol. 132:183-191(1993).	
DR EMBL: S64566; AAB7840; 1; -	
DR InterPro: IPR00493; Herpes_glycopH_1;	
DR Pfam: PF04849; Herpes_glycopH_1;	
SQ SEQUENCE 821 AA; 92511 MW; 1F14D4CC944044F7 CRC64;	
Query Match 100.0%; Score 29; DB 12; Length 821;	
Best Local Similarity 100.0%; Pred. No. 5.5e+02;	
Matches 6; conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 AAAFP 6	
DB 106 AAAFP 111	
RESULT 22	
Q9NDT9 PRELIMINARY; PRN: 860 AA.	
ID Q9NDT9	
AC Q9NDT9;	
DT 01-OCT-2000 (TREMBLrel. 15, Created)	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE BGS-5.	
GN BGS-5.	
OS Balanus amphitrite (Barnacle).	
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Cirripedia;	
OC Thoracica; Sessilia; Balanomorpha; Balanidae; Balanidae.	
OC NCBI_TAXID=32267;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=20314484; PubMed=10854786;	

RA Okazaki Y., Shizuri Y.; "Structures of six cDNAs expressed specifically at cypris larvae of barnacles, *Balanus amphitrite*."; RN [1]; RT SEQUENCE FROM N.A.
 RL Gene 25:127-135(2000).
 DR EMBL; AB021880; BAA9547.1;
 SQ SEQUENCE 860 AA; 88965 MW; E5E9905823A5905A CRC64;

Query Match 100 %; Score 29; DB 5; Length 860;
 Best Local Similarity 100 %; Pred. No. 5.e-02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAAPF 6
 Db 319 AAAAPF 324

RESULT 23
 Q9U122 PRELIMINARY; PRT; 1301 AA.
 ID Q9U122; AC 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE Hypothetical 137.3 kDa protein.
 GN L4768.04.
 OS Leishmania major.
 OC Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TAXID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Bothe G., Pohl T., Ivens A.C., Lawson D., Murphy L., Quail M., Rajandream M.A., Barrell B.G.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RX MEDLINE=9814635; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:1135-145(1998).
 DR EMBL: ALI32763; CBL59861.1; -.
 DR InterPro; IPR01752; kinesin_motor.
 DR Pfam; PF00225; kinesin_1.
 DR PRINS; PR00380; KINESINHEAVY.
 DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Hypothetical protein; Microtubules;
 Motor protein
 SQ SEQUENCE 1301 AA; 137312 MW; 6822477834A0B521 CRC64;

Query Match 100.0%; Score 29; DB 5; Length 1301;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAAPF 6
 Db 325 AAAAPF 330

RESULT 24
 Q951MB PRELIMINARY; PRT; 1598 AA.
 ID Q951MB; AC 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Mjok-1 protein.
 GN MBK-1.
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pierygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Apis.

OX NCBI_TAXID=7460;
 RN [1]; RT SEQUENCE FROM N.A.
 RL Takeuchi H., Kage E., Sawata M., Kamikouchi A., Ohashi K., Ohara M., Fujiyuki T., Kunieda T., Sekinizu K., Natori S., Kubo T.;
 DR "Identification of a novel gene, Mjok-1, that encodes a putative transcription factor expressed preferentially in the large-type Kenyon cells of the honey bee brain.";
 RT Insect Mol. Biol. 10:487-494 (2001).
 RL EMBL; AB047034; BAB64310.1;
 SQ SEQUENCE 1598 AA; 174929 MW; E5475BD3ACB1EEF CRC64;

Query Match 100 %; Score 29; DB 5; Length 1598;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAAPF 6
 Db 769 AAAAPF 774

RESULT 25
 Q96L91 PRELIMINARY; PRT; 3124 AA.
 ID Q96L91; AC 096L91; DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE P400 SWI2/SNF2-related protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2140041; PubMed=11509179;
 RA Fuchs M., Gerber J., Drapkin R., Sif S., Ikura T., Oryzko V., Lane W.S., Nakatani Y., Livingston D.M.;
 RT "The P400 complex is an essential ElA transformation target.";
 RL Cell 106:297-307(2001).
 DR EMBL: AY044863; AAK97785.1; -.
 DR InterPro; IPR01160; Helicase_C.
 DR InterPro; IPR01003; MYD_DNA_binding.
 DR InterPro; IPR00330; SNF2_N.
 DR Pfam; PF0271; helicase_C; 1.
 DR Pfam; PF0176; SNF2_N; 1.
 DR PROSITE; PS50090; MYB_3; 1.
 KW ATP-binding; Helicase.
 SQ SEQUENCE 3124 AA; 340146 MW; E8F57FD6C7BD01E9 CRC64;

Query Match 100.0%; Score 29; DB 4; Length 3124;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAAAPF 6
 Db 1483 AAAAPF 1488

RESULT 26
 P94119 PRELIMINARY; PRT; 64 AA.
 ID P94119; AC P94119; DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE Small hydrophobic subunit of the terminal oxidase with unknown homologue.
 GN DE
 OX DQ5460;
 OC Acidianus ambivalens (Desulfurolobus ambivalens).
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Acidinus.
 OX NCBI_TAXID=2283;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 3772;
 RX MEDLINE=97175566; PubMed=9023221;
 RA Purchke W.G., Schmidt C.L., Petersen A., Schaefer G.;
 RT "The Terminal Quinol Oxidase of the Hyperthermophilic Archeon
Acidianus ambivalens Exhibits a Novel Subunit Structure and Gene
 Organization";
 RL J. Bacteriol. 179:1344-1353 (1997).
 DR EMBL; Y08729; CA69981.1; -.
 SQ SEQUENCE 64 AA; 7196 MW; 81985978BBB16CE9 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 64;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAPF 6
 ||||:
 Db 30 AAAPPY 35

RESULT 27
 O9CVT5 PRELIMINARY; PRT; 119 AA.
 ID O9CVT5;
 AC O9CVT5;
 DT 01-JUN-2001 (TREMBREL 17, Created)
 DT 01-JUN-2001 (TREMBREL 17, Last sequence update)
 DT 01-JUN-2001 (TREMBREL 17, Last annotation update)
 DE 1700034P1ARIK protein (Fragment).
 GN OS *Mus musculus* (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=1121751;
 RA Kawai J., Shiogawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Asburner M., Batalkov S., Casavant T.,
 RA Fleischmann R., Gasser C., King B., Kochiba H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sekai K., Okido T., Furuno M., Kono H., Bajarelli R., Barsh G.,
 RA Blake J., Borrelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher K., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
 RA Sasaki H., Satoh K., Schonbenbach C., Seya T., Shibata Y., Storch K., "F",
 RA Suzuki H., Toyo-oka H., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "functional annotation of a full-length mouse cDNA collection.";
 DR Nature 409: 665-690 (2001).
 DR EMBL; AK006608; BAB4672.1; -.
 DR MGD; MGI:1920524; 1700034P1ARIK.
 SQ SEQUENCE 119 AA; 1299 MW; 2D13BB580033671D CRC64;

Query Match 89.7%; Score 26; DB 11; Length 119;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAPF 6
 ||||:
 Db 20 ANSAPP 25

RESULT 28

Q9AX21 PRELIMINARY; PRT; 132 AA.
 ID Q9AX21;
 AC Q9AX21;
 DT 01-JUN-2001 (TREMBREL 17, Created)
 DT 01-JUN-2001 (TREMBREL 19, Last sequence update)
 DT 01-DEC-2001 (TREMBREL 19, Last annotation update)
 DE P0456A01.14 protein (P0435H01.2 protein).
 GN P0456A01.14 OR P0435H01.2.
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoides; Oryzeae; Oryza.
 OX NCBI_TaxID=45330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV; NIPPONBARE;
 RA STRAIN=CV; NIPPONBARE;
 RT Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0456A01.1";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP002899; BAB2158.1; -.
 DR AP003122; BAB2159.1; -.
 SQ SEQUENCE 132 AA; 14544 MW; 460CE1E90B39DC0A CRC64;

Query Match 89.7%; Score 26; DB 10; Length 132;
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAPF 6
 ||||:
 Db 35 AAAPPY 40

RESULT 29
 O9Y8T1 PRELIMINARY; PRT; 134 AA.
 ID O9Y8T1;
 AC O9Y8T1;
 DT 01-NOV-1999 (TREMBREL 12, Created)
 DT 01-NOV-1999 (TREMBREL 12, Last sequence update)
 DT 01-MAR-2002 (TREMBREL 20, Last annotation update)
 DE Hypothetical protein APE2552.
 GN AP2552.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceales;
 OC Desulfurococcus; Aeropyrum.
 OX NCBI_TaxID=56336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=993110339; PubMed=10382966;
 RA STRAIN=K1;
 RA JIn-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Nakamiyama M., Masuda S., Funahashi T., Tanaka T., Kudo H.,
 RA Yamazaki J., Kishita N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nomura N., Sako Y., Kiuchi H.;
 RT "complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1";
 RT DNA Res. 6:83-101(1999).
 DR EMBL; AP000064; BAB1565.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 134 AA; 13838 MW; AFDDBDE92484FB0 CRC64;

Query Match 89.7%; Score 26; DB 17; Length 134;
 Best Local Similarity 83.3%; Pred. No. 4.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

	Qy	1 AAAAPF 6 :	Query Match Best Local Similarity 89.7%; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db	121 ASAAPP 126		
RESULT 30			
Q8S7D5		PRELIMINARY; PRT; 140 AA.	
ID	Q8S7D5		
AC	Q8S7D5;		
DT	01-JUN-2002 (TREMBLrel. 21, Created) 01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	putative chloroplast chaperonin.		
GN	OSJNRA051U213.		
OS	Oryza sativa (Rice).		
OC	Bukaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophytta;		
SPERMATOPHYTA; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzaceae; Oryza.		
OX	NCBI_TaxID=4530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV_NIPPONBARE;		
RA	Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hiao J., Zissmann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblum T.V., Kalb E., Quackenbush J., Salther S.L., White O., Fasel C.M.,		
RT	"Oryza sativa chromosome 10 BAC OSJNRA051U213 genomic sequence."		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
EMBL	AC08759; AALJ7901_1;		
SQ	SEQUENCE 140 AA; 14764 MW; 409F53C675EDE430 CRC64;		
Query Match	89.7%; Score 26; DB 10; Length 140;		
Best Local Similarity 83.3%; Pred. No. 4.4e+02;			
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 AAAAPP 6 :		
Db	8 AAASPF 13		
RESULT 31			
Q9FP74		PRELIMINARY; PRT; 155 AA.	
ID	Q9FP74		
AC	Q9FP74;		
DT	01-MAR-2001 (TREMBLrel. 16, Created) 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	P0458A05_15 protein (B115F09.5 protein).		
GN	P0458A05_15 OR B115F09.5.		
OS	Oryza sativa (Rice).		
OC	Eukaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophytta;		
OC	Spermatophytta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaceae; Oryza.		
OX	NCBI_TaxID=4530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV_NIPPONBARE;		
RA	Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3)" genomic DNA, chromosome 1, PAC clone:P0458A05_15.		
RT	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV_NIPPONBARE;		
RA	Sasaki T., Matsunoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3)" genomic DNA, chromosome 1, BAC clone:BJ157F09.		
RT	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; APO02870; BAB19406_1; -;		
DR	EMBL; APO03207; BAB64080_1; -;		
SEQUENCE 155 AA; 17208 MW; A3D7ED8E327629DC CRC64;			
Qy	1 AAAAPF 6 :		
Db	77 ASAAPP 82		
RESULT 32			
Q8ZW95		PRELIMINARY; PRT; 159 AA.	
ID	Q8ZW95		
AC	Q8ZW95;		
DT	01-MAR-2002 (TREMBLrel. 20, Created) 01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DE	P.aerophilum family 322 protein part 2, authentic frameshift. PREF1905.		
GN	Pyrobaculum aerophilum.		
OC	Archaea; Crenarchaeota; Thermoproteales; Thermoproteaceae; Pyrobaculum.		
OX	NCBI_TaxID=13773;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SEQUENCE / ARCC 51768 / DSM 7523;		
RX	Pubmed=179269;		
RA	Fritz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Miller J.H.;		
RT	"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum." Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).		
RT	EMBL; AE009846; AAL63807_1; -.		
DR	InterPro; IPR003675; Abi.		
DR	Pfam; PF02517; Abi; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 159 AA; 17712 MW; 6FEIC5A0B5B844AA CRC64;		
Query Match	89.7%; Score 26; DB 17; Length 159;		
Best Local Similarity 83.3%; Pred. No. 5e+02;			
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 AAAAPP 6 :		
Db	89 AAASPF 94		
RESULT 33			
Q9LG37		PRELIMINARY; PRT; 169 AA.	
ID	Q9LG37		
AC	Q9LG37;		
DT	01-OCT-2000 (TREMBLrel. 15, Created) 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	P0512G09_19 protein (P0110E05_30 protein).		
GN	P0512G09_19 OR P0710E05_30.		
OS	Oryza sativa (Rice).		
OC	Eukaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophytta;		
OC	Spermatophytta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaceae; Oryza.		
OX	NCBI_TaxID=4530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV_NIPPONBARE;		
RA	Sasaki T., Matsunoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3)" genomic DNA, chromosome 1, PAC clone:P0458A05_15.		
RT	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV_NIPPONBARE;		
RA	Sasaki T., Matsunoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3)" genomic DNA, chromosome 1, BAC clone:P0512G09_19.		
RT	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; APO02870; BAB19406_1; -;		
DR	EMBL; APO03207; BAB64080_1; -;		
SEQUENCE 155 AA; 17208 MW; A3D7ED8E327629DC CRC64;			

RT coelicolor A3(2).";
 RL Nature 417:147-147(2002)."
 DR EMBL: AL078610; CAB4411.1; -.
 SQ SEQUENCE 206 AA; 21505 MW; .62E4F58985AC2126 CRC64;
 Query Match Best Local Similarity 89.7%; Score 26; DB 16; Length 206;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPP 6
 Db 91 AAAAPP 96

RESULT 38
 ID 042159 PRELIMINARY; PRT; 244 AA.
 AC 042159;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE TRYPSinogen BI precursor (Fragment).
 GN TRYPB1.
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 NCBI_TAXID=7757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Roach J.C.;
 RT "The Molecular Evolution of the Vertebrate Trypsinogens. ";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL: AF011901; AAB69656.1; -.
 DR HSSP: P00763; 1DPO.
 DR MEROPS: S01.128; -.
 DR InterPro: IPR001254; Serine_protease_TRY.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Serine_protease_TRY.
 DR PRINTS: PR00722; CHMOTRIPSPN.
 DR SMART: SM00020; TRYPSIN_SPC; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR KW Hydrolase; Serine protease; Signal.
 FT NON_TER 1
 FT SIGNAL <1 13 POTENTIAL.
 FT CHAIN 14 245 TRYPSIN_B2.
 SQ SEQUENCE 245 AA; 26001 MW; 9A93250BB96C93E CRC64;
 Query Match Best Local Similarity 89.7%; Score 26; DB 13; Length 245;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAAPP 6
 Db 111 AAAAPP 16

RESULT 40
 ID 042158 PRELIMINARY; PRT; 247 AA.
 AC 042158;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE TRYPSinogen a2 precursor.
 GN TRYPA2.
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 NCBI_TAXID=7757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Roach J.C.;
 RT "The Molecular Evolution of the Vertebrate Trypsinogens. ";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL: AF011898; AAB69654.1; -.
 DR HSSP: P00763; 1DPO.
 DR MEROPS: S01.128; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Serine_protease_TRY.
 DR PRINTS: PR00722; CHMOTRIPSPN.
 DR SMART: SM00020; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 247 TRYPSIN_A2.
 SQ SEQUENCE 247 AA; 26309 MW; AD73B88531970324 CRC64;
 Query Match Best Local Similarity 89.7%; Score 26; DB 13; Length 247;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AAAAPF 6
Db 1111:
13 AAAPY 18

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Job time : 30.333 secs

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